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Original Paper

Overexpression of *DWARF AND LESION FORMATION 1* (*DLE1*) causes altered activation of plant defense system in *Arabidopsis thaliana*

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Abstract A novel gain-of-function mutant showing dwarfism and bushy inflorescences was isolated from Arabidopsis activation-tagging lines. Transformed plants, in which the gene responsible for the phenotype of the mutant was overexpressed, exhibited phenotypes similar to constitutive systematic acquired resistance (SAR)-like defense responses including simulation of lesions in leaves and a highly activated *PATHOGENESIS-RELATED 1* gene. We, therefore, designated the gene as *DWARF AND LESION FORMATION 1* (*DLE1*) and showed it encodes a DUF 247 protein. Microarray and gene ontology analyses revealed that defense response genes, especially to biotic stimulus, were enriched in *DLE1* overexpressing plants. Fusion proteins of the N-terminal fragment of DLE1 and GFP were likely to be localized in the endoplasmic reticulum (ER) in tobacco BY-2 cells. DLE1 may function in the plant defense system responding to environmental stimuli including biotic stresses in the ER.

Key words: ER, HR, PR genes.

Plants have evolved a precise system to defend themselves against invading pathogens. The defense mechanisms in plant cells are categorized into basal and inducible systems, and the molecular components of these systems contain various molecules such as cell wall polymers, secondary metabolites and proteins, which can confront pathogen attack (Slusarenko et al. 2000; van Loon et al. 2006). The basal defenses are pre-existing and play an important role in resisting the infection and spread of pathogens. In contrast, inducible resistance is imperceptible or less active in uninfected plants, but is activated by pathogen infection (Carr et al. 2010). In one of these inducible systems, cultivar-specific resistance, plants perceive pathogen attack through recognition of the pathogen's avirulence (Avr) proteins by their resistance (*R*) gene products. Most *R* gene products have nucleotide-binding sites (NBSs) and leucine-rich repeats (LRRs). These NBS-LRR proteins are divided into two types, coiled-coil (CC)-NBS-LRR and toll-interleukin-1-receptor-like (TIR)-NBS-LRR depending on the amino-acid sequence at the N-terminal motif (Dangl and Jones 2001; Meyers et al. 2003). The recognition of the Avr protein subsequently induces activation of a downstream signaling pathway, which initiates biological and physiological changes, such as localized cell death, hypersensitive response (HR), and development of a broad and systemic resistance, systematic acquired resistance (SAR). HR results in programmed cell death to restrict the spread of the pathogen to other plant tissues (Hammond-Kosack and Jones 1996; Loebenstein 2009; Maule et al. 2007). SAR, following induction of the HR, is caused by the production of signaling compounds that systemically spread to plant tissues away from the infection site and increase resistance to secondary infections in more distant tissues (Durrant and Dong 2004). SAR is characterized by elevated resistance to

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Abbreviations: SAR, systematic acquired resistance; HR, hypersensitive response; ER, endoplasmic reticulum; *PR* gene, *PATHOGENESIS-RELATED* gene

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virulent pathogens and strong induction of transcription of *PATHOGENESIS-RELATED* (*PR*) genes (Ryals et al. 1996; Ward et al. 1991).

PR genes encode various characteristic proteins and it has been suggested that these proteins play various roles in increasing resistance to pathogens. The *PR* gene products are categorized from PR-1 to PR-17 according to their biochemical and biological properties (van Loon et al. 2006). Most PR proteins are rapidly induced by pathogens through endogenous phytohormones including salicylic acid (SA), jasmonic acid (JA) and ethylene (ET) (Clarke et al. 2000; Durrant and Dong 2004). Although they are expressed at a basal level under normal conditions, individual *PR* genes are spatially and temporally regulated. Moreover, various growth hormones including SA, abscisic acid (ABA), JA, ET and brassinosteroids (BRs) and abiotic stresses also regulate these genes (Mauch-Mani and Mauch 2005; Thomma et al. 2001). In some defense-related Arabidopsis mutants such as the *constitutive expresser of PR genes* (*cpr*), *accelerated cell death* (*acd*), *lesion simulating disease resistance response* (*lsd*) and *HR-like lesion mimic* (*hlm1*), *PR* genes are constitutively expressed (Balague et al. 2003; Bowling et al. 1994; Dietrich et al. 1994; Gou et al. 2009; Greenberg et al. 1994). The defense responses of these mutants showing HR-like lesion formation and constitutive SAR-like defense responses are constitutively active in the absence of pathogen infection. Growth defects in these mutants are also a characteristic phenotype.

A number of factors related with plant cell death are localized in the endoplasmic reticulum (ER). Arabidopsis BI-1 (AtBI-1), which functions as a suppressor of cell death caused by reactive oxygen species (ROS), is an ER membrane protein. Overexpression of *Bax inhibitor-1* (*BI-1*), which is widely conserved in plants and animals, suppresses cell death that is induced by various stimuli in plants, animals and yeasts (Kawai et al. 1999; Kawai-Yamada et al. 2001, 2004; Sanchez et al. 2000; Xu and Reed 1998). An important part of the signaling pathway of ethylene is also localized around the ER membrane, because ethylene receptors such as ETHYLENE RESPONSE (ETR) 1 are ER membrane proteins (Chen et al. 2002; Grefen et al. 2008). The transmembrane domain of ETR1, which functions as a link between the ER and Golgi apparatus, also includes an ethylene-binding site (Hall et al. 1999; Rodriguez et al. 1999). Ethylene binds to ETR1 and causes a close interaction between this receptor and ETHYLENE INSENSITIVE (EIN) 2, which is also an ER membrane protein and one of the central components of ethylene signaling at the ER membrane (Alonso et al. 1999; Bisson et al. 2009).

Activation tagging is a method of gain-of-function mutagenesis. In this strategy, enhancer elements from the cauliflower mosaic virus (CaMV) *35S* gene positioned in a T-DNA activate genes near the insertion site of the T-DNA (Kondou et al. 2010). We produced approximately 50,000 Arabidopsis activation-tagging lines and have isolated many gain-of-function mutants that show a variety of phenotypes. These mutants have been classified depending on their visible characteristics, such as growth rate, leaf color, fertility, flowering time and morphology (Ichikawa et al. 2003; Nakazawa et al. 2003). In order to determine how the characteristic phenotypes were caused in these gain-of-function mutants we investigated a novel gain-of-function mutant, designated as *dle1-D*, which shows growth defects and bushy inflorescences. This mutant has a T-DNA that inserted close to a gene encoding a protein of unknown function. Our work indicates that overexpression of this gene is likely to cause a defense-related phenotype to environmental stresses and that this protein may play the role of activator for the defense response in the ER.

Materials and methods

Plant material and growth conditions

Arabidopsis thaliana (Col-0 and the transformed lines) was grown at 22°C in long-day conditions (16 h light and 8 h dark) under white fluorescent light (FL40SW, Sanyo, Osaka, Japan). For growing the plants we used a cultivation container system (ARACON). The procedure for Arabidopsis transformation has been described previously (Nakazawa et al. 2003). To confirm cell death in leaf samples, 4-week-old plants were stained according to methods described previously (Bowling et al. 1997).

Construction of vectors for production of overexpressing plants

The PCR primers, DLE1-ATG-GW (GGG GAC AAG TTT GTA CAA AAA AGC AGG CTC GAT GAA CCG AAG GTT GAA TCA TGAACC) and DLE1-STOP-GW (GGG GAC CAC TTT GTA CAA GAA AGC TGG GTTCAC TTT TGC ATA ACC TGA AGA ATA GAA G) were used for amplification from cDNA, which was synthesized using RNA isolated from the whole plant, to produce a *DLE1* overexpression construct. The fragment amplified using these primers was cloned into pBIDAVL-GWR1 as previously described (Nakazawa et al. 2003). This construct was introduced into *Agrobacterium tumefaciens* GV3101pMP90 by electroporation for transformation of Arabidopsis plants. To generate the 35S-*DLE1*$_{1-50}$::*GFP* construct, DLE1-ATG-GW and DLE1-GFP-GW (GGG GAC CAC TTT GTA CAA GAA AGC TGG GTC CGT GTA AGC TTC TGG ATT TAC) were used as primers for amplification from cDNA. The amplified fragment was cloned into pBE2113GFP-GW in-frame with sGFP (S65T) as previously described (Kondou et al. 2008).

Quantitative expression analysis by RT-PCR

RNA was isolated using a NucleoSpin RNA Plant Kit

(MACHEREY-NAGEL, GmbH and Co., Germany) and cDNA was synthesized using a SuperScript First-Strand Synthesis System (Life Technology, Co., USA) according to the instructions. Quantitative RT-PCR was performed using the MX3000P Multiplex Quantitive PCR System (Promega Corp., USA) according to the manufacturer's instructions. SYBR Green I was used as the dye for detection of the amplified fragment from each gene. A part of each gene was employed as a reference DNA fragment for a dilution series. The primers for amplification of the reference DNA fragment were: *DLE1*, TTG TGG GTT CCT GAT GAT GC and CCG AAA ATA GCG TGT TCA CC, *PR1*, ACG TGC AAT GGA GTT TGT GG and CAT CCT GCA TAT GAT GCT CCT TA and *ACT2*, GTA TCG CTG ACC GTA TGA GC and GAT CTT GAG AGC TTA GAA AC. The gene-specific primers for quantitative RT-PCR were: *DLE1*, TGG ATT TCC TCA TCG ACA CTG and CCG CCA CAG AAC TCT TCT CC, *PR1*, CTC GGA TGT GCC AAA GTG AG and CGT CCT TTA TGT ACG TGT GTA TGC and *ACT2*, CTG GAT CGG TGG TTC CAT TC and CCT GGA CCT GCC TCA TCA TAC.

Microarray and gene ontology analyses

The microarray analysis was performed using Agilent Arabidopsis 3 Oligo Microarray (Agilent Technologies, Japan) for 44K Microarray analysis as previously described (Kondou et al. 2008). The genes with altered expression levels were identified using a false discover rate procedure and fold-change from our experimental data set. The calculation for statistical analysis was performed using the software R including a module for the *q*-value calculation, and all default parameters were used in the *q*-value module. Selection of the genes was made by analysis of whether the *q*-values for differential expression of each gene were below 0.005 in two or three experiments. The genes were identified as having altered expression levels if the differential expression ratio was less than 0.125 or more than 8 fold. For gene ontology analysis, the web interface High-throughput GoMiner was used with default parameters (Zeeberg et al. 2005).

Intracellular protein localization

Tobacco BY-2 culture cells were used for transient expression analysis. The suspension cells were spread onto the filter paper by vacuum filtration and were bombarded once with DNA-coated gold particles at a pressure of 1,100 psi using a pneumatic particle gun device (PDS-1000/He, Bio-Rad Laboratories, USA). The cells were then resuspended in MS liquid medium, incubated at 28°C for 12 h in the dark, and then observed by confocal microscopy (LSM510; Carl Zeiss, Inc., Germany).

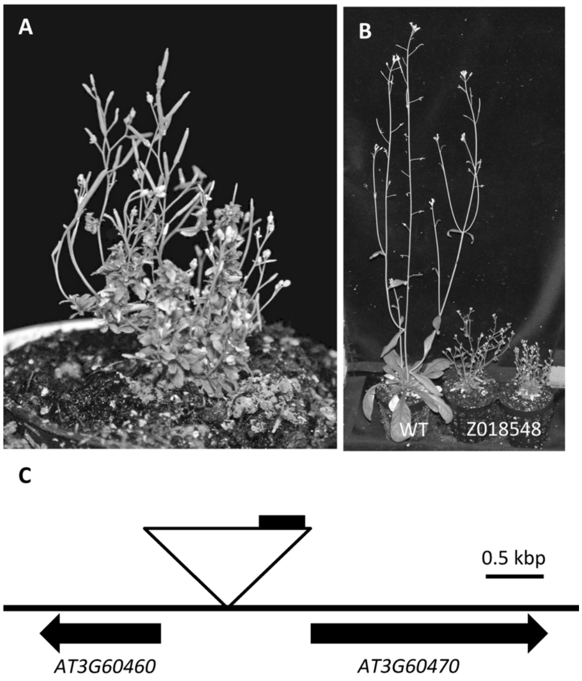

Figure 1. Gain-of-function mutant, Z018548, from activation-tagging lines. (A) The adult phenotype of Z018548 at 5 weeks under long day conditions in the T1 generation. (B) Comparison of the adult phenotype of Z018548 to that of wild type (WT) at 4 weeks in the T2 generation. Plants, from left to right, are wild type, ecotype Col-0, and Z018548 plants. (C) Activation-tagging T-DNA insertion site in the mutant. The activation-tagging T-DNA insertion site in Z01Z54Z is indicated by the triangle. The position of the four copies of the CaMV *35S* enhancer near the right border is indicated by the black bar on the triangle.

Results

Z018548, isolated from activation-tagging lines, is a gain-of-function mutant showing dwarf phenotype

We isolated an Arabidopsis dwarf mutant, Z018548, which had small leaves and shoots, and bushy inflorescences, from activation-tagging lines (Figure 1A and B). The phenotype of this mutant was dominant and co-segregated with the hygromycin resistance derived from the gene on the activation T-DNA. This result suggested that the phenotype of this mutant was caused by the activation of a gene near the T-DNA integration site. Therefore we determined the position of the T-DNA and analyzed the transcriptional levels of genes near the insertion site. The T-DNA was integrated in a region between *AT3G60460* and *AT3G60470* on chromosome 3 (Figure 1C). The distances between the CaMV *35S* enhancers on the T-DNA and the predicted translation start sites of *AT3G60460* and *AT3G60470* were 5,032 bp and 719 bp, respectively. We determined the expression levels of both genes by semi-quantitative RT-PCR to determine which gene was responsible for the mutant. Although the expression level of *AT3G60460* was little

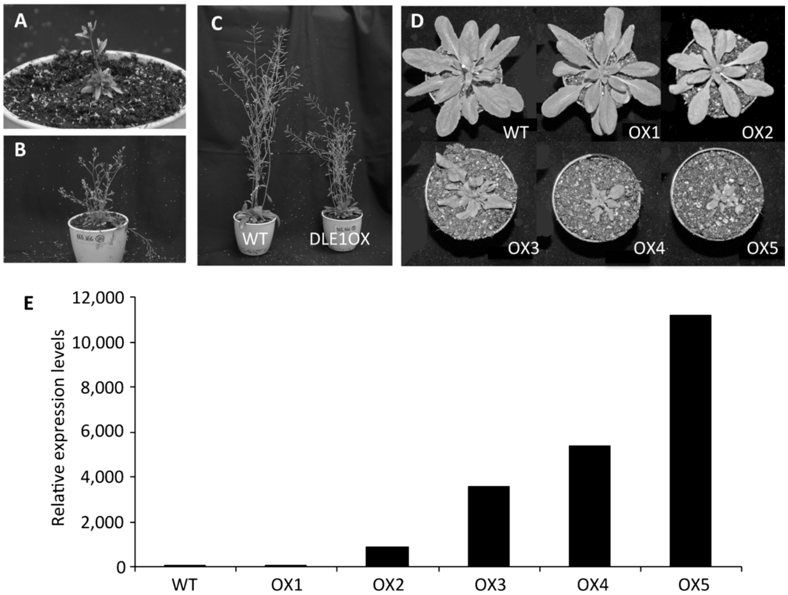

Figure 2. Similar phenotypes of DLE1OXs (overexpressors) to that of *dle1-D* (Z018548). (A, B) The adult phenotype of DLE1OX at 5 weeks under long day conditions in the T1 generation. (C) Comparison of the adult phenotype of DLE1OX to that of wild type (WT) at 5 weeks in the T1 generation. Plants, from left to right, are wild type and DLE1OX plant. (D) Comparison of phenotypes of various DLE1OXs with that of wild type (WT) in the T2 generation. These DLE1OX plants were randomly selected from T2 plants derived from some independent T1 plants. Order of plants from left to right is wild type (WT), OX1, OX2, OX3, OX4 and OX5. (E) Quantitative RT-PCR analysis showing expression of *DLE1* in various DLE1OXs, OX1, OX2, OX3, OX4 and OX5, and wild type (WT) in the T2 generation. Expression levels of the *DLE1* gene were normalized with *ACT2* expression. Relative expression level of the *DLE1* gene in WT was set to 1.

changed in the mutant compared with wild type, the transcriptional product of *AT3G60470* was detected only in the mutant (data not shown). This result suggested that overexpression of *AT3G60470* in the mutant caused the phenotype of Z018548.

We introduced a binary vector, which harbored *AT3G60470* driven by the CaMV *35S* promoter, into Arabidopsis and generated about 30 independent transgenic plants. In the T1 generation some of these transgenic plants showed the characteristic dwarf phenotype and bushy inflorescences similar to those of Z018548 (Figures 2A–C). We also observed dwarf plants in the T2 generation derived from independent T1 plants. We randomly selected some of these T2 plants that showed varying degrees of the phenotype and determined by quantitative PCR their *AT3G60470* expression levels (Figure 2D). The expression level in each plant correlated with the severity of its dwarf phenotype (Figure 2E). These results indicated that the mutant phenotype of the Z018548 plants was derived from enhancement of *AT3G60470* expression.

Overexpression of AT3G60470 causes defense-related phenotypes in response to environmental stresses

We found formation of lesions on the leaves of transgenic plants from the T2 generation overexpressing *AT3G60470* (Figures 3A, B). It is known that some dwarf mutants show defense-related phenotypes, which include

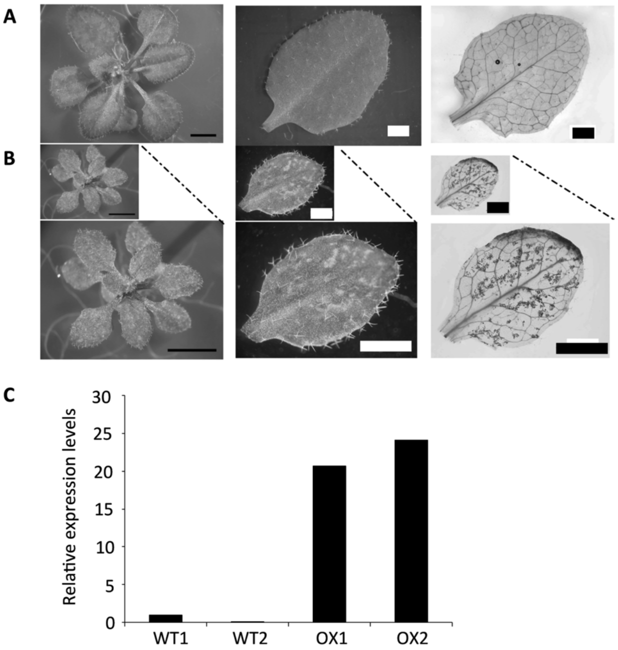

Figure 3. Constitutive cell death in leaves of DLE1OX. (A, B) The adult phenotypes of whole plant (left) and leaves (center) of wild type (A) and DLE1OX (B) at 4 weeks in the T2 generation. Leaves are stained with trypan blue to confirm cell death in leaf areas showing lesion formation (right). Thick and thin scale bars indicate 3 and 1 mm, respectively. (C) Quantitative RT-PCR analysis showing expression of *PR1* in DLE1OX (OX) and wild type (WT). Expression levels of the *PR1* gene were normalized with *ACT2* expression. Relative expression level of the *PR1* gene in WT1 was set to 1.

Table 1. Results of gene ontology analysis using High-throughput GoMiner.

GO ID	Name	FDR
0051707	response to other organism	0
0009607	response to biotic stimulus	0
0051704	multi-organism process	0
0050832	defense response to fungus	0
0006952	defense response	0
0009620	response to fungus	0
0050896	response to stimulus	0
0006950	response to stress	0
0009611	response to wounding	0.00111
0009817	defense response to fungus incompatible interaction	0.001
0009617	response to bacterium	0.000909
0045087	innate immune response	0.000833
0016998	cell wall macromolecule catabolic process	0.000769
0006955	immune response	0.004286
0009814	defense response incompatible interaction	0.006
0002376	immune system process	0.00625
0044036	cell wall macromolecule metabolic process	0.007647

FDR indicates false discovery rate for confidence limits. The gene categories, for which FDR is below 0.008, are shown.

HR-like lesion formation and constitutive SAR-like defense responses. Therefore we stained leaves of these plants with trypan blue to confirm cell death in leaf areas showing the lesion formation (Figures 3A, B). These areas corresponded with the stained cells indicating that overexpression of *AT3G60470* in Arabidopsis caused constitutive cell death similar to HR lesion formation in leaves. We therefore named *AT3G60470* as *DLE1* (*DWARF AND LESION FORMATION 1*). We also designated Z018548 and plants overexpressing *AT3G60470* as *dle1-D* and DLE1OX, respectively.

DLE1 may be positive regulator of inducible defense system caused by biotic stresses in plants

It is known that transcription levels of *PR* genes are enhanced after activation of HR in plants (Ryals et al. 1996). We determined the expression levels of the *PR1* gene (*AT2G14610*) by quantitative PCR in wild type and overexpressors of *DLE1* showing the lesion formation. Transcriptional activation of *PR1* in overexpressors was strongly enhanced (Figure 3C). Overexpression of *DLE1* in Arabidopsis may cause constitutive activation of the signal transduction related with resistance to environmental stresses. If this hypothesis is correct, it is expected that transcriptional products of genes characteristic of the defense response, such as *PR1*, would be up-regulated. We, therefore, carried out genome-wide microarray expression analysis to investigate in detail the differences in the gene expression profiles between DLE1OX and wild type in the T2 generation. Many genes including *PR1*, *PR2* (*AT3G57260*), *PR4* (*AT3G04720*) and *PR5* (*AT1G75040*) were differentially expressed in DLE1OX (Table S1). 324 genes were up-regulated and 115 genes were down-regulated. Gene ontology analysis was performed to classify the function of these genes. Defense response genes were enriched in DLE1OX plants as expected (Table 1 and Table S2). In particular, the genes identified as being involved in the defense response to biotic stimulus were enriched. These results suggest that overexpression of *DLE1* in Arabidopsis causes altered activation of biotic defense response genes inducing activation of SAR. DLE1 may function as a positive regulator of an inducible plant defense system such as SAR derived from biotic stress in Arabidopsis. The expression levels of many positive regulators associated with the plant defense system against biotic stress are induced by pathogen infection (Daniel et al. 1999; del Pozo et al. 2004; Robatzek and Somssich 2001). Therefore we validated how the expression levels of *DLE1* were related with pathogen infection using public microarray data sets. As a result, we found a data set in which the abundance of *DLE1* transcripts was increased by infection of *Pseudomonas syringae* ES4326, registered with the reference number NASCARRAYS-168 in data sets produced by the NASC's International Affymetrix Service. The expression level of *DLE1* may be induced only by some bacteria.

DLE1 is plant-specific protein

DLE1 encodes a 540-aa protein, which has a domain of unknown function (DUF) 247 (Figure 4A). A blast search indicated that 27 genes in Arabidopsis encoded proteins containing a DUF247 domain. We found that proteins encoded by *AT2G28580* and *AT2G44930* were similar to DLE1, although central regions in these homologs were deleted. We also found some similar proteins to DLE1 in several plant species, however no homologous sequences in organisms other than plants were identified. This result suggests that DLE1 is a protein specific to plants.

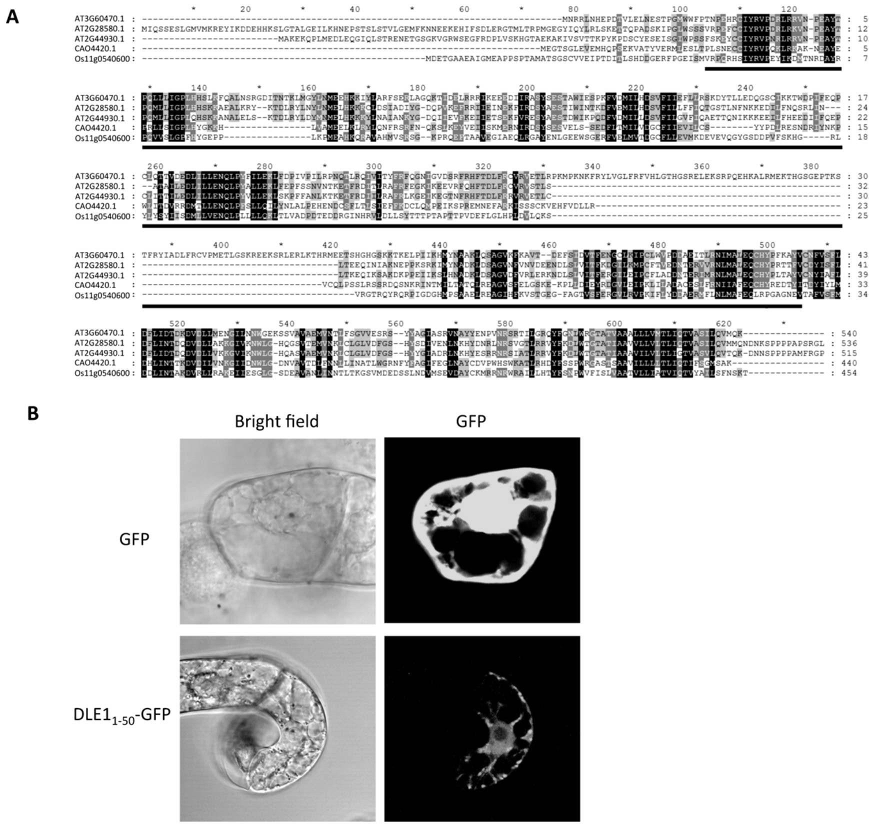

Figure 4. DLE1 is ER protein specific to plants. (A) Alignment of DLE1 and its homologs. The full-length amino acid sequence of DLE1 was aligned with those of *Arabidopsis thaliana* (AT2G28580.1 and AT2G44930.1), *Vitis vinifera* (CAO44201.1) and *Oriza sativa* (Os11g0540600). All alignments were performed using ClustalW software. The DUF247 is indicated by the bold underline. (B) Localization of the N-terminal fragment of DLE1 fused to GFP (DLE1$_{1-50}$-GFP). Only fluorescence of the GFP fusion protein is indicated.

It was predicted by the PSORT prediction program for bacterial/plant sequences that DLE1 was localized in the ER. Therefore we fused GFP to the N-terminal fragment, 1–50 aa, of DLE1 (DLE1$_{1-50}$) to experimentally confirm its intra-cellular localization; the signal peptide for translocation to the ER was located at the N-terminal (Vitale and Denecke 1999). GFP fluorescence of DLE1$_{1-50}$-GFP was observed around the nuclear and plasma membranes. This pattern of localization corresponded to that of proteins localized in the ER (Yang et al. 2005). These results suggested that DLE1 in BY-2 cells was localized in the ER (Figure 4B).

Discussion

We have identified a dominant dwarf mutant designated as *dle1-D* from activation tagging lines. A T-DNA harboring CaMV *35S* enhancers inserted between two genes, *AT3G60460* and *AT3G60470*. There was a great distance between *AT3G60470* and the enhancers (more than 5 kb) but because the expression of genes can be influenced by enhancers several kb away, sometimes more than 10 kb (Hsing et al. 2007), we determined the expression levels of both genes in wild type and *dle1-D*. Only one of these genes, *AT3G60470*, was actually activated in *dle1-D*. The transcripts of *DLE1* were almost undetectable in wild type growing under normal conditions, even though the cDNA of *DLE1* has been registered in GenBank (DQ492234.1). This result may indicate that expression of *DLE1* is suppressed under optimal growing conditions and activated by environmental stimuli such as biotic or abiotic stresses. This hypothesis is supported by public microarray data, in which the expression level of *DLE1* was induced by infection with *Pseudomonas syringae* ES4326.

Transgenic plants, overexpressing the gene responsible for the *dle1-D* phenotype, also exhibited leaf areas showing lesion formation. The lesions in the leaves of some defense-related mutants simulate the phenomenon known as the hypersensitive response (HR), which is characterized by programmed cell death (Balague et al. 2003; Bowling et al. 1994; Dietrich et al. 1994; Gou et al. 2009; Greenberg et al. 1994). Since it was confirmed that cell death occurred in these leaf areas, DLE1OX lines show HR-like lesion formation (Figure 3B). These results suggested that the molecular pathway for the defense response was activated in DLE1OX. This is supported by the correlation between the expression levels of *DLE1* and the severity of the abnormal dwarfism in DLE1OX (Figure 2B), because enhancement of the defense response frequently causes defects in plant growth (Balague et al. 2003; Bowling et al. 1994; Dietrich et al. 1994; Gou et al. 2009; Greenberg et al. 1994). Interestingly, many genes, which are involved in cell wall organization according to gene ontology annotation, were included in the overexpressed genes by microarray. The aberrant activation of the defense response in DLE1OX may cause swelling of the cell wall, because plant cells respond to the invasion of pathogens such as fungi by forming a cell wall apposition at the entry site (Schulze-Lefert 2004). One of the important plant defense systems, SAR, is triggered after an acceleration of the HR (Durrant and Dong 2004). SAR may also be induced in DLE1OX, because strong activation of the *PR1* gene characterizing SAR was confirmed in DLE1OX (Figure 3C). This hypothesis is supported by the result from the microarray analysis showing activation of expression levels of other *PR* genes, *PR2*, *PR4* and *PR5*, in DLE1OX (Table S1). It was interesting that increased expression of the *PR3* gene (*AT3G12500*) was not included in the list of up-regulated genes in DLE1OX. Seo et al. reported that the expression level of *PR3* was significantly induced by high salt stress in an ABA-dependent manner (Seo et al. 2008). DLE1 may function in the defense response in another way apart from being dependent on ABA.

DLE1 encodes a novel protein containing a DUF247, which has been defined as a domain of unknown function. Although we could not find a biochemical function of the proteins that had this domain, some genes encoding similar proteins to DLE1 were found only in plants. DLE1 and its homologous proteins could have a function in the plant immune system. Intracellular localization of DLE1$_{1-50}$ fused to GFP may give us some information about the molecular function. BI1 is one of the putative targets of DLE1, because this protein is an ER membrane protein and overexpression of it suppresses cell death (Kawai-Yamada et al. 2001; Xu and Reed 1998). DLE1 may negatively regulate activity of AtBI1 in the ER. Although this hypothesis is attractive, it is inconsistent with the fact that DLE1 is a plant-specific protein and BI1 regulates cell death in many organisms including animals and yeasts. Ethylene, which is one of the important phytohormones involved in the plant immune system, induces various changes including localized plant cell death associated with HR and the up-regulation of resistance against many types of pathogens (Carr et al. 2010; Clarke et al. 2000; Thomma et al. 2001). The ER, where DLE1$_{1-50}$ (the N-terminal part of DLE1) fused to GFP localized, plays an important role in the signal transduction of ethylene. This is because there is an ethylene receptor, ETR1, and important proteins for the signaling pathway through ETR1 in the ER membrane (Bisson et al. 2009; Grefen et al. 2008). A possible model is that DLE1 serves as an activator of the defense response induced by ethylene in the ER in Arabidopsis, because ethylene-dependent signal transduction is plant specific.

In this study, we have found a plant-specific protein that functions in the plant defense system responding to environmental stimuli including biotic stresses. We are isolating Arabidopsis mutants that have lost *DLE1* function. Detailed functional analysis using the loss-of-function mutants will provide further information to elucidate the molecular function of DLE1 in the plant immune system.

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Table S1. 439 genes differentially detected in whole plants of DLE1OX and Col-0 at 4 weeks

Increase and q-value were obtained from the 1st and 2nd experiments.

Each average is calculated from the Increase and Decrease of each experiment.

DLE1 and *PR* genes are indicated in red and blue, respectively.

Probe Name	AGI code	1st experiment		2nd experiment		Average	Description
		Increase	q-value	Increase	q-value		
A_84_P160753	At2g41800.1	1054.479622	2.35E-20	449.5946319	3.74E-20	752.0371271	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 [At2g41800.1]
A_84_P91639	At2g39030.1	695.365172	2.35E-20	225.6345836	3.74E-20	460.4998778	GCN5-related N-acetyltransferase (GNAT) family protein similar to SPIQ9SMB8 Tyramine N-feruloyltransferase 4/11 (EC 2.3.1.110) (Hydroxycinnamoyl- CoA: tyramine N-hydroxycinnamoyltransferase) {Nicotiana tabacum}; contains Pfam profile PF00583:...
A_84_P15115	At3g24954.1	632.330939	2.35E-20	247.5176166	3.74E-20	439.9242778	leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611 [At3g24954.1]
A_84_P21769	At1g61120.1	148.7355805	2.35E-20	609.3021412	3.74E-20	379.0188609	terpene synthase/cyclase family protein similar to S-linalool synthase GI:1491939 from [Clarkia breweri][PMID: 8768373] [At1g61120.1]
A_84_P14441	At2g29460.1	428.9542573	2.35E-20	252.336431	3.74E-20	340.6453442	glutathione S-transferase, putative [At2g29460.1]
A_84_P196694	At5g44430.1	375.0000558	2.35E-20	299.2127827	3.74E-20	337.1064193	plant defensin-fusion protein, putative (PDF1.2c) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to antifungal protein 1 preprotein [Raphanus sativus] gil609322lgblAAA69541...
A_84_P517367	At3g45130.1	295.8848461	2.35E-20	349.9999729	3.74E-20	322.9424095	cycloartenol synthase, putative / 2,3-epoxysqualene--cycloartenol cyclase, putative / (S)-2,3-epoxysqualene mutase, putative 77% similar to cycloartenol synthase [SPIP38605lgi:452446] [PMID: 7505443]; oxidosqualene cyclase LcOSC2 - Luffa cylindrica,...
A_84_P310613	At2g26020.1	334.261874	2.35E-20	294.59436	3.74E-20	314.428117	plant defensin-fusion protein, putative (PDF1.2b) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to antifungal protein 1 preprotein [Raphanus sativus] gil609322lgblAAA69541...
A_84_P587549	At3g60470.1	323.5951108	2.35E-20	244.8131596	3.74E-20	284.2041352	hypothetical protein contains Pfam profile PF03140: Plant protein of unknown function [At3g60470.1]
A_84_P239215	At2g26010.1	316.3842561	2.35E-20	251.7986434	3.74E-20	284.0914497	plant defensin-fusion protein, putative (PDF1.3) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to antifungal protein 1 preprotein [Raphanus sativus] gil609322lgblAAA69541 [At2g26010.1]
A_84_P558829	At2g29350.2	384.5141821	2.35E-20	169.2491291	3.74E-20	276.8816556	tropinone reductase, putative / tropine dehydrogenase, putative similar to tropinone reductase SP:P50165 from [Datura stramonium] [At2g29350.2]
A_84_P13535	At2g38240.1	240.1314408	2.35E-20	197.4842379	3.74E-20	218.8078394	oxidoreductase, 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 [At2g38240.1]
A_84_P20322	At3g49340.1	218.3761363	2.35E-20	217.0541806	3.74E-20	217.7151585	cysteine proteinase, putative contains PS00640: Eukaryotic thiol (cysteine) proteases asparagine active site; similar to cysteine proteinase GI:535454 from [Alnus glutinosam] [At3g49340.1]
A_84_P18821	At5g61160.1	226.8964143	2.35E-20	197.4248385	3.74E-20	212.1606264	transferase family protein similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains...
A_84_P10609	At2g24850.1	304.8390681	2.35E-20	116.1458423	3.74E-20	210.4924552	aminotransferase, putative similar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:6469087]; contains Pfam profile PF00155 aminotransferase, classes I and II [At2g24850.1]
A_84_P517367	At3g45130.1	228.6750728	2.35E-20	159.837709	3.74E-20	194.2563909	cycloartenol synthase, putative / 2,3-epoxysqualene--cycloartenol cyclase, putative / (S)-2,3-epoxysqualene mutase, putative 77% similar to cycloartenol synthase [SPIP38605lgi:452446] [PMID: 7505443]; oxidosqualene cyclase LcOSC2 - Luffa cylindrica,...
A_84_P18113	At1g76640.1	121.3642498	2.71E-20	262.6016189	3.74E-20	191.9829343	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana tabacum] [At1g76640.1]
A_84_P18315	At3g09940.1	180.3279231	2.35E-20	185.3856417	3.74E-20	182.8567824	monodehydroascorbate reductase, putative similar to monodehydroascorbate reductase (NADH) GB:JU0182 (Cucumis sativus) [At3g09940.1]
A_84_P68884	At4g21840.1	108.5675615	2.87E-20	242.1466108	3.74E-20	175.3570861	methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein weak similarity to pilin-like transcription factor [Homo sapiens] GI:5059062, SPIP14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) {Neisseria...
A_84_P20323	At3g49620.1	156.7227057	2.35E-20	148.0916718	3.74E-20	152.4071888	2-oxoacid-dependent oxidase, putative (DIN11) identical to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554 [Arabidopsis thaliana]; identical to cDNA 2-oxoacid-dependent oxidase (din11) GI:10834553; contains Pfam profile PF03171:...
A_84_P17676	At4g37990.1	185.6461132	2.35E-20	114.6852863	3.74E-20	150.1656997	mannitol dehydrogenase, putative (ELI3-2) identical to GI:16269 [At4g37990.1]
A_84_P701229	CHR4v0121200	202.3345667	2.35E-20	70.9649136	7.72E-20	136.6497402	Unknown
A_84_P17693	At4g16260.1	126.2032016	2.35E-20	126.2916635	3.74E-20	126.2474326	glycosyl hydrolase family 17 protein similar to glucan endo-1,3-beta-glucosidase, basic vacuolar isoform precursor SP:P52407 from [Hevea brasiliensis] [At4g16260.1]
A_84_P115562	At1g73325.1	181.0054592	2.35E-20	61.16320916	5.52E-20	121.0843342	trypsin and protease inhibitor family protein / Kunitz family protein similar to Dr4 [Arabidopsis thaliana] GI:469114; contains Pfam profile PF00197: Trypsin and protease inhibitor [At1g73325.1]
A_84_P156615	At4g12490.1	72.96357935	2.79E-20	145.6311333	3.74E-20	109.2973563	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease...
A_84_P22923	At2g33020.1	133.0226125	2.58E-20	64.77418261	1.38E-19	98.89839756	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611 [At2g33020.1]
A_84_P14442	At2g29350.1	116.0584213	2.47E-20	81.01568825	8.43E-20	98.5370548	tropinone reductase, putative / tropine dehydrogenase, putative similar to tropinone reductase SP:P50165 from [Datura stramonium] [At2g29350.1]
A_84_P245685	At3g44300.1	98.47329994	2.47E-20	94.962677	3.74E-20	96.71798847	nitrilase 2 (NIT2) identical to SPIP32962 Nitrilase 2 (EC 3.5.5.1) {Arabidopsis thaliana} [At3g44300.1]
A_84_P292144	At3g23550.1	92.03144656	2.51E-20	101.0849424	3.74E-20	96.5581945	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family [At3g23550.1]
A_84_P100746	At3g28220.1	119.0476474	2.35E-20	71.91284593	4.61E-20	95.48024665	meprin and TRAF homology domain-containing protein / MATH domain-containing protein similar to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain [At3g28220.1]
A_84_P16673	At4g24340.1	109.8092898	2.87E-20	76.38326584	9.27E-20	93.0962778	phosphorylase family protein contains Pfam PF01048: Phosphorylase family [At4g24340.1]
A_84_P12686	At3g25180.1	65.02177343	2.87E-20	110.6996154	3.74E-20	87.86069443	cytochrome P450 family protein similar to cytochrome P450 monooxygenase GB:AAC49188 [Pisum sativum]; contains Pfam profile: PF00067 cytochrome P450 [At3g25180.1]
A_84_P594753	At4g22230.1	144.8717714	3.47E-20	28.93048091	5.82E-19	86.90112617	expressed protein [At4g22230.1]
A_84_P15194	At1g54020.1	68.20810613	2.82E-20	104.3137842	3.74E-20	86.26094515	myrosinase-associated protein, putative strong similarity to myrosinase-associated proteins GI:1769968, GI:1769970, GI:1216389,GI:1216391 from [Brassica napus]; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family [At1g54020.1]
A_84_P16173	At1g28480.1	108.2191872	2.35E-20	60.11562026	5.52E-20	84.16740371	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) [At1g28480.1]
A_84_P137009	At5g44420.1	70.75474515	2.81E-20	77.57844751	4.29E-20	74.16659633	plant defensin protein, putative (PDF1.2a) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to antifungal protein 1 preprotein [Raphanus sativus] gil609322lgblAAA69541 [At5g44420.1]
A_84_P14560	At3g26830.1	87.60909235	2.58E-20	57.35293452	6E-20	72.48101344	cytochrome P450 71B15, putative (CYP71B15) Identical to Cytochrome P450 (SP:Q9LW27) [Arabidopsis thaliana]; similar to cytochrome P450 71B2 GB:O65788 [Arabidopsis thaliana] [At3g26830.1]
A_84_P22140	At3g23250.1	65.89357975	7.02E-20	75.16254437	9.57E-20	70.52806206	myb family transcription factor (MYB15) similar to myb-related transcription factor GB:CAA66952 from [Lycopersicon esculentum] [At3g23250.1]
A_84_P250315	At2g18660.1	91.53841458	2.77E-20	49.27007286	8.43E-20	70.40424372	expansin family protein (EXPR3) identical to Expansin-related protein 3 precursor (Ath-ExpGamma-1.2) (Swiss-Prot:Q9ZV52) [Arabidopsis thaliana]; contains Prosite PS00092: N-6 Adenine-specific DNA methylases signature; [At2g18660.1]
A_84_P23050	At3g04720.1	85.12820469	2.58E-20	53.92152896	6.34E-20	69.52486683	hevein-like protein (HEL) identical to SPIP43082 Hevein-like protein precursor {Arabidopsis thaliana}; similar to SPIP09762 Wound-induced protein WIN2 precursor {Solanum tuberosum}; contains Pfam profile PF00187: Chitin recognition protein [At3g04720.1]
A_84_P10863	At3g48520.1	68.31434738	6.18E-20	67.04291625	1.09E-19	67.67863181	cytochrome P450 family protein similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:O81117) {Vicia sativa}; contains Pfam profile: PF00067 cytochrome P450 [At3g48520.1]
A_84_P18557	At4g22470.1	39.70149694	5.43E-20	84.15097021	8.03E-20	61.92623358	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to hydroxyproline-rich glycoprotein DZ-HRGP from Volvox carteri f. nagariensis GPI6523547; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family...
A_84_P14336	At1g72260.1	50.7936555	3.32E-20	70.8933795	4.61E-20	60.8435175	thionin (THI2.1) identical to thionin [Arabidopsis thaliana] gil1181531lgblAAC41678 [At1g72260.1]
A_84_P12747	At3g46700.1	78.88284063	4.24E-20	40.91504121	1.74E-18	59.89894092	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At3g46700.1]
A_84_P12477	At1g79680.1	92.75550484	3.26E-20	24.93827896	2.16E-18	58.8468919	wall-associated kinase, putative similar to wall-associated kinase 2 GI:4826399 from [Arabidopsis thaliana] [At1g79680.1]
A_84_P21703	At5g13080.1	87.2641391	2.68E-20	27.33333705	3.6E-19	57.29873808	WRKY family transcription factor WRKY DNA binding protein - Solanum tuberosum, EMBL:AJ278507 [At5g13080.1]
A_84_P22914	At2g15490.1	81.96317694	3.4E-20	27.82258188	2.44E-18	54.89287941	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At2g15490.1]
A_84_P23270	At4g18250.1	89.64612388	3.32E-20	17.42357423	7.89E-18	53.53484905	receptor serine/threonine kinase, putative similar to to receptor serine/threonine kinase PR5K gil1235680lgblAAC49208 [At4g18250.1]
A_84_P10711	At2g39330.1	57.52065903	3.09E-20	42.97411428	8.59E-20	50.24738665	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767, myrosinase binding protein [Brassica napus] GI:1711296; contains Pfam profile PF01419 jacalin-like lectin domain [At2g39330.1]
A_84_P18258	At2g24210.1	20.37444704	3.17E-19	78.34395196	5.02E-20	49.3591995	myrcene/ocimene synthase (TPS10) nearly identical to GI:9957293; contains Pfam profile: PF01397 terpene synthase family [At2g24210.1]
A_84_P11694	At3g01830.1	36.06357715	2.93E-18	61.23849829	1.72E-19	48.65103772	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana tabacum]; Pfam HMM hit: EF hand [At3g01830.1]
A_84_P544532	At1g58225.1	26.68299677	1.26E-16	70.4491649	1.09E-19	48.56608084	expressed protein [At1g58225.1]
A_84_P199304	At1g19610.1	54.04157064	3.24E-20	39.41605815	1.02E-19	46.72881439	plant defensin-fusion 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...
A_84_P13031	At5g19110.1	56.90473508	3.2E-20	36.05838807	1.11E-19	46.48156158	extracellular dermal glycoprotein-related / EDGP-related similar to extracellular dermal glycoprotein EDGP precursor [Daucus carota] GI:285741 [At5g19110.1]
A_84_P22839	At1g73260.1	65.82282315	2.92E-20	25.27273158	3.54E-19	45.54777736	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 [At1g73260.1]
A_84_P10330	At5g65600.1	64.33203408	7.79E-20	24.69286448	5.78E-16	44.51244928	legume lectin family protein / protein kinase family protein contains Pfam domains PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain [At5g65600.1]
A_84_P20045	At1g57630.1	70.63389261	5.63E-20	17.30158735	7.08E-18	43.96773998	disease resistance protein (TIR class), putative domain signature TIR exists, suggestive of a disease resistance protein. [At1g57630.1]
A_84_P65264	At3g15356.1	56.78300522	3.1E-20	30.26114141	1.57E-19	43.52207331	legume lectin family protein contains Pfam domain, PF00139: Legume lectins beta domain [At3g15356.1]
A_84_P16574	At3g57260.1	42.78213869	4.02E-20	43.88892413	8.43E-20	43.33553141	glycosyl hydrolase family 17 protein similar to glucan endo-1,3-beta-glucosidase, acidic isoform precursor SP:P33157 from [Arabidopsis thaliana] [At3g57260.1]
A_84_P13172	At5g67080.1	54.19500562	3.26E-20	32.11991122	1.57E-19	43.15745842	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At5g67080.1]
A_84_P21212	At3g16530.1	47.06897398	3.49E-20	38.13085565	1.01E-19	42.59991481	legume lectin family protein contains Pfam domain, PF00139: Legume lectins beta domain [At3g16530.1]
A_84_P10009	At4g08870.1	54.16664011	3.2E-20	30.58459782	1.54E-19	42.37561897	arginase, putative similar to Swiss-Prot:P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana] [At4g08870.1]
A_84_P268160	At3g13950.1	64	3.24E-20	19.06104618	5.05E-18	41.53052309	expressed protein [At3g13950.1]
A_84_P97476	At5g24780.1	40.06848342	4.48E-20	42.55818147	8.59E-20	41.31333244	vegetative storage protein 1 (VSP1) identical to SPIO49195 Vegetative storage protein 1 precursor {Arabidopsis thaliana}; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase [At5g24780.1]
A_84_P11918	At4g13410.1	49.01532555	3.47E-20	31.81357287	1.43E-19	40.41444921	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium japonicum], cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains...
A_84_P172941	At2g18690.1	50.90180815	3.4E-20	29.85384812	1.9E-19	40.37782814	expressed protein [At2g18690.1]
A_84_P21958	At2g43510.1	51.05821865	3.32E-20	28.29133793	1.86E-19	39.67477829	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) {Sinapis alba} [At2g43510.1]
A_84_P21851	At1g66370.1	51.76151719	3.4E-20	27.10280565	2.17E-19	39.43216142	myb family transcription factor (MYB113) contains Pfam profile: PF00249 myb-like DNA-binding domain [At1g66370.1]
A_84_P74014	At3g11340.1	43.75001177	5.02E-20	33.53235725	2.25E-19	38.64118451	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At3g11340.1]
A_84_P20237	At1g26420.1	53.33334834	1.72E-19	23.08642052	1.9E-15	38.20988443	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At1g26420.1]
A_84_P21673	At1g52400.1	40.46690759	4.44E-20	34.63476548	1.15E-19	37.55083654	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:6651430 from [Arabidopsis thaliana] [At1g52400.1]
A_84_P12382	At1g53830.1	49.8422572	3.61E-20	24.61278489	5.39E-19	37.22752105	pectinesterase family protein identical to pectinesterase 2 (PME2/ PE 2) SP:Q42534 from [Arabidopsis thaliana];contains Pfam profiles: PF01095 pectinesterase, PF04043 plant invertase/pectin methylesterase inhibitor [At1g53830.1]
A_84_P181974	At1g20310.1	35.35763809	3.45E-18	38.82353552	2.64E-18	37.09058681	expressed protein [At1g20310.1]
A_84_P19191	At1g19670.1	46.23958037	3.59E-20	27.75261863	1.94E-19	36.9960995	coronatine-responsive protein / coronatine-induced protein 1 (CORI1) identical to coronatine-induced protein 1 (CORI1) GI:30912637 from [Arabidopsis thaliana] [At1g19670.1]

A_84_P210768	At5g19230.1	36.90647385	5.31E-20	35.94061025	1.09E-19	36.42354205	expressed protein [At5g19230.1]
A_84_P594753	At4g22230.1	50.27323423	3.47E-20	22.31706499	5.82E-19	36.29514961	expressed protein [At4g22230.1]
A_84_P12550	At2g32660.1	53.37001457	1.67E-19	16.92913083	7.97E-13	35.1495727	disease resistance family protein / LRR family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4 [Lycopersicon hirsutum] gil2808683lemblCAA05268 [At2g32660.1]
A_84_P13709	At3g50770.1	14.91228466	1.4E-18	54.67104323	8.59E-20	34.79166394	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana tabacum] [At3g50770.1]
A_84_P515859	At5g25250.1	60.34722388	2.97E-20	8.244146831	2.8E-16	34.29568536	expressed protein [At5g25250.1]
A_84_P290004	At4g21850.1	25.8300942	1.3E-19	42.42991843	8.59E-20	34.13000632	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein low similarity to pilin-like transcription factor [Homo sapiens] GI:5059062, SPIP14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) {Neisseria...
A_84_P542288	At4g17470.1	57.37228209	3.09E-20	10.59891515	2.72E-17	33.98559862	palmitoyl protein thioesterase family protein [At4g17470.1]
A_84_P17546	At3g44860.1	55.05052052	3.2E-20	12.048194	1.07E-17	33.54935726	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cjs1 [Brassica carinata][GI:14009292][Mol Plant Pathol (2001) 2(3):159-169] [At3g44860.1]
A_84_P188254	At4g23140.1	46.14394676	3.99E-19	20.50847909	1.19E-16	33.32621292	receptor-like protein kinase 5 (RLK5) identical to receptor-like protein kinase 5 [Arabidopsis thaliana] GI:13506747; contains Pfam domain PF00069: Protein kinase domain; identical to cDNA receptor-like protein kinase 5 (RLK5) GI:13506746 [At4g23140.1]
A_84_P15797	At4g15100.1	46.46194678	3.81E-19	20.13157303	2.25E-14	33.2967599	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (EC 3.4.16.6) [Triticum aestivum (Wheat)] [At4g15100.1]
A_84_P535346	At5g22540.1	39.58904059	1.18E-18	26.05156252	2.48E-16	32.82030155	expressed protein contains Pfam profile PF03140: Plant protein of unknown function [At5g22540.1]
A_84_P10528	At1g51800.1	44.65649759	4.52E-20	19.30131183	3.3E-18	31.97890471	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gil1321686lemblCAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069...
A_84_P272600	At5g21960.1	32.6639713	7.75E-18	31.22629936	2.2E-17	31.94513533	AP2 domain-containing transcription factor, putative similar to TINY (GI:1246403) [Arabidopsis thaliana] [At5g21960.1]
A_84_P595141	At1g30135.1	29.02857807	1.05E-17	34.34935253	5.05E-18	31.6889653	expressed protein [At1g30135.1]
A_84_P600236	At5g22545.1	49.14003568	2.36E-19	14.13978913	3.76E-16	31.6399124	expressed protein [At5g22545.1]
A_84_P582597	At1g09932.1	28.79044933	1.05E-19	34.43982006	1.33E-19	31.6151347	phosphoglycerate/bisphosphoglycerate mutase-related weak hit to Pfam profile PF00300: phosphoglycerate mutase family [At1g09932.1]
A_84_P12241	At5g20230.1	37.02929045	5.22E-20	25.84614839	2.35E-19	31.43771942	plastocyanin-like domain-containing protein [At5g20230.1]
A_84_P17584	At1g17380.1	29.53020568	9.55E-20	32.5916164	1.38E-19	31.06091104	expressed protein [At1g17380.1]
A_84_P241225	At5g39520.1	41.11801175	9.55E-20	19.91388778	8.7E-15	30.51594976	expressed protein predicted protein, Synechocystis sp., PIR:S77152 [At5g39520.1]
A_84_P544235	At5g28237.1	45.3804434	4.32E-19	15.56122467	4.19E-17	30.47083403	tryptophan synthase, beta subunit, putative similar to SPIP14671 Tryptophan synthase beta chain 1, chloroplast precursor (EC 4.2.1.20) {Arabidopsis thaliana}; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme [At5g28237.1]
A_84_P19362	At3g46090.1	40.64516106	1.04E-19	19.75459275	1.74E-18	30.19987691	zinc finger (C2H2 type) family protein (ZAT7) identical to zinc finger protein ZAT7 [Arabidopsis thaliana] gil1418341lemblCAA67234; contains Pfam domain, PF00096: Zinc finger, C2H2 type [At3g46090.1]
A_84_P18100	At1g69930.1	20.62068995	6.92E-18	38.31774086	3E-18	29.46921541	glutathione S-transferase, putative similar to glutathione transferase GB:CAA09188 [Alopecurus myosuroides] [At1g69930.1]
A_84_P544827	At3g25760.1	27.32672379	3.17E-19	29.88022279	6.25E-19	28.60347329	early-responsive to dehydration stress protein (ERD12) nearly identical to early-responsive to dehydration (ERD12) protein [GI:15320414]; similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; identical to cDNA ERD12 partial cds...
A_84_P14273	At1g14780.1	37.05235921	2.17E-18	19.52191398	4.67E-14	28.28713659	expressed protein [At1g14780.1]
A_84_P592948	At4g11910.1	43.77511307	5.02E-20	12.06106668	1.19E-17	27.91808988	expressed protein hypothetical protein F7H19.100 -Arabidopsis thaliana,PID:e1310060 [At4g11910.1]
A_84_P24128	At3g54150.1	42.31885827	9.37E-20	12.54417425	7.22E-17	27.43151626	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531 [At3g54150.1]
A_84_P13039	At5g24420.1	25.4506571	1.35E-19	28.99583943	1.76E-19	27.22324827	glucosamine/galactosamine-6-phosphate isomerase-related contains weak similarity to Swiss-Prot:O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) [Homo sapiens] [At5g24420.1]
A_84_P12432	At1g74590.1	31.86694912	2.37E-18	22.4844642	3.13E-15	27.17570666	glutathione S-transferase, putative similar to putative glutathione S-transferase GB:CAA10060 [Arabidopsis thaliana]; contains Pfam profile: PF00043 Glutathione S-transferases [At1g74590.1]
A_84_P557523	At5g33355.1	32.38805663	4.41E-19	21.65948447	1.27E-15	27.02377055	expressed protein [At5g33355.1]
A_84_P16846	At5g38900.1	32.08555426	8.73E-20	21.81184646	9.27E-19	26.94870036	DSBA oxidoreductase family protein contains Pfam profile: PF01323 DSBA-like thioredoxin domain [At5g38900.1]
A_84_P14882	At1g06620.1	32.46575827	7.26E-20	20.1803739	6.25E-19	26.32306608	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SPIP10967); contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family [At1g06620.1]
A_84_P15574	At3g45140.1	28.49675026	9.65E-20	23.25442722	3.34E-19	25.87558874	lipoxygenase (LOX2) identical to SPIP38418 [At3g45140.1]
A_84_P22797	At1g33030.1	24.2537345	1.58E-19	27.40156713	2.21E-19	25.82765081	O-methyltransferase family 2 protein similar to caffeic acid 3-O-methyltransferase [SPIQ00763] [Populus tremuloides], catechol O-methyltransferase [GI:4808524][Thalictrum tuberosum] [At1g33030.1]
A_84_P18663	At5g05340.1	32.79411416	1.34E-19	18.48341463	6.83E-18	25.63876439	peroxidase, putative similar to peroxidase [Nicotiana tabacum] gil5381253ldbjlBAA82306; similar to Peroxidase P7 [Brassica rapa (Turnip)] SWISS-PROT:P00434 [At5g05340.1]
A_84_P21007	At2g43570.1	33.90245399	6.18E-20	17.30263673	1.25E-18	25.60254536	chitinase, putative similar to chitinase class IV GI:722272 from [Brassica napus] [At2g43570.1]
A_84_P91079	At5g22520.1	25.60000168	2E-16	24.1025603	8.49E-16	24.85128099	expressed protein [At5g22520.1]
A_84_P529186	At5g44575.1	30.34783092	8.06E-19	18.72385639	2.19E-15	24.53584366	expressed protein [At5g44575.1]
A_84_P23754	At1g33960.1	22.10526309	5.35E-18	26.96366124	3.59E-17	24.53446217	avirulence-responsive protein / avirulence induced gene (AIG1) identical to AIG1 (exhibits RPS2- and avrRpt2-dependent induction early after infection with Pseudomonas) SP:U40856 [Arabidopsis thaliana] (Plant Cell 8 (2), 241-249 (1996)) [At1g33960.1]
A_84_P22829	At1g68290.1	28.77192015	3.99E-19	19.99999868	3.13E-15	24.38595941	bifunctional nuclease, putative similar to bifunctional nuclease [Zinnia elegans] gil4099833lgblAAD00694 [At1g68290.1]
A_84_P22787	At1g02920.1	20.17619613	3.08E-19	28.58406114	1.85E-19	24.38012864	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA GI:443697. [At1g02920.1]
A_84_P18619	At4g37410.1	31.45833478	7.43E-20	16.91357351	1.35E-18	24.18595414	cytochrome P450, putative similar to cytochrome p450 SP:O65790 from [Arabidopsis thaliana] [At4g37410.1]
A_84_P178164	At1g70850.1	11.1538456	1.04E-15	36.69064852	1.33E-19	23.92224706	Bet v I allergen family protein similar to Csf-2 [Cucumis sativus][GI:5762258][J Am Soc Hortic Sci 124, 136-139 (1999)] contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family [At1g70850.1]
A_84_P212238	At5g13220.1	17.80876664	5.1E-19	28.48781368	1.85E-19	23.14829016	expressed protein [At5g13220.1]
A_84_P12851	At4g10500.1	16.52892851	1.31E-12	29.26510399	5.01E-17	22.89701625	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to hyoscyamine 6 beta-hydroxylase [Atropa belladona][GI:4996123]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain [At4g10500.1]
A_84_P13831	At4g23150.1	26.87164991	1.12E-16	18.58489974	1.24E-15	22.72827482	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain [At4g23150.1]
A_84_P549255	At3g28600.1	25.10067054	2.99E-16	20.31662421	1.94E-14	22.70864738	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 [At3g28600.1]
A_84_P572473	At4g21920.1	23.94927371	3.17E-19	21.05769324	2.68E-18	22.50348347	expressed protein [At4g21920.1]
A_84_P17963	At1g13300.1	16.53846003	7.96E-19	28.44067893	2.88E-19	22.48956948	myb family transcription factor contains Pfam domain, PF00249: Myb-like DNA-binding domain [At1g13300.1]
A_84_P12195	At5g59580.1	9.408288498	7.17E-10	35.39475048	0.000000019	22.40151949	Unknown
A_84_P10248	At5g44380.1	28.973101	3.91E-17	15.21738966	5.96E-14	22.09524533	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At5g44380.1]
A_84_P289964	At1g19020.1	23.10606208	2.36E-19	21.0611017	6.08E-19	22.08358189	expressed protein [At1g19020.1]
A_84_P61660	At2g15220.1	17.414969	3.41E-13	26.65799553	1.67E-16	22.03648227	secretory protein, putative similar to NtPRp27 [Nicotiana tabacum] GI:5360263; contains Pfam profile PF04450: Plant Basic Secretory Protein [At2g15220.1]
A_84_P15812	At5g01380.1	30.45268014	1.85E-17	13.52940605	3.84E-14	21.99104309	expressed protein [At5g01380.1]
A_84_P15826	At5g05600.1	19.54224896	3.4E-19	24.43890939	2.87E-19	21.99057918	oxidoreductase, 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 [At5g05600.1]
A_84_P11746	At3g27400.1	29.43575037	9.02E-20	14.53531266	3.22E-18	21.98553152	pectate lyase family protein similar to pectate lyase GP:7547009 from [Vitis vinifera]; contains Pfam profile: PF00544 pectate lyase [At3g27400.1]
A_84_P15536	At3g16470.1	21.67033724	2.31E-19	22.2670109	3.95E-19	21.96867407	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767 [At3g16470.1]
A_84_P101906	At1g70700.1	22.55245524	2.03E-19	21.35977137	4.61E-19	21.95611331	expressed protein [At1g70700.1]
A_84_P79105	At1g66860.1	20.40088736	4.01E-19	23.23651008	4.32E-19	21.81869872	expressed protein similar to Hypothetical protein RP404. (Swiss-Prot:Q9ZDC7) [Rickettsia prowazekii]; similar to Hypothetical protein yvdE homolog (Fragment) (Swiss-Prot:P22347) [Lactococcus lactis] [At1g66860.1]
A_84_P14672	At1g23850.1	10.69915015	1.6E-17	32.10784649	2.8E-19	21.40349832	expressed protein [At1g23850.1]
A_84_P16942	At5g64120.1	15.61061641	9.82E-19	26.95032938	2.19E-19	21.28047289	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gil1483222lemblCAA67551 [At5g64120.1]
A_84_P16943	At1g52410.1	24.37811042	1.54E-19	17.92453764	9.91E-19	21.15132403	caldesmon-related weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957) [Gallus gallus] [At1g52410.1]
A_84_P73644	At3g59930.1	28.58156482	1.54E-19	13.71257589	1.86E-17	21.14707036	expressed protein [At3g59930.1]
A_84_P229729	At2g20142.1	30.90908411	9.88E-20	11.34831109	2.31E-17	21.1286976	expressed protein [At2g20142.1]
A_84_P23919	At2g35980.1	20.73170694	5.09E-17	21.46957905	6.39E-15	21.100643	harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (GI:1619321) [Nicotiana tabacum]; identical to cDNA YLS9 mRNA for hin1 homolog GI:13122295 [At2g35980.1]
A_84_P524680	At5g13220.2	17.56301957	5.33E-19	24.54829635	2.85E-19	21.05565796	expressed protein [At5g13220.2]
A_84_P18001	At1g65500.1	25.08835546	2.6E-19	16.8652091	4.38E-18	20.97678228	expressed protein [At1g65500.1]
A_84_P16777	At5g07010.1	28.2369136	5.04E-17	13.69389927	7.45E-12	20.96540643	sulfotransferase family protein similar to steroid sulfotransferase 3 [Brassica napus] GI:3420008, steroid sulfotransferase 1 [Brassica napus] GI:3420004; contains Pfam profile PF00685: Sulfotransferase domain [At5g07010.1]
A_84_P610481	At2g34600.1	17.1400047	9.12E-19	24.78404906	4.61E-19	20.96202688	expressed protein [At2g34600.1]
A_84_P530502	At2g34820.1	9.457542143	1.97E-16	32.37625024	1.92E-18	20.91689619	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain [At2g34820.1]
A_84_P12086	At5g19100.1	21.76781507	3.69E-15	19.90521294	8.49E-15	20.836514	extracellular dermal glycoprotein-related / EDGP-related low similarity to extracellular dermal glycoprotein EDGP precursor [Daucus carota] GI:285741, SPIP13917 Basic 7S globulin precursor {Glycine max} [At5g19100.1]
A_84_P740321	CHR3v0121200	22.50397578	2.33E-19	19.11289616	1.46E-18	20.80843597	Unknown
A_84_P13493	At2g30670.1	31.17647041	2.15E-19	10.37037098	8.5E-14	20.7734207	tropinone reductase, putative / tropine dehydrogenase, putative similar to tropinone reductase SP:P50165 from [Datura stramonium] [At2g30670.1]
A_84_P11129	At5g14180.1	17.85387716	5.03E-19	23.28243426	3.62E-19	20.56815571	lipase family protein similar to SPIQ64194 Lysosomal acid lipase/cholesteryl ester hydrolase precursor (EC 3.1.1.13) {Rattus norvegicus}; contains Pfam profile PF04083: ab-hydrolase associated lipase region [At5g14180.1]
A_84_P505670	At2g36080.1	20.52896516	3.17E-19	20.58346986	6.4E-19	20.55621751	DNA-binding protein, putative strong similarity to DNA-binding proteins from [Arabidopsis thaliana] RAV1 GI:3868857, RAV2 GI:3868859; contains Pfam profile PF02362: B3 DNA binding domain [At2g36080.1]
A_84_P11903	At1g06160.1	23.90110146	1.63E-19	16.91517268	1.35E-18	20.40813707	ethylene-responsive factor, putative similar to ethylene response factor 1 GB:AAD03544 GI:4128208 from [Arabidopsis thaliana] [At1g06160.1]
A_84_P18072	At1g72520.1	12.43956128	1.02E-17	28.36237224	2.88E-19	20.40096676	lipoxygenase, putative similar to lipoxygenase gi:1495804 [Solanum tuberosum], gi:1654140 [Lycopersicon esculentum], GB:CAB56692 [Arabidopsis thaliana] [At1g72520.1]
A_84_P11802	At3g46690.1	22.1381598	4.29E-19	18.16177119	1.66E-16	20.14996549	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At3g46690.1]
A_84_P17866	At1g01680.1	30.41237541	1.86E-17	9.259257446	4.2E-13	19.83581643	U-box domain-containing protein [At1g01680.1]
A_84_P15207	At1g14120.1	28.31818703	2.27E-19	11.35014718	2.72E-17	19.8341671	2-oxoglutarate-dependent dioxygenase, putative similar to adventitious rooting related oxygenase ARRO-1 from Malus x domestica, gil3492806; contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily [At1g14120.1]
A_84_P113182	At4g39670.1	9.543649106	1.38E-16	30.00000841	4.28E-19	19.77182876	expressed protein [At4g39670.1]
A_84_P13546	At2g42360.1	25.06061649	2.2E-19	14.4654099	1.44E-17	19.76301319	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) [At2g42360.1]

A_84_P280890	At3g10320.1	26.96477331	1.12E-16	12.17273797	2.49E-09	19.56875564	expressed protein contains Pfam domain, PF04577: Protein of unknown function (DUF563) [At3g10320.1]
A_84_P128906	At2g15390.1	26.71233525	1.47E-19	12.4161088	1.46E-17	19.56422203	xyloglucan fucosyltransferase, putative (FUT4) identical to SPIQ9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AtFUT4) {Arabidopsis thaliana}; similar to SPIQ9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan...
A_84_P12305	At1g52050.1	23.63388668	8.16E-16	14.9863755	1.67E-11	19.31013109	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain [At1g52050.1]
A_84_P19294	At1g26380.1	24.23123447	5.4E-16	13.88564415	9.6E-11	19.05843931	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At1g26380.1]
A_84_P15382	At2g30770.1	19.94474814	4.33E-18	17.99999998	5.74E-17	18.97237406	cytochrome P450 71A13, putative (CYP71A13) Identical to Cytochrome P450 71A13 (SP:O49342) [Arabidopsis thaliana]; similar to Cytochrome P450 (gi:5713172) [Nicotiana tabacum]. [At2g30770.1]
A_84_P82539	At1g14870.1	21.66665597	3.4E-19	16.20787446	4.38E-18	18.93726522	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614 [At1g14870.1]
A_84_P163493	At5g26260.1	21.35592526	2.48E-17	16.47058623	3.93E-15	18.91325574	meprin and TRAF homology domain-containing protein / MATH domain-containing protein similar to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain [At5g26260.1]
A_84_P106016	At1g15125.1	24.8520852	1.58E-19	12.9533675	7.89E-18	18.90272635	S-adenosyl-L-methionine:carboxyl methyltransferase family protein low similarity to caffeine synthase [Camellia sinensis] GI:9967143; contains Pfam profile PF03492: SAM dependent carboxyl methyltransferase [At1g15125.1]
A_84_P15752	At4g29690.1	19.68610241	1.89E-18	17.86207772	1.61E-16	18.77409007	type I phosphodiesterase/nucleotide pyrophosphatase family protein similar to SPIP22413 Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide...
A_84_P21194	At3g23240.1	26.10525417	1.54E-19	11.34593894	2.2E-17	18.72559655	ethylene-responsive factor 1 / ethylene response factor 1 (ERF1) identical to ethylene response factor 1 GB:AAD03544 from [Arabidopsis thaliana] [At3g23240.1]
A_84_P564785	At1g14250.1	25.59006665	1.33E-19	11.41892157	1.54E-17	18.50449411	nucleoside phosphatase family protein / GDA1/CD39 family protein low similarity to SPIP97687 Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) {Rattus norvegicus}; contains Pfam profile PF01150: GDA1/CD39 (nucleoside...
A_84_P21573	At5g38120.1	12.18487208	5.54E-18	24.62599992	2.99E-19	18.405436	4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to 4CL2, Arabidopsis thaliana [gi:12229665], 4CL1, Nicotiana tabacum [gi:12229631]; contains Pfam AMP-binding enzyme domain PF00501 [At5g38120.1]
A_84_P15531	At3g26500.1	23.72504634	2.33E-19	12.74314083	2.96E-17	18.23409358	leucine-rich repeat family protein [At3g26500.1]
A_84_P206058	At4g37290.1	26.91326653	1.12E-16	9.15094097	1.46E-13	18.03210375	expressed protein [At4g37290.1]
A_84_P12972	At4g36700.1	27.17537428	9.26E-17	8.737373117	3.54E-13	17.9563737	cupin family protein low similarity to preproMP27-MP32 from Cucurbita cv. Kurokawa Amakuri [GI:691752]; contains Pfam profile PF00190: Cupin [At4g36700.1]
A_84_P11360	At1g52040.1	16.74155929	6.64E-19	18.99122418	7.47E-19	17.86639174	jacalin lectin family protein nearly identical to myrosinase-binding protein homolog GI:2997767 from [Arabidopsis thaliana]; contains Pfam profile PF01419 jacalin-like lectin domain; identical to cDNA myrosinase-binding protein homolog GI:2997766...
A_84_P11446	At1g15520.1	12.77669419	7.52E-18	22.76881652	6.25E-19	17.77275536	ABC transporter family protein similar to ABC1 protein GI:14331118 from [Nicotiana plumbaginifolia] [At1g15520.1]
A_84_P18293	At2g25470.1	23.21428594	1.12E-15	12.31824054	1.88E-09	17.76626324	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to disease resistance protein [Lycopersicon esculentum] gil3894383lgblAAC78591 [At2g25470.1]
A_84_P21841	At1g02930.1	24.39351916	1.54E-19	10.99999986	2.13E-17	17.69675951	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus] [At1g02930.1]
A_84_P595805	At5g36925.1	20.91583951	8.53E-15	14.43661597	4.19E-11	17.67622774	expressed protein [At5g36925.1]
A_84_P268790	At5g43350.1	19.82366764	5.08E-19	15.31645799	2.39E-17	17.57006282	inorganic phosphate transporter (PHT1) (PT1) identical to inorganic phosphate transporter [Arabidopsis thaliana] GI:2258116 [At5g43350.1]
A_84_P18030	At1g30720.1	24.51923394	4.22E-16	10.25316705	0.00000013	17.38620049	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At1g30720.1]
A_84_P18553	At4g21390.1	18.67186979	1.66E-18	16.02510606	1.63E-17	17.34848792	S-locus lectin protein kinase family protein contains Pfam profiles: PF00954 S-locus glycoprotein family, PF00069 protein kinase domain, PF01453 lectin (probable mannose binding) [At4g21390.1]
A_84_P21931	At1g28370.1	19.93333225	3.22E-19	14.44914478	3.3E-18	17.19123852	ERF domain protein 11 (ERF11) identical to ERF domain protein 11 (AtERF11) GI:15207789 from [Arabidopsis thaliana] [At1g28370.1]
A_84_P15590	At3g48850.1	21.09275152	7.24E-15	13.06954762	4.59E-10	17.08114957	mitochondrial phosphate transporter, putative similar to mitochondrial phosphate transporter GI:3318617 from [Arabidopsis thaliana] [At3g48850.1]
A_84_P16072	At1g65690.1	21.93676678	3.1E-19	12.20560413	2.53E-17	17.07118546	harpin-induced protein-related / HIN1-related / harpin-responsive protein-related similar to hin1 homolog (GI:13122296) [Arabidopsis thaliana]; similar to hin1 (GI:22830759) [Nicotiana tabacum]; contains 1 transmembrane domain; [At1g65690.1]
A_84_P564785	At1g14250.1	18.92551298	1.33E-19	14.92957509	1.54E-17	16.92754403	nucleoside phosphatase family protein / GDA1/CD39 family protein low similarity to SPIP97687 Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) {Rattus norvegicus}; contains Pfam profile PF01150: GDA1/CD39 (nucleoside...
A_84_P726268	CHR4v012120	12.58064775	1.14E-16	21.19815795	6.82E-15	16.88940285	Unknown
A_84_P536372	At5g66640.1	19.85383221	2.46E-14	13.50737382	1.25E-10	16.68060302	LIM domain-containing protein-related contains low similarity to Pfam profile PF00412: LIM domain [At5g66640.1]
A_84_P222669	At1g76930.1	20.08797732	3.1E-19	12.85714843	6.83E-18	16.47256288	proline-rich extensin-like family protein contains extensin-like region, Pfam:PF04554 [At1g76930.1]
A_84_P19115	At2g43590.1	17.23202568	5.79E-19	15.71181345	1.99E-18	16.47191956	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43590.1]
A_84_P18416	At3g46080.1	17.42647056	1.99E-18	15.39924058	1.31E-17	16.41285557	zinc finger (C2H2 type) family protein contains zinc finger, C2H2 type, domain, PROSITE:PS00028 [At3g46080.1]
A_84_P16138	At1g30700.1	18.5106455	3.18E-15	13.76623559	1.28E-10	16.13844054	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At1g30700.1]
A_84_P23284	At4g21680.1	10.10694795	3.11E-14	22.05323353	3.86E-15	16.08009074	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At4g21680.1]
A_84_P18510	At4g04490.1	22.65717366	3.74E-16	9.487181186	3.21E-10	16.07217742	protein kinase family protein contains Pfam PF00069: Protein kinase domain [At4g04490.1]
A_84_P613251	At3g18250.1	13.55828409	1.26E-17	17.94392263	4.66E-15	15.75110336	expressed protein ; expression supported by MPSS [At3g18250.1]
A_84_P13801	At4g11650.1	19.39586887	4.18E-19	11.94617371	2.62E-17	15.67102129	osmotin-like protein (OSM34) nearly identical to SPIP50700IOSL3_ARATH Osmotin-like protein OSM34 precursor {Arabidopsis thaliana}; contains Pfam profile PF00314: Thaumatin family [At4g11650.1]
A_84_P141619	At1g66870.1	21.71136761	3.91E-15	9.47955542	0.000000786	15.59546152	glycosyl hydrolase family protein 17 similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from [Triticum aestivum] [At1g66870.1]
A_84_P12788	At3g55970.1	15.95577744	8.68E-19	14.63877575	3E-18	15.29727659	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygenase, Malus domestica, SPIP51091; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family [At3g55970.1]
A_84_P18624	At4g38540.1	18.44396592	4.29E-19	12.07048215	1.07E-17	15.25722404	monooxygenase, putative (MO2) identical to GI:3426064 [At4g38540.1]
A_84_P18989	At1g16420.1	14.11428948	1.47E-16	16.36747647	2.64E-14	15.24088298	latex-abundant protein, putative (AMC8) / caspase family protein similar to latex-abundant protein [Hevea brasiliensis] gb:AAD13216; contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain [At1g16420.1]
A_84_P83519	At1g62225.1	12.3118299	8.9E-16	18.12339586	2.2E-13	15.21761288	expressed protein [At1g62225.1]
A_84_P11606	At2g29480.1	22.05882438	2.98E-15	8.36492613	0.0000101	15.21187526	glutathione S-transferase, putative similar to Glutathione S-Transferase [Arabidopsis thaliana] gi:940381l16226389lgblAF428387. [At2g29480.1]
A_84_P17343	At2g44840.1	9.684603606	2.97E-17	20.72493971	5.24E-19	15.20477166	ethylene-responsive element-binding protein, putative [At2g44840.1]
A_84_P17268	At2g14610.1	21.2142872	6.09E-18	9.182389947	2.16E-12	15.19833857	pathogenesis-related protein 1 (PR-1) identical to GB:M90508 SPIP33154 [At2g14610.1]
A_84_P14505	At2g32140.1	20.05457517	1.85E-14	10.22727292	8.18E-14	15.14092405	disease resistance protein (TIR class), putative domain signature TIR exists, suggestive of a disease resistance protein. [At2g32140.1]
A_84_P14299	At1g75040.1	18.02197228	4.69E-19	12.07264595	1.04E-17	15.04730912	pathogenesis-related protein 5 (PR-5) identical to SPIP28493 Pathogenesis-related protein 5 precursor (PR-5) {Arabidopsis thaliana}; contains Pfam profile: PF00314 Thaumatin family [At1g75040.1]
A_84_P12373	At1g14240.1	19.7604706	3.25E-19	10.30946813	3.42E-17	15.03496936	nucleoside phosphatase family protein / GDA1/CD39 family protein low similarity to nod factor binding lectin-nucleotide phosphohydrolase [Dolichos biflorus] GI:4868375; contains Pfam profile PF01150: GDA1/CD39 (nucleoside phosphatase) family...
A_84_P186914	At3g11480.1	8.384615927	1.86E-16	21.60714271	2.53E-18	14.99587932	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to SAM:benzoic acid carboxyl methyltransferase (BAMT)[GI:9789277][Antirrhinum majus] and to SAM:salicylic acid carboxyl methyltransferase (SAMT)[GI:6002712][Clarkia breweri]...
A_84_P711324	CHR1v012120	13.98514493	7.54E-11	15.70743604	5.41E-12	14.84629048	Unknown
A_84_P11920	At4g13860.1	16.21117323	7.92E-17	13.28358453	3.76E-14	14.74737888	glycine-rich RNA-binding protein, putative similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor (AtGRP2) (Swiss-Prot:Q9SVM8) [Arabidopsis thaliana] ; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif)...
A_84_P11194	At5g44390.1	17.86236992	6.03E-19	11.5171456	2.12E-17	14.68975776	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At5g44390.1]
A_84_P592168	At5g05300.1	18.53211327	2.98E-18	10.79645516	3.38E-15	14.66428421	expressed protein similar to unknown protein (gblAAF01528.1); expression supported by MPSS [At5g05300.1]
A_84_P16848	At5g39580.1	18.21561753	5.17E-19	10.77727994	3.99E-17	14.49644874	peroxidase, putative identical to peroxidase ATP24a [Arabidopsis thaliana] gil1890313lemblCAA72484 [At5g39580.1]
A_84_P20061	At2g43580.1	13.15136827	1.01E-17	15.76922769	6.56E-17	14.46029798	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43580.1]
A_84_P21275	At3g50930.1	14.89532916	1.97E-18	13.99160635	5.86E-18	14.44346776	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 [At3g50930.1]
A_84_P725988	CHR2v012120	15.69343216	4.27E-12	13.16648736	1.27E-10	14.42995976	AV440386 Arabidopsis thaliana above-ground organ two to six-week old Arabidopsis thaliana cDNA clone APD60g01_f 3', mRNA sequence [AV440386]
A_84_P18976	At1g30730.1	18.7563734	2.85E-15	9.964370738	0.000000241	14.36037207	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At1g30730.1]
A_84_P20425	At4g12480.1	19.17126061	4.11E-18	9.532158891	3.67E-13	14.35170975	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein identical to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease...
A_84_P286390	At3g25780.1	15.73704324	6.1E-18	12.86907362	2.6E-17	14.30305843	allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; similar to early-responsive to dehydration (ERD12) protein...
A_84_P15199	At1g59950.1	17.57812517	3.38E-13	10.94872068	2.99E-08	14.26342292	aldo/keto reductase, putative similar to NADPH-dependent codeinone reductase GI:6478210 [Papaver somniferum], NAD(P)H dependent 6'-deoxychalcone synthase [Glycine max][GI:18728] [At1g59950.1]
A_84_P69204	At1g21110.1	11.31979558	3.72E-17	17.09029743	4.45E-18	14.2050465	O-methyltransferase, putative similar to GI:2781394 [At1g21110.1]
A_84_P22966	At2g44480.1	15.98173353	1.38E-17	12.38095246	1.18E-14	14.181343	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) [Prunus serotina] [At2g44480.1]
A_84_P10039	At1g27020.1	15.30487652	1.1E-18	12.96296917	6.69E-18	14.13392284	expressed protein [At1g27020.1]
A_84_P18172	At2g19970.1	13.52657141	1.89E-16	14.63767993	8.83E-15	14.08212567	pathogenesis-related protein, putative similar to pathogenesis-related protein 1 {Arabidopsis thaliana} GI:166805; contains Pfam profile PF00188: SCP-like extracellular protein [At2g19970.1]
A_84_P235603	At1g58190.1	19.58621335	3.15E-14	8.452220473	0.00000934	14.01921691	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.2 [Lycopersicon pimpinellifolium] gil1184077lgblAAC15780 [At1g58190.1]
A_84_P541993	At2g27310.1	17.16980798	6.14E-19	10.84112222	2.44E-17	14.0054651	F-box family protein contains Pfam PF00646: F-box domain;; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 [At2g27310.1]
A_84_P23149	At3g46660.1	19.04161579	6E-14	8.795622583	0.00000394	13.91861919	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At3g46660.1]
A_84_P572262	At3g10815.1	14.01575542	9.16E-15	13.61322519	1.49E-10	13.81449031	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) [At3g10815.1]
A_84_P18359	At3g25250.1	11.65384482	5.87E-09	15.7831351	4.6E-12	13.71848996	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At3g25250.1]
A_84_P562774	At5g12340.1	12.6301354	8.28E-10	14.76063825	2.56E-11	13.69538682	expressed protein ; expression supported by MPSS [At5g12340.1]
A_84_P18540	At4g18170.1	17.81955371	5.17E-19	9.333330608	9.52E-17	13.57644216	WRKY family transcription factor similar to DNA-binding protein 2 GI:4322940 from [Nicotiana tabacum]; contains Pfam profile: PF03106 WRKY DNA -binding domain [At4g18170.1]
A_84_P172221	At4g27860.1	14.54114632	1.46E-18	12.33153937	9.04E-18	13.43634284	integral membrane family protein contains Pfam PF01988: Integral membrane protein [At4g27860.1]
A_84_P17210	At1g51890.1	15.4609954	2.51E-16	11.39999906	0.000000011	13.43049723	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gil1321686lemblCAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069...
A_84_P14118	At5g67310.1	18.15789048	7.02E-17	8.611422067	0.00000617	13.38465627	cytochrome P450 family protein [At5g67310.1]
A_84_P726774	CHR4v012120	14.20518288	1.01E-11	12.50000096	1.49E-09	13.35259192	T055 tyrosine transaminase homolog F9D16.70 - Arabidopsis thaliana, partial (23%) [AI996914]
A_84_P11822	At3g51450.1	16.13662541	8.06E-19	10.52173635	2.96E-17	13.32918088	strictosidine synthase family protein similar to hemomucin [Drosophila melanogaster][GI:1280434], strictosidine synthase [Rauvolfia serpentina][SPIP15324] [At3g51450.1]
A_84_P18925	At1g61610.1	16.99248566	6.51E-19	9.54081824	7.19E-17	13.26665195	S-locus lectin protein kinase family protein similar to KI domain interacting kinase 1 [Zea mays] gil2735017lgblAAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954 [At1g61610.1]
A_84_P169033	At1g65970.1	16.61585585	9.21E-19	9.872727449	1.54E-16	13.24429165	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 [At1g65970.1]
A_84_P21341	At4g02330.1	16.55737429	7.24E-19	9.797293092	5.32E-17	13.17733369	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase [At4g02330.1]
A_84_P54570	At3g61930.1	10.29762119	1.01E-13	15.96009905	3.73E-12	13.12886012	expressed protein [At3g61930.1]

A_84_P556661	At5g43230.1	14.2857156	4.44E-11	11.93317219	3.3E-09	13.10944389	hypothetical protein [At5g43230.1]
A_84_P280220	At2g32210.1	11.04827554	2.13E-08	15.1351325	1.2E-11	13.09170402	expressed protein [At2g32210.1]
A_84_P84999	At3g28580.1	14.6923025	1.52E-18	11.36363427	2E-17	13.02796838	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 [At3g28580.1]
A_84_P69564	At3g21710.1	11.68514232	2.12E-17	14.36507281	4.6E-17	13.02510756	expressed protein [At3g21710.1]
A_84_P13104	At5g49520.1	9.553567725	1.38E-14	16.29999594	4.12E-14	12.92678183	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain [At5g49520.1]
A_84_P611334	At2g22880.1	9.605268882	7.11E-17	16.02649459	3.1E-18	12.81588174	VQ motif-containing protein contains PF05678: VQ motif [At2g22880.1]
A_84_P89769	At2g35930.1	9.90740343	3.05E-17	15.63786225	2.69E-18	12.77263284	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200; contains Pfam profile PF04564: U-box domain [At2g35930.1]
A_84_P21986	At2g22760.1	8.01388996	0.001553044	17.29729335	3.81E-09	12.65559165	Unknown
A_84_P236643	At1g44350.1	13.90710766	1.95E-18	11.16592913	1.86E-17	12.53651839	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...
A_84_P23380	At5g01540.1	12.67715405	4.07E-18	12.38195744	1.11E-17	12.52955574	lectin protein kinase, putative similar to receptor lectin kinase 3 [Arabidopsis thaliana] gil4100060lgblAAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139 [At5g01540.1]
A_84_P11721	At3g15500.1	13.36841759	2.56E-18	11.61111006	1.47E-17	12.48976383	no apical meristem (NAM) family protein (NAC3) identical to AtNAC3 [Arabidopsis thaliana] GI:12060424; contains Pfam PF02365: No apical meristem (NAM) domain; similar to jasmonic acid 2 GB:AAF04915 from [Lycopersicon esculentum] [At3g15500.1]
A_84_P701779	CHR3v012120	13.40153918	6.79E-18	11.47608775	3.6E-17	12.43881347	AV522912 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APZL09g03F 3', mRNA sequence [AV522912]
A_84_P12620	At2g02990.1	9.312171318	4.75E-17	15.49295357	3.53E-18	12.40256244	ribonuclease 1 (RNS1) identical to ribonuclease SP:P42813 Ribonuclease 1 precursor (EC 3.1.27.1) {Arabidopsis thaliana}, GI:561998 from [Arabidopsis thaliana] [At2g02990.1]
A_84_P15993	At5g63450.1	8.356163378	2.62E-10	16.16279279	3.03E-12	12.25947809	cytochrome P450, putative [At5g63450.1]
A_84_P193424	At1g19180.1	11.82941644	5.74E-18	12.64501637	7.51E-18	12.23721641	expressed protein [At1g19180.1]
A_84_P16057	At1g45145.1	14.92956991	1.24E-18	9.226360732	9.16E-17	12.07796532	thioredoxin H-type 5 (TRX-H-5) (TOUL) identical to SPIQ39241 Thioredoxin H-type 5 (TRX-H-5) {Arabidopsis thaliana}; identical to cDNA (TOUL) mRNA for thioredoxin GI:992965 [At1g45145.1]
A_84_P212918	At4g39030.1	12.29592189	4.62E-18	11.74311381	1.34E-17	12.01951785	enhanced disease susceptibility 5 (EDS5) / salicylic acid induction deficient 1 (SID1) identical to SPIQ945F0; contains Pfam profile PF01554: Uncharacterized membrane protein family [At4g39030.1]
A_84_P152118	At1g52200.1	15.31250065	1.11E-18	8.580246529	2.38E-16	11.94637359	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614 [At1g52200.1]
A_84_P611898	At5g59580.1	12.71683546	5.52E-16	11.17503155	6.46E-18	11.9459335	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At5g59580.1]
A_84_P223429	At5g43650.1	10.7894708	3.76E-08	13.0820978	4.46E-10	11.9357843	basic helix-loop-helix (bHLH) family protein similar to unknown protein (pirllT04030) [At5g43650.1]
A_84_P733533	CHR3v012120	13.35877673	2.18E-10	10.44524698	0.000000085	11.90201185	Unknown
A_84_P10160	At5g07100.1	14.82268605	1.32E-18	8.937730229	1.3E-16	11.88020814	WRKY family transcription factor SPF1 protein - Ipomoea batatas (sweet potato), PIR:S51529 [At5g07100.1]
A_84_P22181	At3g28210.1	12.56173034	2.24E-17	11.16838596	2.39E-16	11.86505815	zinc finger (AN1-like) family protein contains Pfam profile: PF01428 AN1-like zinc finger [At3g28210.1]
A_84_P249535	At1g13340.1	11.55830949	8.63E-18	12.14642963	2.04E-17	11.85236956	expressed protein contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292 [At1g13340.1]
A_84_P13393	At1g66090.1	11.83999692	6.61E-18	11.76211829	1.33E-17	11.8010576	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein. [At1g66090.1]
A_84_P56360	At5g57010.1	11.52380701	6.66E-16	12.05555363	2.84E-15	11.78968032	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif [At5g57010.1]
A_84_P88159	At2g45360.1	12.83185465	1.45E-13	10.6738549	5.45E-08	11.75285478	expressed protein [At2g45360.1]
A_84_P52340	At3g26840.1	14.40734107	2.3E-18	9.072465717	2.12E-16	11.73990339	esterase/lipase/thioesterase family protein contains Pfam profile PF03096: Ndr family [At3g26840.1]
A_84_P21945	At1g32350.1	12.1653574	8.1E-17	11.17187785	6.23E-13	11.66861763	alternative oxidase, putative similar to Alternative oxidase 1a, mitochondrial precursor from Arabidopsis thaliana [SPIQ39219], alternative oxidase 2, mitochondrial precursor from Nicotiana tabacum [SPIQ40578]; contains Pfam profile PF01786...
A_84_P703001	CHR4v012120	15.08064679	1.55E-15	8.199999376	5.88E-11	11.64032308	Unknown
A_84_P20248	At3g23230.1	8.34261923	0.0000103	14.71389708	2.75E-11	11.52825815	ethylene-responsive factor, putative similar to EREBP-4 GB:BAA07323 from [Nicotiana tabacum] [At3g23230.1]
A_84_P13078	At5g42650.1	11.05768137	9.1E-18	11.90475479	1.12E-17	11.48121808	allene oxide synthase (AOS) / hydroperoxide dehydrase / cytochrome P450 74A (CYP74A) identical to Allene oxide synthase, chloroplast precursor (Hydroperoxide dehydrase) (Cytochrome P450 74A) (SP:Q96242) {Arabidopsis thaliana} [At5g42650.1]
A_84_P175491	At5g62520.1	13.79691203	7.2E-12	9.081012741	0.00000198	11.43896239	expressed protein [At5g62520.1]
A_84_P226889	At4g20000.1	9.598659896	7.17E-16	13.21353156	2.16E-12	11.40609573	VQ motif-containing protein contains PF05678: VQ motif [At4g20000.1]
A_84_P13077	At5g42380.1	12.12328695	9.14E-17	10.62761968	5.32E-17	11.37545331	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana tabacum] [At5g42380.1]
A_84_P11789	At3g43250.1	11.13184407	1.76E-08	11.60566672	7.46E-09	11.3687554	cell cycle control protein-related contains similarity to Swiss-Prot:Q9P7C5 cell cycle control protein cwf16 [Schizosaccharomyces pombe] [At3g43250.1]
A_84_P220868	At2g17740.1	13.0281714	3.37E-14	9.501134557	0.000000739	11.26465298	DC1 domain-containing protein [At2g17740.1]
A_84_P704033	CHR1v012120	10.71789662	6.32E-10	11.77515136	2.99E-14	11.24652399	10709 Lambda-PRL2 Arabidopsis thaliana cDNA clone 148F11T7, mRNA sequence [T75931]
A_84_P23455	At1g68620.1	14.22459824	2.02E-18	8.243844544	5.01E-16	11.23422139	expressed protein similar to PrMC3 [Pinus radiata] GI:5487873 [At1g68620.1]
A_84_P16882	At5g48540.1	13.90533118	1.99E-18	8.235293115	3.24E-16	11.07031215	33 kDa secretory protein-related contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa secretory proteins [At5g48540.1]
A_84_P139169	At1g67810.1	13.72603183	8.53E-18	8.295458368	1.16E-14	11.0107451	Fe-S metabolism associated domain-containing protein contains Pfam PF02657: Fe-S metabolism associated domain [At1g67810.1]
A_84_P13916	At4g36430.1	11.69653012	7.64E-18	10.26578467	7.22E-17	10.9811574	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gil6822093lemblCAB71009; identical to cDNA class III peroxidase ATP31, GI:17530561 [At4g36430.1]
A_84_P23274	At1g29290.1	12.46835299	2.69E-15	9.407897879	2.38E-12	10.93812544	expressed protein [At1g29290.1]
A_84_P10611	At2g43530.1	11.4875959	7.35E-18	10.36496687	3.11E-17	10.92628138	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) {Sinapis alba} [At2g43530.1]
A_84_P17614	At4g23210.1	9.603173214	2.52E-15	12.24137915	4.64E-13	10.92227618	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain [At4g23210.1]
A_84_P197444	At3g22160.1	12.29885411	4.46E-18	9.210522496	9.63E-17	10.7546883	VQ motif-containing protein contains PF05678: VQ motif [At3g22160.1]
A_84_P146458	At5g24290.1	12.64285777	4.08E-18	8.756219984	1.71E-16	10.69953888	integral membrane family protein contains Pfam domain PF01988: Integral membrane protein [At5g24290.1]
A_84_P12888	At4g23600.1	12.47618115	4.11E-18	8.823540731	1.3E-16	10.64986094	coronatine-responsive tyrosine aminotransferase / tyrosine transaminase similar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:6469087]; contains Pfam profile PF00155 aminotransferase, classes I and II; identical to cDNA...
A_84_P12877	At4g20860.1	11.7857168	6.29E-18	9.42857406	9E-17	10.60714543	FAD-binding domain-containing protein simlar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At4g20860.1]
A_84_P20213	At3g04000.1	12.19917094	4.73E-18	8.944951748	1.37E-16	10.57206134	short-chain dehydrogenase/reductase (SDR) family protein similar to SPIQ08632 Short-chain type dehydrogenase/reductase (EC 1.-.-.-) {Picea abies}; contains Pfam:PF00106 oxidoreductase, short chain dehydrogenase/reductase family [At3g04000.1]
A_84_P206488	At1g35230.1	12.49032404	1.14E-09	8.449152279	0.000000008	10.46973816	arabinogalactan-protein (AGP5) identical to gi_3883128_gb_AAC77827 [At1g35230.1]
A_84_P12640	At3g01420.1	9.962408026	0.000000233	10.8907394	3.54E-08	10.42657371	pathogen-responsive alpha-dioxygenase, putative similar to pathogen-inducible alpha-dioxygenase [Nicotiana attenuata] GI:12539609; contains Pfam profile PF03098: Animal haem peroxidase [At3g01420.1]
A_84_P13494	At2g36690.1	11.19265894	6.6E-12	9.571234395	0.000000712	10.38194667	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to IDS3 [Hordeum vulgare][GI:4514655], leucoanthocyanidin dioxygenase [SPIP51091][Malus domestica]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain [At2g36690.1]
A_84_P211958	At5g43580.1	11.0952387	9.42E-18	9.59677321	7.82E-17	10.34600595	protease inhibitor, putative similar to SPIP19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}; contains Pfam profile PF00280: Potato inhibitor I family [At5g43580.1]
A_84_P23398	At5g06870.1	11.76055631	5.89E-18	8.823529111	1.32E-16	10.29204271	polygalacturonase inhibiting protein 2 (PGIP2) identical to polygalacturonase inhibiting protein 2 (PGIP2) [Arabidopsis thaliana] gil7800201lgblAAF69828; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611 [At5g06870.1]
A_84_P23654	At1g52000.1	12.11573648	4.77E-18	8.449438667	2.19E-16	10.28258758	jacalin lectin family protein similar to myrosinase binding protein [Brassica napus] GI:1711296, myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile: PF01419 jacalin-like lectin domain [At1g52000.1]
A_84_P66214	At3g02840.1	10.55118769	2.2E-12	9.999999342	2.77E-15	10.27559352	immediate-early fungal elicitor family protein similar to immediate-early fungal elicitor protein CMPG1 (GI:14582200) [Petroselinum crispum] [At3g02840.1]
A_84_P19210	At2g46400.1	10.87324006	1.09E-17	9.662918544	6.02E-17	10.2680793	WRKY family transcription factor [At2g46400.1]
A_84_P159845	At3g28290.1	8.163264482	1.56E-16	12.29165863	9.13E-18	10.22746155	integrin-related protein 14a identical to At14a protein GI:11994573 [Arabidopsis thaliana] [Gene 230 (1), 33-40 (1999)], At14a protein [Arabidopsis thaliana] GI:4589123 [At3g28290.1]
A_84_P521700	At3g04300.1	9.841268601	7.8E-11	10.60676864	6.07E-08	10.22401862	expressed protein [At3g04300.1]
A_84_P14331	At1g76650.1	10.12270251	2.24E-17	10.11718692	4.12E-17	10.11994472	calcium-binding EF hand family protein similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana tabacum]; contains INTERPRO:IPR002048 calcium-binding EF-hand domain [At1g76650.1]
A_84_P10439	At1g09080.1	9.677423513	3.56E-16	10.51281774	1.54E-14	10.09512063	luminal binding protein 3 (BiP-3) (BP3) Similar to Arabidopsis luminal binding protein (gblD89342); contains Pfam domain PF00012: dnaK protein [At1g09080.1]
A_84_P103016	At4g12500.1	10.50131797	2.31E-17	9.633026937	9.39E-16	10.06717245	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease...
A_84_P511454	At5g43570.1	11.91919255	1.88E-11	8.079800659	0.000021	9.999496603	serine protease inhibitor, potato inhibitor I-type family protein similar to SPIP24076 Glu S.griseus protease inhibitor (BGIA) {Momordica charantia}; contains Pfam profile PF00280: Potato inhibitor I family [At5g43570.1]
A_84_P21578	At5g39670.1	9.823631882	6.61E-17	10.09118155	8.04E-17	9.957406714	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain [At5g39670.1]
A_84_P270170	At1g21100.1	9.032679377	1.02E-16	10.75324812	1.19E-16	9.892963748	O-methyltransferase, putative similar to GI:2781394 [At1g21100.1]
A_84_P585099	At5g24200.1	10.89431211	2.97E-17	8.691908577	4.66E-16	9.793110346	expressed protein ; expression supported by MPSS [At5g24200.1]
A_84_P569018	At5g20770.1	8.320611159	2.22E-10	11.1805519	0.000000019	9.75058153	hypothetical protein [At5g20770.1]
A_84_P215028	At3g25770.1	8.604651725	9.23E-17	10.89285782	2.2E-17	9.748754772	allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative strong similarity to early-responsive to dehydration (ERD12) protein [GI:15320414]; similar to allene oxide cyclase GI:8977961 from...
A_84_P17453	At3g11180.1	8.321578987	0.00000901	11.06848913	2.37E-08	9.695034059	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygenase GB:BAA20143 [Perilla frutescens], Malus domestica, SPIP51091; contains PF03171 2OG-Fe(II) oxygenase superfamily domain [At3g11180.1]
A_84_P18552	At4g21120.1	8.063781235	2.37E-15	11.00558555	6.82E-14	9.534683391	amino acid permease family protein similar to cationic amino acid transporter-1 [Rattus norvegicus] GI:1589917; contains Pfam profile PF00324: Amino acid permease [At4g21120.1]
A_84_P61820	At1g17250.1	10.90000506	2.97E-17	8.064516273	3.48E-15	9.482260668	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-0B [Lycopersicon esculentum] gil3894387lgblAAC78593 [At1g17250.1]
A_84_P20289	At3g28270.1	9.132950411	5.13E-17	9.540232991	6.66E-17	9.336591701	expressed protein similar to At14a protein (GI:11994571 and GI:11994573) [Arabidopsis thaliana] [At3g28270.1]
A_84_P724781	CHR4v012120	10.26246929	0.000000106	8.339671749	0.0000112	9.30107052	BP604606 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-63-F08 3', mRNA sequence [BP604606]
A_84_P17278	At2g29440.1	10.32719824	2.2E-17	8.148601055	5.78E-16	9.237899647	glutathione S-transferase, putative [At2g29440.1]
A_84_P20166	At2g39200.1	10.14056267	5.95E-17	8.044162356	1.61E-14	9.092362512	seven transmembrane MLO family protein / MLO-like protein 12 (MLO12) identical to SPIO80961 MLO-like protein 12 (AtMlo12) {Arabidopsis thaliana}, membrane protein Mlo12 [Arabidopsis thaliana] gil14091594lgblAAK53805; similar to MLO protein...
A_84_P12547	At2g30750.1	8.928575373	8.46E-16	9.0058472	1.85E-12	8.967211287	cytochrome P450 71A12, putative (CYP71A12) Identical to Cytochrome P450 (SP:O49340) [Arabidopsis thaliana]; contains Pfam profile: PF00067 cytochrome P450 [At2g30750.1]
A_84_P718360	CHR3v012120	9.660196262	3.41E-09	8.169460455	0.00000175	8.914828359	Unknown
A_84_P20180	At2g32030.1	9.383889337	1.75E-14	8.279569752	1.84E-12	8.831729545	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family [At2g32030.1]
A_84_P12066	At5g11410.1	9.101123805	5.99E-17	8.365217201	3.49E-16	8.733170503	protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719 [At5g11410.1]
A_84_P12601	At2g42350.1	8.952378291	1.7E-13	8.455880568	1.9E-09	8.704129429	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger) [At2g42350.1]

A_84_P18737	At5g38710.1	8.246266006	1.5E-16	9.066669522	1.29E-16	8.656467764	proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative similar to proline oxidase, mitochondrial precursor (Osmotic stress- induced proline dehydrogenase) [Arabidopsis thaliana] SWISS-PROT:P92983 [At5g38710.1]
A_84_P211588	At4g24110.1	8.107641512	5.95E-16	9.071426907	7E-16	8.58953421	expressed protein [At4g24110.1]
A_84_P17613	At4g22950.1	8.95652316	8.46E-17	8.014182703	4.91E-16	8.485352932	MADS-box protein (AGL19) MADS-box protein AGL14, Arabidopsis thaliana, gb:U20184 [At4g22950.1]
A_84_P706671	CHR1v012120	8.130606085	0.00000398	8.825173857	0.0000038	8.477889971	AV541119 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clone RZ16d04F 3', mRNA sequence [AV541119]
A_84_P14449	At2g34810.1	8.545451388	9.92E-17	8.287032614	2.72E-16	8.416242001	FAD-binding domain-containing protein similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain [At2g34810.1]
A_84_P609600	At2g40200.1	8.012421404	3.03E-11	8.756753496	3.08E-09	8.38458745	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain [At2g40200.1]
A_84_P10171	At5g10300.1	8.666661756	8.82E-17	8.043013826	3.79E-16	8.354837791	hydrolase, alpha/beta fold family protein similar to ethylene-induced esterase [Citrus sinensis] GI:14279437, alpha-hydroxynitrile lyase [Manihot esculenta] GI:2780225; contains Pfam profile PF00561: hydrolase, alpha/beta fold family [At5g10300.1]

Probe Name	AGI code	1st experiment		2nd experiment		Average	Description
		Decrease	q-value	Decrease	q-value		
A_84_P12450	At1g75940.1	0.001898735	2.35E-20	0.002994154	3.74E-20	0.002446444	glycosyl hydrolase family 1 protein / anther-specific protein ATA27 contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; identical to anther-specific protein ATA27 (GI:2746341) [Arabidopsis...
A_84_P23763	At1g66850.1	0.00256542	2.35E-20	0.003240093	3.74E-20	0.002902757	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to GPI3062791 Lipid transfer protein {Brassica rapa}; contains Pfam profile: PF00234: protease inhibitor/seed storage/LTP family [At1g66850.1]
A_84_P17165	At1g67990.1	0.001641337	2.35E-20	0.004725663	3.74E-20	0.0031835	caffeoyl-CoA 3-O-methyltransferase, putative similar to GI:2960356 [Populus balsamifera subsp. trichocarpa], GI:684942 [Medicago sativa subsp. sativa] [At1g67990.1]
A_84_P24111	At1g62940.1	0.001261194	2.35E-20	0.005553121	3.74E-20	0.003407157	4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to gi:112801 from Petroselinum crispum, GB:AAD40664 from [Solanum tuberosum] (J. Biol. Chem. 266 (13), 8551-8559 (1991)); contains Pfam AMP-binding enzyme domain...
A_84_P12958	At4g14080.1	0.006086333	2.35E-20	0.003991343	3.74E-20	0.005038838	glycosyl hydrolase family 17 protein / anther-specific protein (A6) identical to probable glucan endo-1,3-beta-glucosidase A6 precursor SP:Q06915 from [Arabidopsis thaliana] [At4g14080.1]
A_84_P21510	At5g07530.1	0.002794117	2.35E-20	0.007462689	3.74E-20	0.005128403	glycine-rich protein (GRP17) olesin; glycine-rich protein 17 (GRP17) PMID:11431566; function: pollen recognition (PMID:10655594) [At5g07530.1]
A_84_P10877	At3g51590.1	0.007220773	2.35E-20	0.004409092	3.74E-20	0.005814933	lipid transfer protein, putative similar to lipid transfer protein E2 precursor, Brassica napus, PIR:T07984 [GI:899224]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 [At3g51590.1]
A_84_P15251	At1g69500.1	0.006357666	2.35E-20	0.005333333	3.74E-20	0.005845499	cytochrome P450 family protein similar to Cytochrome P450 86A2 (SP:O23066) [Arabidopsis thaliana]contains Pfam profile: PF00067: Cytochrome P450 [At1g69500.1]
A_84_P11283	At1g47980.1	0.00842623	2.35E-20	0.004130436	3.74E-20	0.006278333	expressed protein [At1g47980.1]
A_84_P21877	At1g75910.1	0.008385651	2.35E-20	0.004273503	3.74E-20	0.006329577	family II extracellular lipase 4 (EXL4) EXL4 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana (Mouse-ear cress)] [At1g75910.1]
A_84_P12424	At1g01280.1	0.004410482	2.35E-20	0.008811189	3.74E-20	0.006610836	cytochrome P450 family protein similar to cytochrome P450 GB:BAA92894 GI:7339658 from [Petunia hybrida] [At1g01280.1]
A_84_P584547	At1g68875.1	0.00491057	2.35E-20	0.009269566	8.43E-20	0.007090068	expressed protein [At1g68875.1]
A_84_P17290	At2g03740.1	0.004379747	2.35E-20	0.011304343	8.43E-20	0.007842045	late embryogenesis abundant domain-containing protein / LEA domain-containing protein similar to cold-regulated gene cor15b [Arabidopsis thaliana] GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein [At2g03740.1]
A_84_P19321	At3g13220.1	0.010960006	2.77E-20	0.006405578	3.74E-20	0.008682792	ABC transporter family protein contains Pfam profile: PF00005 ABC transporter; similar to white protein GB:Q27256 [Anopheles gambiae] [At3g13220.1]
A_84_P22823	At1g75930.1	0.003306748	2.35E-20	0.016288339	8.84E-19	0.009797544	family II extracellular lipase 6 (EXL6) EXL6 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana] [At1g75930.1]
A_84_P22834	At1g74540.1	0.011090913	2.67E-20	0.008908291	7.82E-20	0.009999602	cytochrome P450, putative similar to cytochrome P450 GB:O48922 [Glycine max]; contains Pfam profile: PF00067 cytochrome P450 [At1g74540.1]
A_84_P20419	At1g06280.1	0.011122663	2.87E-20	0.010000001	9.61E-20	0.010561332	LOB domain family protein / lateral organ boundaries domain family protein (LBD2) nearly identical to SPIQ9LNB9 Putative LOB domain protein 2 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis...
A_84_P17460	At3g42960.1	0.010946747	2.68E-20	0.01028419	1.02E-19	0.010615468	alcohol dehydrogenase (ATA1) identical to alcohol dehydrogenase (ATA1) GI:2501781 from [Arabidopsis thaliana] [At3g42960.1]
A_84_P23905	At2g19070.1	0.01291878	2.71E-20	0.011441434	4.91E-20	0.012180107	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus [gi:2239091]; contains Pfam profile PF02458: Transferase family [At2g19070.1]
A_84_P13426	At1g57750.1	0.003422331	2.35E-20	0.022579376	1.85E-17	0.013000853	cytochrome P450, putative similar to cytochrome P450 GI:4688670 from [Catharanthus roseus] [At1g57750.1]
A_84_P23402	At5g07550.1	0.014341805	2.82E-20	0.011730758	1.09E-19	0.013036281	glycine-rich protein (GRP19) oleosin; glycine-rich protein 19 (GRP19) PMID:11431566 [At5g07550.1]
A_84_P24118	At3g52160.1	0.008654147	3.26E-20	0.017999991	1.94E-18	0.013327069	beta-ketoacyl-CoA synthase family protein beta-ketoacyl-CoA synthase - Simmondsia chinensis,PID:g1045614 [At3g52160.1]
A_84_P212618	At3g25050.1	0.001381334	2.35E-20	0.025949999	1.07E-16	0.013665666	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to endoxyloglucan transferase EXGT-A4 GI:5533315 from [Arabidopsis thaliana] [At3g25050.1]
A_84_P548554	At4g33355.1	0.004583333	2.35E-20	0.026618351	1.58E-16	0.015600842	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family [At4g33355.1]
A_84_P548554	At4g33355.1	0.004846845	2.35E-20	0.02806283	1.58E-16	0.016454837	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family [At4g33355.1]
A_84_P17122	At1g44970.1	0.005986079	2.35E-20	0.027351605	1.09E-19	0.016668842	peroxidase, putative similar to peroxidase GI:993004 from [Mercurialis annua] [At1g44970.1]
A_84_P13477	At2g03850.1	0.01063776	2.51E-20	0.023305076	1.01E-19	0.016971418	late embryogenesis abundant domain-containing protein / LEA domain-containing protein low similarity to low-temperature-regulated 14.8 kda protein [Brassica napus] GI:544698, cold-regulated gene cor15b [Arabidopsis thaliana] GI:456016; contains Pfam...
A_84_P20010	At1g56360.1	0.007782487	2.97E-20	0.026372552	1.36E-16	0.01707752	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase [At1g56360.1]
A_84_P18743	At5g40260.1	0.017451207	3.86E-20	0.01715447	4.61E-19	0.017302839	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula] [At5g40260.1]
A_84_P13883	At4g34850.1	0.007601859	2.35E-20	0.027244094	1.27E-19	0.017422976	chalcone and stilbene synthase family protein similar to chalcone synthase homolog PrChS1, Pinus radiata, gb:U90341; similar to anther-specific protein [Nicotiana sylvestris][GI:2326774], YY2 protein [Oryza sativa][GI:2645170] [At4g34850.1]
A_84_P15688	At1g06260.1	0.016410261	2.97E-20	0.019867561	1.09E-19	0.018138911	cysteine proteinase, putative contains similarity to thiol-protease, pre-pro-TPE4A protein GI:3688528 [Pisum sativum] [At1g06260.1]
A_84_P15203	At1g13140.1	0.017321428	3.47E-20	0.019027779	2.23E-19	0.018174604	cytochrome P450 family protein similar to Cytochrome P450 86A2 (SP:O23066) [Arabidopsis thaliana]; contains Pfam PFI00067 Cytochrome P450 family [At1g13140.1]
A_84_P21900	At1g75790.1	0.007629428	2.92E-20	0.030103624	1.06E-15	0.018866526	multi-copper oxidase type I family protein contains Pfam profile: PF00394 Multicopper oxidase [At1g75790.1]
A_84_P17744	At5g13380.1	0.01116371	5.66E-20	0.0267143	1.64E-16	0.018939005	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter [At5g13380.1]
A_84_P21029	At2g16910.1	0.009425444	2.97E-20	0.030000014	9.44E-16	0.019712729	basic helix-loop-helix (bHLH) family protein [At2g16910.1]
A_84_P10733	At2g23800.1	0.006308335	2.35E-20	0.035359491	1.86E-14	0.020833913	geranylgeranyl pyrophosphate synthase (GGPS2) (GGPS5) / GGPP synthetase / farnesyltranstransferase identical to GB:U44876; sequence disagrees at N-Terminus, sequence submitted has been confirmed from three electropherograms. [At2g23800.1]
A_84_P731276	CHR4v012120	0.018270691	8.87E-20	0.024289406	9.68E-19	0.021280048	SLY1_ARATH (Q9SL48) SEC1-family transport protein SLY1 (AtSLY1), partial (4%) [TC269252]
A_84_P146818	At5g37940.1	0.008875736	2.35E-20	0.034285705	1.76E-19	0.021580721	NADP-dependent oxidoreductase, putative similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 [SPIQ39172][gi:886428], Arabidopsis thaliana [At5g37940.1]
A_84_P23792	At1g71160.1	0.009533211	3.7E-20	0.035804184	2.18E-14	0.022668698	beta-ketoacyl-CoA synthase family protein similar to fatty acid elongase 3-ketoacyl-CoA synthase 1 GB:AAC99312, very-long-chain fatty acid condensing enzyme CUT1 [GI:5001734] [At1g71160.1]
A_84_P19227	At1g07340.1	0.021383643	5.43E-20	0.02454106	4.58E-17	0.022962352	hexose transporter, putative similar to hexose transporter [Lycopersicon esculentum] GI:5734440; contains Pfam profile PF00083: major facilitator superfamily protein [At1g07340.1]
A_84_P10163	At5g07560.1	0.014907409	3.2E-20	0.033533326	6.62E-15	0.024220367	glycine-rich protein (GRP20) oleosin; glycine-rich protein 20 (GRP20); similar to - Brassica napus, PIR:S50195 [At5g07560.1]
A_84_P196974	At5g26730.1	0.029707597	3.05E-16	0.019804687	5.06E-18	0.024756142	expressed protein ; expression supported by MPSS [At5g26730.1]
A_84_P10801	At1g26720.1	0.008946541	3.4E-20	0.041366898	4.95E-13	0.02515672	expressed protein ; expression supported by MPSS [At1g26720.1]
A_84_P21482	At4g36350.1	0.013373501	1.16E-19	0.038226934	8.22E-14	0.025800217	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase [At4g36350.1]
A_84_P550260	At4g14815.1	0.025113118	1.91E-19	0.027777778	2.68E-16	0.026445448	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 [At4g14815.1]
A_84_P14930	At5g24820.1	0.012720928	9.65E-20	0.040592593	3.29E-13	0.02665676	aspartyl protease family protein low similarity to CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease [At5g24820.1]
A_84_P542422	At5g17340.1	0.039816494	3.99E-19	0.019741686	4.41E-18	0.02977909	expressed protein weak similarity to M3.4 protein [Brassica napus] GI:4574746 [At5g17340.1]
A_84_P196514	At1g23570.1	0.036158534	1.23E-19	0.024013149	2.3E-19	0.030085841	expressed protein contains Pfam profile PF02713: Domain of unknown function DUF220 [At1g23570.1]
A_84_P13080	At5g43340.1	0.02176471	4.03E-18	0.039844958	1.81E-13	0.030804834	inorganic phosphate transporter identical to inorganic phosphate transporter [Arabidopsis thaliana] GI:3869190 [At5g43340.1]
A_84_P602531	At2g46880.1	0.035099347	2.01E-18	0.031304366	1.75E-15	0.033201857	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase [At2g46880.1]
A_84_P17176	At1g75920.1	0.02509091	5.63E-20	0.043060504	1.31E-17	0.034075707	family II extracellular lipase 5 (EXL5) EXL5 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana (Mouse-ear cress)] [At1g75920.1]
A_84_P12703	At3g23770.1	0.015063293	3.84E-20	0.054259253	2.31E-10	0.034661273	glycosyl hydrolase family 17 protein similar to A6 anther-specific protein SP:Q06915 [Arabidopsis thaliana] [At3g23770.1]
A_84_P22542	At5g44540.1	0.017659349	3.7E-20	0.052764229	3.8E-12	0.035211789	tapetum-specific protein-related similar to SaTAP 35 [Sinapis alba] GI:408108 [At5g44540.1]
A_84_P83099	At5g07600.1	0.021121728	1.69E-19	0.049316219	3.4E-12	0.035218974	oleosin / glycine-rich protein [At5g07600.1]
A_84_P13222	At1g08065.1	0.016026662	2.33E-19	0.065197742	1.28E-08	0.040612202	carbonic anhydrase family protein similar to storage protein (dioscorin) [Dioscorea cayenensis] GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase [At1g08065.1]
A_84_P152588	At5g16920.1	0.028626379	1.38E-16	0.053488368	1.58E-10	0.041057374	expressed protein [At5g16920.1]
A_84_P20704	At5g59320.1	0.014375002	2.87E-20	0.070029651	4.48E-17	0.042202326	lipid transfer protein 3 (LTP3) identical to lipid transfer protein 3 from Arabidopsis thaliana [gi:8571921]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 [At5g59320.1]
A_84_P23780	At1g74550.1	0.034491962	9.89E-20	0.050293264	1.21E-18	0.042392613	cytochrome P450, putative similar to cytochrome P450 98A3 (SP:O22203)[Arabidopsis thaliana]; cytochrome P450 (GB:O48922) [Glycine max]; contains Pfam profile: PF00067 cytochrome P450 [At1g74550.1]
A_84_P12174	At5g54010.1	0.049575083	2.93E-18	0.037641014	2.53E-16	0.043608048	glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase [At5g54010.1]
A_84_P16899	At5g53510.1	0.041806162	3.98E-17	0.050673068	4.83E-11	0.046239615	oligopeptide transporter OPT family protein similar to SPIP40900 Sexual differentiation process protein isp4 {Schizosaccharomyces pombe}, oligopeptide transporter Opt1p [Candida albicans] GI:2367386; contains Pfam profile PF03169: OPT oligopeptide...
A_84_P16926	At5g60510.1	0.036794596	4.41E-19	0.055849919	4.36E-10	0.046322257	undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein contains putative undecaprenyl diphosphate synthase domain [PF01255]; similar to S. cerevisiae dehydrodolichyl diphosphate synthetase (DEDOL-PP...
A_84_P586474	At2g39855.1	0.049245285	7.96E-12	0.05057692	4.76E-11	0.049911102	expressed protein [At2g39855.1]
A_84_P17970	At1g23670.1	0.030786522	4.44E-18	0.069211199	5.82E-08	0.04999886	expressed protein contains Pfam profile PF02713: Domain of unknown function DUF220 [At1g23670.1]

A_84_P19722	At5g49070.1	0.026887753	5.58E-17	0.076162804	0.000000434	0.051525278	beta-ketoacyl-CoA synthase family protein similar to very-long-chain fatty acid condensing enzyme CUT1 [GI:5001734], beta-ketoacyl-CoA synthase [Simmondsia chinensis][GI:1045614] [At5g49070.1]
A_84_P599242	At4g28395.1	0.069021718	1.15E-17	0.034123237	8.57E-19	0.051572477	lipid transfer protein, putative identical to anther-specific gene ATA7 [gi:2746339]; contains Pfam protease inhibitor/seed storage/LTP family domain [At4g28395.1]
A_84_P20015	At1g33430.1	0.036619731	1.11E-19	0.068666641	3.91E-18	0.052643186	galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase [At1g33430.1]
A_84_P15944	At5g50790.1	0.047701155	5.68E-19	0.059178072	3.04E-17	0.053439613	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula] [At5g50790.1]
A_84_P18672	At5g07520.1	0.054457856	2.55E-18	0.055026463	2.88E-10	0.054742159	glycine-rich protein (GRP18) Oleosin; glycine-rich protein 18 (GRP18) PMID:11431566; [At5g07520.1]
A_84_P593106	At5g19470.1	0.060739044	9.89E-10	0.049801983	3.04E-11	0.055270513	MutT/nudix family protein similar to SPIP41888 Thiamine pyrophosphokinase (EC 2.7.6.2) (TPK) (Thiamine kinase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain [At5g19470.1]
A_84_P18921	At1g55560.1	0.093750052	4.78E-11	0.018071431	1.92E-18	0.055910742	multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SPIQ00624][Brassica napus]; contains Pfam profile: PF00394 Multicopper oxidase [At1g55560.1]
A_84_P19758	At5g59310.1	0.019574998	3.32E-20	0.093364532	3.3E-17	0.056469765	lipid transfer protein 4 (LTP4) identical to lipid transfer protein 4 from Arabidopsis thaliana [gi:8571923]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 [At5g59310.1]
A_84_P14137	At5g13170.1	0.050914613	3.38E-19	0.065697678	2.66E-18	0.058306146	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula]; identical to cDNA senescence-associated protein (SAG29) mRNA, partial cds GI:4426938 [At5g13170.1]
A_84_P18051	At1g47610.1	0.040362697	2.54E-16	0.078470843	6.54E-10	0.05941677	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); similar to En/Spm-like transposon protein (GI:2739374) [Arabidopsis thaliana] [At1g47610.1]
A_84_P14653	At3g50580.1	0.020219778	1.97E-18	0.101444039	0.00010318	0.060831909	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965 [At3g50580.1]
A_84_P18639	At4g16270.1	0.017134983	3.09E-20	0.105092601	7.22E-17	0.061113792	peroxidase 40 (PER40) (P40) identical to SPIO23474 Peroxidase 40 precursor (EC 1.11.1.7) (Atperox P40) {Arabidopsis thaliana} [At4g16270.1]
A_84_P15697	At4g12920.1	0.024420609	1.4E-17	0.09881355	0.0000574	0.06161708	aspartyl protease family protein low similarity to CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease [At4g12920.1]
A_84_P579082	At1g28375.1	0.027295917	6.4E-17	0.098320884	0.0000565	0.062808401	expressed protein [At1g28375.1]
A_84_P17831	At1g29610.1	0.083935714	1.89E-17	0.043268131	5.33E-19	0.063601922	hypothetical protein [At1g29610.1]
A_84_P23297	At4g24890.1	0.046305745	4.75E-15	0.081948878	0.00000194	0.064127311	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase [At4g24890.1]
A_84_P10574	At1g06990.1	0.023408073	8.75E-18	0.106224061	0.000197258	0.064816067	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 [At1g06990.1]
A_84_P16204	At1g20150.1	0.115536107	0.000400678	0.01538941	5.74E-19	0.065462759	subtilase family protein similar to subtilisin-type protease precursor GI:14150446 from [Glycine max] [At1g20150.1]
A_84_P12140	At5g44700.1	0.060729614	3.02E-18	0.071428582	2.04E-15	0.066079098	leucine-rich repeat transmembrane protein kinase, putative [At5g44700.1]
A_84_P17912	At5g28470.1	0.0230837	7.35E-18	0.113260837	0.000494653	0.068172268	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At5g28470.1]
A_84_P554054	At5g60140.1	0.027486627	9.11E-17	0.111940283	0.000486175	0.069713455	transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain [At5g60140.1]
A_84_P16963	At5g16960.1	0.058506227	6.47E-19	0.081042669	1.44E-17	0.069774448	NADP-dependent oxidoreductase, putative similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 [SPIQ39172][gi:886428] and P2 [SPIQ39173][gi:886430], Arabidopsis thaliana [At5g16960.1]
A_84_P16149	At1g13150.1	0.033035706	2.42E-19	0.110000028	1.85E-09	0.071517867	cytochrome P450, putative strong similarity to gil3313615 F21J9.9 from Arabidopsis thaliana and is a member of the PFI00067 Cytochrome P450 family [At1g13150.1]
A_84_P22667	At5g59040.1	0.056074797	3E-16	0.088749992	0.00000679	0.072412394	copper transporter family protein similar to SPIQ39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}; contains Pfam profile PF04145: Ctr copper transporter family [At5g59040.1]
A_84_P15526	At1g26710.1	0.027272731	1.55E-17	0.118085146	1.01E-08	0.072678938	expressed protein [At1g26710.1]
A_84_P16177	At1g78440.1	0.064724898	3.64E-17	0.081021927	6.03E-12	0.072873412	gibberellin 2-oxidase / GA2-oxidase (GA2OX1) identical to gibberellin 2- oxidase ga2ox1 [GI:4678366] from [Arabidopsis thaliana] [At1g78440.1]
A_84_P580614	At5g24790.1	0.051132076	1.63E-11	0.096880747	0.0000451	0.074006411	expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF599 [At5g24790.1]
A_84_P19732	At5g51950.1	0.041473408	2.71E-19	0.10694986	8.06E-08	0.074211634	glucose-methanol-choline (GMC) oxidoreductase family protein similar to mandelonitrile lyase from Prunus serotina [SPIP52706, SPIP52707]; contains Pfam profile PF00732 GMC oxidoreductase [At5g51950.1]
A_84_P726808	CHR5v012120	0.066639381	1.81E-11	0.082710913	0.00000273	0.074675147	Unknown
A_84_P11352	At1g23580.1	0.029029127	1.77E-16	0.121104569	0.001429567	0.075066848	expressed protein contains Pfam profile PF02713: Domain of unknown function DUF220 [At1g23580.1]
A_84_P526945	At2g33880.1	0.057920802	1.11E-15	0.092455868	0.0000186	0.075188335	expressed protein [At2g33880.1]
A_84_P558738	At1g74130.2	0.047844835	3.92E-12	0.103113548	0.000135525	0.075479191	rhomboid family protein contains Pfam profile PF01694: Rhomboid family [At1g74130.2]
A_84_P89649	At3g26125.1	0.051570238	8.14E-19	0.103763431	1.06E-13	0.077666834	cytochrome P450, putative [At3g26125.1]
A_84_P233609	At5g62080.1	0.067203361	1.68E-18	0.0887851	1.01E-14	0.077994231	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to tapetum-specific protein a9 precursor {Brassica napus} SPIQ05772; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234; supported by full-length...
A_84_P14098	At5g62320.1	0.119711089	1.59E-08	0.037272722	5.57E-14	0.078491906	myb family transcription factor (MYB99) contains PFAM profile: myb DNA binding domain PF00249 [At5g62320.1]
A_84_P715912	CHR1v012120	0.05175879	3.05E-11	0.110021303	0.000362637	0.080890047	Unknown
A_84_P514216	At3g46770.1	0.060782255	1.03E-09	0.101943472	0.000118999	0.081362863	transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain [At3g46770.1]
A_84_P598819	At1g73890.1	0.095808403	7.72E-14	0.070113769	8.43E-10	0.082961086	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234 [At1g73890.1]
A_84_P23860	At1g64110.1	0.064532043	1.1E-18	0.10200807	5.32E-17	0.083270056	AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family [At1g64110.1]
A_84_P21553	At5g25110.1	0.090659367	9.78E-18	0.088186828	1.72E-17	0.089423098	CBL-interacting protein kinase 25 (CIPK25) identical to CBL-interacting protein kinase 25 [Arabidopsis thaliana] gil17646697lgblAAL41008 [At5g25110.1]
A_84_P606561	At5g59845.1	0.076212106	5.91E-18	0.105405401	6.87E-15	0.090808754	gibberellin-regulated family protein similar to SPIP27057 GAST1 protein precursor {Lycopersicon esculentum}; contains Pfam profile PF02704: Gibberellin regulated protein [At5g59845.1]
A_84_P600903	At3g58060.1	0.069788513	5.72E-10	0.112692351	0.000462484	0.091240432	cation efflux family protein / metal tolerance protein, putative (MTPc3) member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563 [At3g58060.1]
A_84_P20471	At4g27330.1	0.076923078	6.46E-15	0.108914278	2.96E-08	0.092918678	sporocyteless (SPL) identical to sporocyteless SPL (MADS-box related protein) [Arabidopsis thaliana] gil5566240lgblAAD45344 [At4g27330.1]
A_84_P14274	At1g52690.1	0.119379887	3.48E-16	0.06709795	7.77E-18	0.093238919	late embryogenesis abundant protein, putative / LEA protein, putative similar to SPIP13934 Late embryogenesis abundant protein 76 (LEA 76) {Brassica napus}; contains Pfam profile PF02987: Late embryogenesis abundant protein [At1g52690.1]
A_84_P78785	At3g03650.1	0.119771844	4.54E-15	0.068800015	6.48E-18	0.09428593	exostosin family protein contains Pfam profile: PF03016 Exostosin family [At3g03650.1]
A_84_P10821	At3g21040.1	0.121061144	0.0000101	0.072802217	0.000000171	0.096931681	contains similarity to retroelement pol polyprotein~gene_id:MSA6.7 [NP301363]
A_84_P503428	At5g24105.1	0.07514452	2.78E-18	0.124030978	4.2E-16	0.099587749	expressed protein [At5g24105.1]
A_84_P23143	At3g45480.1	0.096437028	0.000000022	0.104331456	0.000159824	0.100384242	zinc finger (C3HC4-type RING finger) family protein contains a zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518 [At3g45480.1]
A_84_P594944	At5g47635.1	0.092819633	0.0000109	0.109158418	7.18E-08	0.100989026	expressed protein [At5g47635.1]
A_84_P19357	At3g44990.1	0.090839653	9.66E-18	0.117919114	2.01E-16	0.104379384	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative [At3g44990.1]
A_84_P181494	At3g48280.1	0.10265485	3.68E-17	0.12487308	5.12E-16	0.113763965	cytochrome P450, putative nearly identical to cytochrome P450 71A25 (SP:Q9STK8) [Arabidopsis thaliana]; [At3g48280.1]
A_84_P311113	At5g43840.1	0.116733067	7.8E-15	0.119407884	5.14E-15	0.118070476	heat shock transcription factor family protein contains Pfam profile: PF00447 HSF-type DNA-binding domain [At5g43840.1]

Table S2. Many genes categorized in defense response to biotic stimulus using High-throughput GoMiner for gene ontology analysis

For the analysis, genes over-expressed in DLE1OX in comparison with Col-0 are used.

HYPERLINKED GO CATEGORY	TOTAL GENES	OVER-EXPRESSED GENES	ENRICHMENT	LOG10(p)	CUMULATIVE NUMBER OF CATEGORIES	CUMULATIVE RANDOMS LOWER BOUND	CUMULATIVE RANDOMS MEAN	CUMULATIVE RANDOMS UPPER BOUND	FALSE DISCOVERY RATE
GO:0051707_response_to_other_organism	135	14	7.482343	-8.490438	1	0	0	0	0
GO:0009607_response_to_biotic_stimulus	140	14	7.215116	-8.282112	2	0	0	0	0
GO:0051704_multi-organism_process	245	17	5.006407	-7.560497	3	0	0	0	0
GO:0050832_defense_response_to_fungus	31	7	16.292198	-6.81202	4	0	0	0	0
GO:0006952_defense_response	286	17	4.288705	-6.576038	5	0	0	0	0
GO:0009620_response_to_fungus	35	7	14.430233	-6.423706	6	0	0	0	0
GO:0050896_response_to_stimulus	1106	34	2.218029	-5.809681	7	0	0	0	0
GO:0006950_response_to_stress	732	25	2.464179	-4.957159	8	0	0	0	0
GO:0009611_response_to_wounding	49	6	8.834836	-4.287483	9	-0.09	0.01	0.11	0.001111
GO:0009817_defense_response_to_fungus__incompatible_inte	16	4	18.037791	-4.25853	10	-0.09	0.01	0.11	0.001
GO:0009617_response_to_bacterium	74	7	6.82511	-4.185735	11	-0.09	0.01	0.11	0.000909
GO:0045087_innate_immune_response	134	9	4.845974	-4.056231	12	-0.09	0.01	0.11	0.000833
GO:0016998_cell_wall_macromolecule_catabolic_process	19	4	15.189718	-3.944017	13	-0.09	0.01	0.11	0.000769
GO:0006955_immune_response	152	9	4.272108	-3.637282	14	-0.178683	0.06	0.298683	0.004286
GO:0009814_defense_response__incompatible_interaction	25	4	11.544186	-3.457866	15	-0.230826	0.09	0.410826	0.006
GO:0002376_immune_system_process	166	9	3.91181	-3.35241	16	-0.233333	0.1	0.433333	0.00625
GO:0044036_cell_wall_macromolecule_metabolic_process	28	4	10.307309	-3.262489	17	-0.311645	0.13	0.571645	0.007647
GO:0010193_response_to_ozone	3	2							
GO:0009753_response_to_jasmonic_acid_stimulus	20	3	10.822674	-2.607059	18	-0.615321	0.98	2.575321	0.054444
GO:0006032_chitin_catabolic_process	6	2	24.050388	-2.561135	19	-0.466729	1.35	3.166729	0.071053
GO:0009751_response_to_salicylic_acid_stimulus	23	3	9.411021	-2.428754	20	-0.576324	1.62	3.816324	0.081
GO:0006026_aminoglycan_catabolic_process	7	2	20.614618	-2.418929	22	-0.533263	1.88	4.293263	0.085455
GO:0006030_chitin_metabolic_process	7	2	20.614618	-2.418929	22	-0.533263	1.88	4.293263	0.085455
GO:0042221_response_to_chemical_stimulus	521	15	2.077289	-2.316582	23	-0.846768	2.27	5.386768	0.098696
GO:0042742_defense_response_to_bacterium	51	4	5.658915	-2.280929	24	-0.864465	2.68	6.224465	0.111667
GO:0006022_aminoglycan_metabolic_process	11	2	13.118393	-2.016435	25	-0.315088	5.14	10.595088	0.2056
GO:0010033_response_to_organic_substance	229	8	2.520565	-1.867196	26	-0.004736	6.88	13.764736	0.264615
GO:0001561_fatty_acid_alpha-oxidation	1	1							
GO:0006562_proline_catabolic_process	1	1							
GO:0007562_eclosion	1	1							
GO:0007563_regulation_of_eclosion	1	1							
GO:0008407_bristle_morphogenesis	1	1							
GO:0009065_glutamine_family_amino_acid_catabolic_process	1	1							
GO:0015690_aluminum_ion_transport	1	1							
GO:0022416_bristle_development	1	1							
GO:0042262_DNA_protection	1	1							
GO:0051131_chaperone-mediated_protein_complex_assembly	1	1							
GO:0070983_dendrite_guidance	1	1							
GO:0071684_organism_emergence_from_protective_structure	1	1							
GO:0072512_trivalent_inorganic_cation_transport	1	1							
GO:0006800_oxygen_and_reactive_oxygen_species_metabolic	17	2	8.488372	-1.646608	27	0.572816	10.56	20.547184	0.391111
GO:0055114_oxidation-reduction_process	624	15	1.734403	-1.633618	28	0.555668	10.78	21.004332	0.385
GO:0009651_response_to_salt_stress	80	4	3.607558	-1.610655	29	0.535349	11.29	22.044651	0.38931
GO:0071554_cell_wall_organization_or_biogenesis	166	6	2.607873	-1.567189	30	1.105493	12.23	23.354507	0.407667
GO:0006911_phagocytosis__engulfment	2	1							
GO:0007472_wing_disc_morphogenesis	2	1							
GO:0007476_imaginal_disc-derived_wing_morphogenesis	2	1							
GO:0009646_response_to_absence_of_light	2	1							
GO:0035120_post-embryonic_appendage_morphogenesis	2	1							
GO:0035220_wing_disc_development	2	1							
GO:0080027_response_to_herbivore	2	1							
GO:0007154_cell_communication	88	4	3.279598	-1.477912	31	2.051819	14.47	26.888181	0.466774
GO:0006970_response_to_osmotic_stress	90	4	3.206718	-1.447146	32	2.443353	15.51	28.576647	0.484688
GO:0002237_response_to_molecule_of_bacterial_origin	3	1							
GO:0006537_glutamate_biosynthetic_process	3	1							
GO:0006560_proline_metabolic_process	3	1							
GO:0007411_axon_guidance	3	1							

GO:0007560_imaginal_disc_morphogenesis	3	1							
GO:0009694_jasmonic_acid_metabolic_process	3	1							
GO:0009695_jasmonic_acid_biosynthetic_process	3	1							
GO:0009900_dehiscence	3	1							
GO:0009901_anther_dehiscence	3	1							
GO:0033194_response_to_hydroperoxide	3	1							
GO:0035114_imaginal_disc-derived_appendage_morphogenes	3	1							
GO:0042273_ribosomal_large_subunit_biogenesis	3	1							
GO:0048737_imaginal_disc-derived_appendage_development	3	1							
GO:0000272_polysaccharide_catabolic_process	24	2	6.012597	-1.366289	33	4.145947	19.38	34.614053	0.587273
GO:0007568_aging	26	2	5.550089	-1.303005	34	5.618489	22.51	39.401511	0.662059
GO:0019748_secondary_metabolic_process	101	4	2.857472	-1.292671	35	5.614262	23.16	40.705738	0.661714
GO:0048544_recognition_of_pollen	27	2	5.344531	-1.27342	36	6.115931	24.07	42.024069	0.668611
GO:0000162_tryptophan_biosynthetic_process	4	1							
GO:0001302_replicative_cell_aging	4	1							
GO:0007444_imaginal_disc_development	4	1							
GO:0007569_cell_aging	4	1							
GO:0009867_jasmonic_acid_mediated_signaling_pathway	4	1							
GO:0035107_appendage_morphogenesis	4	1							
GO:0042255_ribosome_assembly	4	1							
GO:0046219_indolalkylamine_biosynthetic_process	4	1							
GO:0046836_glycolipid_transport	4	1							
GO:0048736_appendage_development	4	1							
GO:0071395_cellular_response_to_jasmonic_acid_stimulus	4	1							
GO:0008652_cellular_amino_acid_biosynthetic_process	63	3	3.43577	-1.249214	37	6.261532	24.64	43.018468	0.665946
GO:0008037_cell_recognition	28	2	5.153654	-1.245071	39	6.994143	25.7	44.405857	0.658974
GO:0009875_pollen-pistil_interaction	28	2	5.153654	-1.245071	39	6.994143	25.7	44.405857	0.658974
GO:0016054_organic_acid_catabolic_process	30	2	4.810078	-1.19173	41	7.852207	27.83	47.807793	0.67878
GO:0046395_carboxylic_acid_catabolic_process	30	2	4.810078	-1.19173	41	7.852207	27.83	47.807793	0.67878
GO:0006909_phagocytosis	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0007350_blastoderm_segmentation	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0009626_plant-type_hypersensitive_response	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0009816_defense_response_to_bacterium__incompatible_	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0030448_hyphal_growth	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0034050_host_programmed_cell_death_induced_by_symb	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0035282_segmentation	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0080086_stamen_filament_development	5	1	14.430233	-1.171175	49	15.502467	39.53	63.557533	0.806735
GO:0006869_lipid_transport	68	3	3.18314	-1.169226	50	15.682463	39.88	64.077537	0.7976
GO:0031668_cellular_response_to_extracellular_stimulus	31	2	4.654914	-1.166588	52	15.97414	40.3	64.62586	0.775
GO:0071496_cellular_response_to_external_stimulus	31	2	4.654914	-1.166588	52	15.97414	40.3	64.62586	0.775
GO:0009309_amine_biosynthetic_process	71	3	3.048641	-1.124759	54	16.886336	41.91	66.933664	0.776111
GO:0010876_lipid_localization	71	3	3.048641	-1.124759	54	16.886336	41.91	66.933664	0.776111
GO:0009719_response_to_endogenous_stimulus	164	5	2.199731	-1.115868	55	17.693544	43.04	68.386456	0.782545
GO:0008299_isoprenoid_biosynthetic_process	34	2	4.244186	-1.096517	56	18.390818	44.39	70.389182	0.792679
GO:0006536_glutamate_metabolic_process	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0007409_axonogenesis	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0009627_systemic_acquired_resistance	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0009880_embryonic_pattern_specification	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0031407_oxylipin_metabolic_process	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0031408_oxylipin_biosynthetic_process	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0031505_fungal-type_cell_wall_organization	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0042398_cellular_modified_amino_acid_biosynthetic_proce	6	1	12.025194	-1.094953	64	25.741329	54.77	83.798671	0.855781
GO:0016053_organic_acid_biosynthetic_process	121	4	2.385162	-1.063034	66	26.826414	56.36	85.893586	0.853939
GO:0046394_carboxylic_acid_biosynthetic_process	121	4	2.385162	-1.063034	66	26.826414	56.36	85.893586	0.853939
GO:0009605_response_to_external_stimulus	76	3	2.848072	-1.055816	67	26.950367	56.65	86.349633	0.845522
GO:0006568_tryptophan_metabolic_process	7	1	10.307309	-1.030959	73	34.561179	67.18	99.798821	0.920274
GO:0006586_indolalkylamine_metabolic_process	7	1	10.307309	-1.030959	73	34.561179	67.18	99.798821	0.920274
GO:0007423_sensory_organ_development	7	1	10.307309	-1.030959	73	34.561179	67.18	99.798821	0.920274
GO:0048653_anther_development	7	1	10.307309	-1.030959	73	34.561179	67.18	99.798821	0.920274
GO:0048707_instar_larval_or_pupal_morphogenesis	7	1	10.307309	-1.030959	73	34.561179	67.18	99.798821	0.920274
GO:0070925_organelle_assembly	7	1	10.307309	-1.030959	73	34.561179	67.18	99.798821	0.920274

GO:0048569_post-embryonic_organ_development	39	2	3.70006	-0.994641	74	36.575351	69.71	102.844649	0.942027
GO:0006979_response_to_oxidative_stress	130	4	2.220036	-0.976456	75	37.458219	70.97	104.481781	0.946267
GO:0006720_isoprenoid_metabolic_process	40	2	3.607558	-0.976147	76	37.948449	71.62	105.291551	0.942368
GO:0007552_metamorphosis	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0042744_hydrogen_peroxide_catabolic_process	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0046246_terpene_biosynthetic_process	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0048563_post-embryonic_organ_morphogenesis	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0048813_dendrite_morphogenesis	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0052482_defense_response_by_cell_wall_thickening	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0052543_callose_deposition_in_cell_wall	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0052544_defense_response_by_callose_deposition_in_cel	8	1	9.018895	-0.975913	84	44.448823	81.18	117.911177	0.966429
GO:0002165_instar_larval_or_pupal_development	9	1	8.016796	-0.927699	88	49.779099	88.93	128.080901	1.010568
GO:0052386_cell_wall_thickening	9	1	8.016796	-0.927699	88	49.779099	88.93	128.080901	1.010568
GO:0052542_defense_response_by_callose_deposition	9	1	8.016796	-0.927699	88	49.779099	88.93	128.080901	1.010568
GO:0052545_callose_localization	9	1	8.016796	-0.927699	88	49.779099	88.93	128.080901	1.010568
GO:0009991_response_to_extracellular_stimulus	43	2	3.355868	-0.923876	89	50.079899	89.6	129.120101	1.006742
GO:0000077_DNA_damage_checkpoint	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0009615_response_to_virus	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0009813_flavonoid_biosynthetic_process	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0009821_alkaloid_biosynthetic_process	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0016358_dendrite_development	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0033037_polysaccharide_localization	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0042435_indole-containing_compound_biosynthetic_proces	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0042743_hydrogen_peroxide_metabolic_process	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0070301_cellular_response_to_hydrogen_peroxide	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0071852_fungal-type_cell_wall_organization_or_biogenesis	10	1	7.215116	-0.884875	99	57.826581	100.99	144.153419	1.020101
GO:0009820_alkaloid_metabolic_process	11	1	6.559197	-0.846408	100	63.848452	109.22	154.591548	1.0922
GO:0071702_organic_substance_transport	95	3	2.278458	-0.840529	101	64.723252	110.57	156.416748	1.094752
GO:0009056_catabolic_process	320	7	1.578307	-0.812366	102	66.767925	113.46	160.152075	1.112353
GO:0006935_chemotaxis	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0009642_response_to_light_intensity	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0009812_flavonoid_metabolic_process	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0030447_filamentous_growth	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0042330_taxis	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0042401_cellular_biogenic_amine_biosynthetic_process	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0048443_stamen_development	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0048466_androecium_development	12	1	6.012597	-0.811539	110	71.760041	120.03	168.299959	1.091182
GO:0009060_aerobic_respiration	13	1	5.550089	-0.77969	116	76.542604	126.58	176.617396	1.091207
GO:0009062_fatty_acid_catabolic_process	13	1	5.550089	-0.77969	116	76.542604	126.58	176.617396	1.091207
GO:0009073_aromatic_amino_acid_family_biosynthetic_proces	13	1	5.550089	-0.77969	116	76.542604	126.58	176.617396	1.091207
GO:0042214_terpene_metabolic_process	13	1	5.550089	-0.77969	116	76.542604	126.58	176.617396	1.091207
GO:0046417_chorismate_metabolic_process	13	1	5.550089	-0.77969	116	76.542604	126.58	176.617396	1.091207
GO:0048667_cell_morphogenesis_involved_in_neuron_differen	13	1	5.550089	-0.77969	116	76.542604	126.58	176.617396	1.091207
GO:0009063_cellular_amino_acid_catabolic_process	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0009084_glutamine_family_amino_acid_biosynthetic_proce	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0009310_amine_catabolic_process	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0019395_fatty_acid_oxidation	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0022618_ribonucleoprotein_complex_assembly	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0032990_cell_part_morphogenesis	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0034440_lipid_oxidation	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0034614_cellular_response_to_reactive_oxygen_species	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0042430_indole-containing_compound_metabolic_process	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0042542_response_to_hydrogen_peroxide	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0048812_neuron_projection_morphogenesis	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0048858_cell_projection_morphogenesis	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0071826_ribonucleoprotein_complex_subunit_organization	14	1	5.153654	-0.750412	129	82.871527	135.54	188.208473	1.050698
GO:0044255_cellular_lipid_metabolic_process	161	4	1.792575	-0.735864	130	84.46666	137.57	190.67334	1.058231
GO:0030030_cell_projection_organization	15	1	4.810078	-0.723348	133	87.612644	142.52	197.427356	1.071579
GO:0031175_neuron_projection_development	15	1	4.810078	-0.723348	133	87.612644	142.52	197.427356	1.071579
GO:0051701_interaction_with_host	15	1	4.810078	-0.723348	133	87.612644	142.52	197.427356	1.071579
GO:0009856_pollination	59	2	2.445802	-0.706015	134	90.04211	145.74	201.43789	1.087612

GO:0006928_cellular_component_movement	16	1	4.509448	-0.698213	136	93.419463	150.05	206.680537	1.103309
GO:0031570_DNA_integrity_checkpoint	16	1	4.509448	-0.698213	136	93.419463	150.05	206.680537	1.103309
GO:0030258_lipid_modification	17	1	4.244186	-0.67477	138	99.518065	158.05	216.581935	1.14529
GO:0072329_monocarboxylic_acid_catabolic_process	17	1	4.244186	-0.67477	138	99.518065	158.05	216.581935	1.14529
GO:0009737_response_to_abscisic_acid_stimulus	62	2	2.327457	-0.673638	139	99.937609	158.59	217.242391	1.140935
GO:0006576_cellular_biogenic_amine_metabolic_process	18	1	4.008398	-0.652827	140	103.15769	162.78	222.40231	1.162714
GO:0006897_endocytosis	19	1	3.79743	-0.632219	146	108.205901	169.55	230.894099	1.161301
GO:0016114_terpenoid_biosynthetic_process	19	1	3.79743	-0.632219	146	108.205901	169.55	230.894099	1.161301
GO:0034599_cellular_response_to_oxidative_stress	19	1	3.79743	-0.632219	146	108.205901	169.55	230.894099	1.161301
GO:0044403_symbiosis__encompassing_mutualism_through_	19	1	3.79743	-0.632219	146	108.205901	169.55	230.894099	1.161301
GO:0045333_cellular_respiration	19	1	3.79743	-0.632219	146	108.205901	169.55	230.894099	1.161301
GO:0048666_neuron_development	19	1	3.79743	-0.632219	146	108.205901	169.55	230.894099	1.161301
GO:0019438_aromatic_compound_biosynthetic_process	67	2	2.153766	-0.62409	147	108.914392	170.44	231.965608	1.159456
GO:0016052_carbohydrate_catabolic_process	68	2	2.122093	-0.614781	148	110.015149	171.76	233.504851	1.160541
GO:0009723_response_to_ethylene_stimulus	20	1	3.607558	-0.612809	150	111.902771	174.37	236.837229	1.162467
GO:0044242_cellular_lipid_catabolic_process	20	1	3.607558	-0.612809	150	111.902771	174.37	236.837229	1.162467
GO:0006631_fatty_acid_metabolic_process	70	2	2.061462	-0.596715	151	113.87229	177.11	240.34771	1.172914
GO:0009072_aromatic_amino_acid_family_metabolic_process	21	1	3.43577	-0.59448	156	116.166205	179.82	243.473795	1.152692
GO:0009267_cellular_response_to_starvation	21	1	3.43577	-0.59448	156	116.166205	179.82	243.473795	1.152692
GO:0009886_post-embryonic_morphogenesis	21	1	3.43577	-0.59448	156	116.166205	179.82	243.473795	1.152692
GO:0010324_membrane_invagination	21	1	3.43577	-0.59448	156	116.166205	179.82	243.473795	1.152692
GO:0030182_neuron_differentiation	21	1	3.43577	-0.59448	156	116.166205	179.82	243.473795	1.152692
GO:0000302_response_to_reactive_oxygen_species	22	1	3.279598	-0.57713	162	120.697912	185.47	250.242088	1.144877
GO:0003002_regionalization	22	1	3.279598	-0.57713	162	120.697912	185.47	250.242088	1.144877
GO:0006575_cellular_modified_amino_acid_metabolic_process	22	1	3.279598	-0.57713	162	120.697912	185.47	250.242088	1.144877
GO:0009064_glutamine_family_amino_acid_metabolic_process	22	1	3.279598	-0.57713	162	120.697912	185.47	250.242088	1.144877
GO:0009887_organ_morphogenesis	22	1	3.279598	-0.57713	162	120.697912	185.47	250.242088	1.144877
GO:0031669_cellular_response_to_nutrient_levels	22	1	3.279598	-0.57713	162	120.697912	185.47	250.242088	1.144877
GO:0051726_regulation_of_cell_cycle	74	2	1.950031	-0.562647	163	122.893736	188.6	254.306264	1.157055
GO:0000075_cell_cycle_checkpoint	23	1	3.137007	-0.560672	169	126.983905	193.74	260.496095	1.146391
GO:0006721_terpenoid_metabolic_process	23	1	3.137007	-0.560672	169	126.983905	193.74	260.496095	1.146391
GO:0007389_pattern_specification_process	23	1	3.137007	-0.560672	169	126.983905	193.74	260.496095	1.146391
GO:0009405_pathogenesis	23	1	3.137007	-0.560672	169	126.983905	193.74	260.496095	1.146391
GO:0048438_floral_whorl_development	23	1	3.137007	-0.560672	169	126.983905	193.74	260.496095	1.146391
GO:0071156_regulation_of_cell_cycle_arrest	23	1	3.137007	-0.560672	169	126.983905	193.74	260.496095	1.146391
GO:0009628_response_to_abiotic_stimulus	320	6	1.352834	-0.548724	170	128.379298	195.44	262.500702	1.149647
GO:0007005_mitochondrion_organization	24	1	3.006298	-0.545029	171	131.919939	199.91	267.900061	1.169064
GO:0008610_lipid_biosynthetic_process	136	3	1.59157	-0.535228	172	133.139333	201.58	270.020667	1.171977
GO:0022008_neurogenesis	25	1	2.886047	-0.530134	177	138.460957	208.57	278.679043	1.178362
GO:0040011_locomotion	25	1	2.886047	-0.530134	177	138.460957	208.57	278.679043	1.178362
GO:0042594_response_to_starvation	25	1	2.886047	-0.530134	177	138.460957	208.57	278.679043	1.178362
GO:0044419_interspecies_interaction_between_organisms	25	1	2.886047	-0.530134	177	138.460957	208.57	278.679043	1.178362
GO:0048699_generation_of_neurons	25	1	2.886047	-0.530134	177	138.460957	208.57	278.679043	1.178362
GO:0007165_signal_transduction	328	6	1.319838	-0.519804	178	139.378515	209.52	279.661485	1.177079
GO:0009116_nucleoside_metabolic_process	26	1	2.775045	-0.515928	181	143.964972	215.09	286.215028	1.188343
GO:0043648_dicarboxylic_acid_metabolic_process	26	1	2.775045	-0.515928	181	143.964972	215.09	286.215028	1.188343
GO:0048437_floral_organ_development	26	1	2.775045	-0.515928	181	143.964972	215.09	286.215028	1.188343
GO:0007050_cell_cycle_arrest	27	1	2.672265	-0.502358	183	148.971808	220.53	292.088192	1.205082
GO:0015980_energy_derivation_by_oxidation_of_organic_com	27	1	2.672265	-0.502358	183	148.971808	220.53	292.088192	1.205082
GO:0005976_polysaccharide_metabolic_process	82	2	1.759784	-0.501756	184	149.250156	220.91	292.569844	1.200598
GO:0016042_lipid_catabolic_process	28	1	2.576827	-0.489378	185	153.80299	225.64	297.47701	1.219676
GO:0006629_lipid_metabolic_process	275	5	1.311839	-0.477323	186	155.021503	226.99	298.958497	1.220376
GO:0006417_regulation_of_translation	29	1	2.487971	-0.476945	187	156.628856	228.88	301.131144	1.223957
GO:0023060_signal_transmission	342	6	1.26581	-0.47265	188	157.117438	229.49	301.862562	1.220691
GO:0023046_signaling_process	344	6	1.258451	-0.466254	189	157.731965	230.2	302.668035	1.217989
GO:0007399_nervous_system_development	30	1	2.405039	-0.465023	190	160.359261	233.4	306.440739	1.228421
GO:0019752_carboxylic_acid_metabolic_process	280	5	1.288414	-0.459587	192	161.273356	234.51	307.746644	1.221406
GO:0043436_oxoacid_metabolic_process	280	5	1.288414	-0.459587	192	161.273356	234.51	307.746644	1.221406
GO:0006082_organic_acid_metabolic_process	282	5	1.279276	-0.452675	193	164.652793	238.44	312.227207	1.23544
GO:0009308_amine_metabolic_process	217	4	1.329975	-0.450476	194	165.158683	238.93	312.701317	1.231598
GO:0042180_cellular_ketone_metabolic_process	283	5	1.274756	-0.449257	195	165.304966	239.1	312.895034	1.226154

GO:0044271_cellular_nitrogen_compound_biosynthetic_proces	218	4	1.323875	-0.446593	196	166.834673	240.96	315.085327	1.229388
GO:0010200_response_to_chitin	32	1	2.254724	-0.442576	199	169.386197	244.04	318.693803	1.226332
GO:0045786_negative_regulation_of_cell_cycle	32	1	2.254724	-0.442576	199	169.386197	244.04	318.693803	1.226332
GO:0080167_response_to_karrikin	32	1	2.254724	-0.442576	199	169.386197	244.04	318.693803	1.226332
GO:0009725_response_to_hormone_stimulus	155	3	1.396474	-0.438766	200	169.810734	244.6	319.389266	1.223
GO:0031667_response_to_nutrient_levels	34	1	2.122093	-0.421802	204	177.306923	253.56	329.813077	1.242941
GO:0032504_multicellular_organism_reproduction	34	1	2.122093	-0.421802	204	177.306923	253.56	329.813077	1.242941
GO:0043623_cellular_protein_complex_assembly	34	1	2.122093	-0.421802	204	177.306923	253.56	329.813077	1.242941
GO:0048609_multicellular_organismal_reproductive_process	34	1	2.122093	-0.421802	204	177.306923	253.56	329.813077	1.242941
GO:0009699_phenylpropanoid_biosynthetic_process	36	1	2.004199	-0.402508	205	181.727743	258.57	335.412257	1.261317
GO:0048610_cellular_process_involved_in_reproduction	99	2	1.457599	-0.39749	206	182.180346	259.14	336.099654	1.257961
GO:0045941_positive_regulation_of_transcription	37	1	1.950031	-0.393363	207	184.144333	261.21	338.275667	1.261884
GO:0042545_cell_wall_modification	100	2	1.443023	-0.392219	208	184.36912	261.45	338.53088	1.256971
GO:0010628_positive_regulation_of_gene_expression	38	1	1.898715	-0.384529	209	191.414808	268.67	345.925192	1.285502
GO:0008219_cell_death	170	3	1.273256	-0.376023	210	192.853624	270.38	347.906376	1.287524
GO:0032268_regulation_of_cellular_protein_metabolic_process	39	1	1.85003	-0.37599	211	194.191403	272.07	349.948597	1.289431
GO:0006468_protein_phosphorylation	655	10	1.101544	-0.373336	212	194.36596	272.24	350.11404	1.284151
GO:0070887_cellular_response_to_chemical_stimulus	104	2	1.387522	-0.371948	213	194.496795	272.39	350.283205	1.278826
GO:0016265_death	172	3	1.258451	-0.368411	214	195.024876	273.09	351.155124	1.276121
GO:0009555_pollen_development	40	1	1.803779	-0.367729	217	197.206847	275.51	353.813153	1.269631
GO:0010557_positive_regulation_of_macromolecule_biosynthe	40	1	1.803779	-0.367729	217	197.206847	275.51	353.813153	1.269631
GO:0010564_regulation_of_cell_cycle_process	40	1	1.803779	-0.367729	217	197.206847	275.51	353.813153	1.269631
GO:0044283_small_molecule_biosynthetic_process	241	4	1.19753	-0.366057	218	197.334829	275.76	354.185171	1.264954
GO:0010608_posttranscriptional_regulation_of_gene_expressio	41	1	1.759784	-0.359734	219	199.456358	277.89	356.323642	1.268904
GO:0033554_cellular_response_to_stress	176	3	1.229849	-0.353673	220	200.558607	279.29	358.021393	1.2695
GO:0042493_response_to_drug	42	1	1.717885	-0.35199	223	202.4899	281.5	360.5101	1.262332
GO:0045935_positive_regulation_of_nucleobase__nucleoside_	42	1	1.717885	-0.35199	223	202.4899	281.5	360.5101	1.262332
GO:0051173_positive_regulation_of_nitrogen_compound_meta	42	1	1.717885	-0.35199	223	202.4899	281.5	360.5101	1.262332
GO:0051246_regulation_of_protein_metabolic_process	43	1	1.677934	-0.344486	224	206.103379	285.81	365.516621	1.275938
GO:0032787_monocarboxylic_acid_metabolic_process	110	2	1.311839	-0.343798	226	207.048569	286.96	366.871431	1.269735
GO:0034622_cellular_macromolecular_complex_assembly	110	2	1.311839	-0.343798	226	207.048569	286.96	366.871431	1.269735
GO:0006520_cellular_amino_acid_metabolic_process	179	3	1.209237	-0.343028	227	207.271067	287.17	367.068933	1.265066
GO:0000904_cell_morphogenesis_involved_in_differentiation	44	1	1.639799	-0.33721	228	210.000033	290.31	370.619967	1.273289
GO:0016310_phosphorylation	674	10	1.070492	-0.337034	229	210.20358	290.51	370.81642	1.268603
GO:0009891_positive_regulation_of_biosynthetic_process	45	1	1.603359	-0.330152	231	212.509529	293.18	373.850471	1.269177
GO:0031328_positive_regulation_of_cellular_biosynthetic_proc	45	1	1.603359	-0.330152	231	212.509529	293.18	373.850471	1.269177
GO:0006725_cellular_aromatic_compound_metabolic_process	115	2	1.254803	-0.32221	232	215.472954	296.21	376.947046	1.276767
GO:0051716_cellular_response_to_stimulus	256	4	1.127362	-0.321522	233	215.610928	296.43	377.249072	1.272232
GO:0006633_fatty_acid_biosynthetic_process	47	1	1.535131	-0.316651	236	217.810722	298.88	379.949278	1.266441
GO:0016044_cellular_membrane_organization	47	1	1.535131	-0.316651	236	217.810722	298.88	379.949278	1.266441
GO:0061024_membrane_organization	47	1	1.535131	-0.316651	236	217.810722	298.88	379.949278	1.266441
GO:0006461_protein_complex_assembly	48	1	1.503149	-0.31019	238	221.238324	302.58	383.921676	1.271345
GO:0070271_protein_complex_biogenesis	48	1	1.503149	-0.31019	238	221.238324	302.58	383.921676	1.271345
GO:0044106_cellular_amine_metabolic_process	190	3	1.139229	-0.306774	239	221.846227	303.3	384.753773	1.269038
GO:0010604_positive_regulation_of_macromolecule_metabolic	49	1	1.472473	-0.303911	240	224.210418	306.02	387.829582	1.275083
GO:0044282_small_molecule_catabolic_process	120	2	1.202519	-0.302156	242	225.324117	307.14	388.955883	1.269174
GO:0065003_macromolecular_complex_assembly	120	2	1.202519	-0.302156	242	225.324117	307.14	388.955883	1.269174
GO:0031325_positive_regulation_of_cellular_metabolic_proces	50	1	1.443023	-0.297806	243	229.124501	310.96	392.795499	1.279671
GO:0009893_positive_regulation_of_metabolic_process	52	1	1.387522	-0.286091	244	234.136609	316.38	398.623391	1.296639
GO:0023052_signaling	487	7	1.03708	-0.285799	245	234.46307	316.75	399.03693	1.292857
GO:0009743_response_to_carbohydrate_stimulus	53	1	1.361343	-0.280468	246	236.544329	319.18	401.815671	1.29748
GO:0034621_cellular_macromolecular_complex_subunit_organ	129	2	1.118623	-0.269498	248	242.045892	325.17	408.294108	1.311169
GO:0040007_growth	129	2	1.118623	-0.269498	248	242.045892	325.17	408.294108	1.311169
GO:0009908_flower_development	56	1	1.288414	-0.264465	249	244.342147	327.52	410.697853	1.315341
GO:0006796_phosphate_metabolic_process	719	10	1.003493	-0.262789	250	244.61387	327.79	410.96613	1.31116
GO:0006793_phosphorus_metabolic_process	720	10	1.002099	-0.261312	251	245.186982	328.54	411.893018	1.308924
GO:0009698_phenylpropanoid_metabolic_process	58	1	1.243986	-0.254465	253	250.502175	333.97	417.437825	1.32004
GO:0048229_gametophyte_development	58	1	1.243986	-0.254465	253	250.502175	333.97	417.437825	1.32004
GO:0071555_cell_wall_organization	134	2	1.076883	-0.25306	254	251.745838	335.14	418.534162	1.319449
GO:0071844_cellular_component_assembly_at_cellular_level	135	2	1.068906	-0.249907	255	252.441507	335.93	419.418493	1.317373
GO:2000026_regulation_of_multicellular_organismal_developm	60	1	1.202519	-0.244956	256	256.056277	339.71	423.363723	1.326992

GO:0043933_macromolecular_complex_subunit_organization	138	2	1.045669	-0.240702	257	256.562876	340.24	423.917124	1.323891
GO:0009057_macromolecule_catabolic_process	139	2	1.038146	-0.237716	258	258.504016	342.35	426.195984	1.326938
GO:0018130_heterocycle_biosynthetic_process	62	1	1.163728	-0.235904	260	259.574787	343.61	427.645213	1.321577
GO:0071495_cellular_response_to_endogenous_stimulus	62	1	1.163728	-0.235904	260	259.574787	343.61	427.645213	1.321577
GO:0071822_protein_complex_subunit_organization	64	1	1.127362	-0.227277	261	263.57517	347.67	431.76483	1.332069
GO:0022607_cellular_component_assembly	144	2	1.002099	-0.223377	262	264.582795	348.82	433.057205	1.331374
GO:0007047_cellular_cell_wall_organization	68	1	1.061047	-0.211195	263	269.25449	353.71	438.16551	1.344905
GO:0045454_cell_redox_homeostasis	69	1	1.045669	-0.2074	265	272.147034	356.78	441.412966	1.34634
GO:0051239_regulation_of_multicellular_organismal_process	69	1	1.045669	-0.2074	265	272.147034	356.78	441.412966	1.34634
GO:0007049_cell_cycle	151	2	0.955645	-0.204844	266	273.165648	357.76	442.354352	1.344962
GO:0046700_heterocycle_catabolic_process	70	1	1.030731	-0.20369	267	274.487106	359.15	443.812894	1.345131
GO:0033036_macromolecule_localization	312	4	0.925015	-0.197278	268	276.50766	361.33	446.15234	1.348246
GO:0050793_regulation_of_developmental_process	72	1	1.002099	-0.196514	269	277.19822	362.13	447.06178	1.346208
GO:0044248_cellular_catabolic_process	236	3	0.917176	-0.192814	270	278.819021	363.63	448.440979	1.346778
GO:0045229_external_encapsulating_structure_organization	74	1	0.975016	-0.189647	272	281.495651	366.09	450.684349	1.345919
GO:0071310_cellular_response_to_organic_substance	74	1	0.975016	-0.189647	272	281.495651	366.09	450.684349	1.345919
GO:0012501_programmed_cell_death	159	2	0.907562	-0.18565	273	282.563709	367.23	451.896291	1.345165
GO:0016567_protein_ubiquitination	77	1	0.937028	-0.179888	274	285.846637	370.5	455.153363	1.35219
GO:0032446_protein_modification_by_small_protein_conjugatio	78	1	0.925015	-0.176772	275	287.210772	371.87	456.529228	1.352255
GO:0030001_metal_ion_transport	79	1	0.913306	-0.17372	276	288.242575	372.97	457.697425	1.351341
GO:0006091_generation_of_precursor_metabolites_and_energ	80	1	0.90189	-0.170732	278	290.651645	375.36	460.068355	1.350216
GO:0070882_cellular_cell_wall_organization_or_biogenesis	80	1	0.90189	-0.170732	278	290.651645	375.36	460.068355	1.350216
GO:0048468_cell_development	81	1	0.890755	-0.167805	279	292.504185	377.34	462.175815	1.352473
GO:0071840_cellular_component_organization_or_biogenesis	651	8	0.88665	-0.158939	280	295.218304	379.98	464.741696	1.357071
GO:0048522_positive_regulation_of_cellular_process	85	1	0.848837	-0.15668	282	296.730258	381.5	466.269742	1.352837
GO:0070647_protein_modification_by_small_protein_conjugatio	85	1	0.848837	-0.15668	282	296.730258	381.5	466.269742	1.352837
GO:0006464_protein_modification_process	892	11	0.889756	-0.149088	283	298.68071	383.37	468.05929	1.354664
GO:0048513_organ_development	177	2	0.815267	-0.149043	285	299.081178	383.78	468.478822	1.346596
GO:0055086_nucleobase__nucleoside_and_nucleotide_metabo	177	2	0.815267	-0.149043	285	299.081178	383.78	468.478822	1.346596
GO:0000902_cell_morphogenesis	90	1	0.80168	-0.143975	286	303.053145	387.54	472.026855	1.355035
GO:0044281_small_molecule_metabolic_process	595	7	0.848837	-0.136337	287	305.794929	390.17	474.545071	1.359477
GO:0050794_regulation_of_cellular_process	908	11	0.874078	-0.135488	288	305.975451	390.39	474.804549	1.355521
GO:0006457_protein_folding	96	1	0.751575	-0.13028	290	309.083575	393.44	477.796425	1.35669
GO:0032989_cellular_component_morphogenesis	96	1	0.751575	-0.13028	290	309.083575	393.44	477.796425	1.35669
GO:0048731_system_development	194	2	0.743826	-0.121298	291	313.31859	397.37	481.42141	1.365533
GO:0019725_cellular_homeostasis	101	1	0.714368	-0.120002	292	317.098852	401.01	484.921148	1.373322
GO:0016192_vesicle-mediated_transport	103	1	0.700497	-0.116151	294	319.308674	403.16	487.011326	1.371293
GO:0048518_positive_regulation_of_biological_process	103	1	0.700497	-0.116151	294	319.308674	403.16	487.011326	1.371293
GO:0022402_cell_cycle_process	107	1	0.67431	-0.108861	295	322.258006	406.19	490.121994	1.376915
GO:0009416_response_to_light_stimulus	110	1	0.65592	-0.10373	297	325.745163	409.42	493.094837	1.378519
GO:0048523_negative_regulation_of_cellular_process	110	1	0.65592	-0.10373	297	325.745163	409.42	493.094837	1.378519
GO:0043412_macromolecule_modification	955	11	0.831061	-0.101415	298	326.28853	409.98	493.67147	1.375772
GO:0042254_ribosome_biogenesis	114	1	0.632905	-0.097302	299	327.034176	410.69	494.345824	1.373545
GO:0006974_response_to_DNA_damage_stimulus	117	1	0.616677	-0.09277	300	329.153773	412.6	496.046227	1.375333
GO:0022414_reproductive_process	308	3	0.702771	-0.092586	301	329.301186	412.75	496.198814	1.371262
GO:0009791_post-embryonic_development	219	2	0.658915	-0.089694	302	330.696573	413.85	497.003427	1.370364
GO:0009314_response_to_radiation	120	1	0.60126	-0.088469	303	332.48359	415.42	498.35641	1.371023
GO:0006508_proteolysis	403	4	0.716141	-0.086657	304	334.202081	417.02	499.837919	1.371776
GO:0022613_ribonucleoprotein_complex_biogenesis	124	1	0.581864	-0.083071	305	336.215379	418.66	501.104621	1.372656
GO:0000003_reproduction	321	3	0.67431	-0.080921	306	337.092595	419.42	501.747405	1.370654
GO:0030154_cell_differentiation	126	1	0.572628	-0.080507	307	337.448007	419.74	502.031993	1.367231
GO:0005975_carbohydrate_metabolic_process	500	5	0.721512	-0.078921	308	338.207044	420.39	502.572956	1.364903
GO:0048519_negative_regulation_of_biological_process	131	1	0.550772	-0.074465	309	341.297756	422.93	504.562244	1.368706
GO:0006812_cation_transport	133	1	0.54249	-0.072187	310	342.324616	423.87	505.415384	1.367323
GO:0009790_embryo_development	134	1	0.538442	-0.071076	311	343.067242	424.66	506.252758	1.365466
GO:0050789_regulation_of_biological_process	1019	11	0.778864	-0.066884	312	344.989359	426.27	507.550641	1.36625
GO:0046483_heterocycle_metabolic_process	244	2	0.591403	-0.066317	313	345.60716	426.74	507.87284	1.363387
GO:0071843_cellular_component_biogenesis_at_cellular_level	139	1	0.519073	-0.06579	314	346.334299	427.34	508.345701	1.360955
GO:0042592_homeostatic_process	142	1	0.508107	-0.062821	315	347.931522	428.78	509.628478	1.361206
GO:0006915_apoptosis	145	1	0.497594	-0.059994	316	349.531655	429.99	510.448345	1.360728
GO:0051179_localization	708	7	0.713359	-0.058163	317	350.07528	430.4	510.72472	1.357729

GO:0010035_response_to_inorganic_substance	148	1	0.487508	-0.057302	318	351.032021	431.11	511.187979	1.355692
GO:2000112_regulation_of_cellular_macromolecule_biosynthet	449	4	0.642772	-0.0561	319	351.32334	431.37	511.41666	1.352257
GO:0010556_regulation_of_macromolecule_biosynthetic_proce	450	4	0.641344	-0.055564	320	351.474057	431.5	511.525943	1.348438
GO:0070727_cellular_macromolecule_localization	153	1	0.471576	-0.053094	321	352.856501	432.63	512.403499	1.347757
GO:0016043_cellular_component_organization	457	4	0.63152	-0.051938	322	353.391446	433.02	512.648554	1.344783
GO:0006355_regulation_of_transcription__DNA-dependent	265	2	0.544537	-0.051414	323	353.971147	433.5	513.028853	1.342105
GO:0044085_cellular_component_biogenesis	266	2	0.54249	-0.050793	324	354.12242	433.66	513.19758	1.338457
GO:0010468_regulation_of_gene_expression	460	4	0.627401	-0.050452	326	354.854555	434.26	513.665445	1.332086
GO:0031326_regulation_of_cellular_biosynthetic_process	460	4	0.627401	-0.050452	326	354.854555	434.26	513.665445	1.332086
GO:0009889_regulation_of_biosynthetic_process	461	4	0.62604	-0.049966	327	355.212456	434.52	513.827544	1.328807
GO:0006753_nucleoside_phosphate_metabolic_process	157	1	0.459562	-0.049962	329	355.852102	435.12	514.387898	1.322553
GO:0009117_nucleotide_metabolic_process	157	1	0.459562	-0.049962	329	355.852102	435.12	514.387898	1.322553
GO:0051252_regulation_of_RNA_metabolic_process	268	2	0.538442	-0.049573	330	356.083035	435.29	514.496965	1.319061
GO:0006996_organelle_organization	276	2	0.522835	-0.044973	331	358.099819	436.94	515.780181	1.32006
GO:0006811_ion_transport	165	1	0.43728	-0.044265	332	358.569938	437.38	516.190062	1.31741
GO:0006810_transport	662	6	0.653938	-0.041499	333	360.91031	439.36	517.80969	1.319399
GO:0048869_cellular_developmental_process	172	1	0.419484	-0.039835	334	361.929322	440.21	518.490678	1.317994
GO:0051234_establishment_of_localization	667	6	0.649036	-0.039741	335	362.267691	440.52	518.772309	1.314985
GO:0032501_multicellular_organismal_process	486	4	0.593837	-0.039127	336	362.436096	440.62	518.803904	1.311369
GO:0009653_anatomical_structure_morphogenesis	175	1	0.412292	-0.038079	337	362.916722	440.91	518.903278	1.308338
GO:0060255_regulation_of_macromolecule_metabolic_process	491	4	0.58779	-0.037239	338	363.795146	441.47	519.144854	1.306124
GO:0006351_transcription__DNA-dependent	293	2	0.492499	-0.036539	339	364.582827	442.11	519.637173	1.304159
GO:0032774_RNA_biosynthetic_process	294	2	0.490824	-0.036094	340	364.842224	442.3	519.757776	1.300882
GO:0032502_developmental_process	506	4	0.570365	-0.03207	341	365.92486	442.98	520.03514	1.299062
GO:0045449_regulation_of_transcription	409	3	0.529226	-0.031705	342	366.287726	443.21	520.132274	1.295936
GO:0080090_regulation_of_primary_metabolic_process	508	4	0.568119	-0.031434	343	366.580947	443.37	520.159053	1.292624
GO:0006259_DNA_metabolic_process	190	1	0.379743	-0.030424	344	367.609988	444.17	520.730012	1.291192
GO:0065007_biological_regulation	1132	11	0.701116	-0.030031	345	367.826198	444.29	520.753802	1.287797
GO:0048608_reproductive_structure_development	194	1	0.371913	-0.028663	346	368.668579	444.94	521.211421	1.285954
GO:0031323_regulation_of_cellular_metabolic_process	520	4	0.555009	-0.027854	347	369.000305	445.13	521.259695	1.282795
GO:0071842_cellular_component_organization_at_cellular_leve	324	2	0.445378	-0.024944	348	370.790258	446.47	522.149742	1.28296
GO:0008152_metabolic_process	4038	49	0.875534	-0.020518	349	371.391702	447.04	522.688298	1.280917
GO:0055085_transmembrane_transport	224	1	0.322103	-0.018366	350	373.304419	448.37	523.435581	1.281057
GO:0019219_regulation_of_nucleobase__nucleoside__nucleoti	461	3	0.46953	-0.017803	351	374.155311	448.82	523.484689	1.278689
GO:0051171_regulation_of_nitrogen_compound_metabolic_pro	466	3	0.464492	-0.016826	352	374.818879	449.22	523.621121	1.276193
GO:0019538_protein_metabolic_process	1712	17	0.716454	-0.015847	353	374.977184	449.31	523.642816	1.272833
GO:0006350_transcription	476	3	0.454734	-0.015021	354	375.369656	449.7	524.030344	1.270339
GO:0003006_developmental_process_involved_in_reproductio	242	1	0.298145	-0.014077	355	375.832306	449.99	524.147694	1.267577
GO:0044267_cellular_protein_metabolic_process	1411	13	0.664752	-0.012786	356	376.384535	450.38	524.375465	1.265112
GO:0019222_regulation_of_metabolic_process	598	4	0.482616	-0.012369	357	376.750114	450.58	524.409886	1.262129
GO:0006412_translation	382	2	0.377755	-0.012062	358	376.8595	450.65	524.4405	1.258799
GO:0051641_cellular_localization	253	1	0.285182	-0.011967	359	377.037737	450.76	524.482263	1.255599
GO:0071841_cellular_component_organization_or_biogenesis_	501	3	0.432043	-0.011279	360	377.390877	451	524.609123	1.252778
GO:0065008_regulation_of_biological_quality	276	1	0.261417	-0.008524	361	379.427571	452.28	525.132429	1.252853
GO:0048856_anatomical_structure_development	410	2	0.351957	-0.00844	362	379.615699	452.39	525.164301	1.249696
GO:0023033_signaling_pathway	282	1	0.255855	-0.007802	363	380.065217	452.68	525.294783	1.247052
GO:0007275_multicellular_organismal_development	440	2	0.32796	-0.005731	364	381.215011	453.36	525.504989	1.245495
GO:0006807_nitrogen_compound_metabolic_process	1228	9	0.528795	-0.002845	365	383.085433	454.39	525.694567	1.244904
GO:0043170_macromolecule_metabolic_process	2480	23	0.669144	-0.001534	366	383.649513	454.7	525.750487	1.24235
GO:0044249_cellular_biosynthetic_process	1294	9	0.501824	-0.001462	367	383.649513	454.7	525.750487	1.238965
GO:0016070_RNA_metabolic_process	546	2	0.26429	-0.001405	368	383.667582	454.72	525.772418	1.235652
GO:0034641_cellular_nitrogen_compound_metabolic_process	1208	8	0.477822	-0.001323	369	383.746113	454.76	525.773887	1.232412
GO:0006139_nucleobase__nucleoside__nucleotide_and_nucle	1043	6	0.415059	-0.000898	370	383.940752	454.89	525.839248	1.229432
GO:0034645_cellular_macromolecule_biosynthetic_process	958	5	0.376572	-0.0007	371	383.940752	454.89	525.839248	1.226119
GO:0009059_macromolecule_biosynthetic_process	963	5	0.374617	-0.00066	372	383.961059	454.9	525.838941	1.222849
GO:0009058_biosynthetic_process	1376	9	0.471919	-0.000613	373	384.064347	454.98	525.895653	1.219786
GO:0090304_nucleic_acid_metabolic_process	863	4	0.33442	-0.000568	374	384.150084	455.02	525.889916	1.216631
GO:0044238_primary_metabolic_process	3240	31	0.690335	-0.000362	375	384.355714	455.16	525.964286	1.21376
GO:0010467_gene_expression	1013	5	0.356126	-0.00036	376	384.3916	455.18	525.9684	1.210585
GO:0044237_cellular_metabolic_process	2778	24	0.623336	-0.000177	377	384.544377	455.26	525.975623	1.207586
GO:0044260_cellular_macromolecule_metabolic_process	2160	16	0.534453	-0.000119	378	384.5672	455.27	525.9728	1.204418

GO:0009987_cellular_process	3659	33	0.650721	-0.000015	379	384.727726	455.42	526.112274	1.201636
GO:0005996_monosaccharide_metabolic_process	73	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006066_alcohol_metabolic_process	128	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006163_purine_nucleotide_metabolic_process	120	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006164_purine_nucleotide_biosynthetic_process	72	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006260_DNA_replication	73	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006281_DNA_repair	109	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006325_chromatin_organization	103	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006396_RNA_processing	167	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006399_tRNA_metabolic_process	75	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006511_ubiquitin-dependent_protein_catabolic_process	89	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0006886_intracellular_protein_transport	130	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0007017_microtubule-based_process	83	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0007166_cell_surface_receptor_linked_signaling_pathway	75	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0007264_small_GTPase_mediated_signal_transduction	80	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0008104_protein_localization	225	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0008150_biological_process	6205	86	1	0	439	425.11131	487.36	549.60869	1.110159
GO:0008361_regulation_of_cell_size	90	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009141_nucleoside_triphosphate_metabolic_process	103	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009144_purine_nucleoside_triphosphate_metabolic_proce	101	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009150_purine_ribonucleotide_metabolic_process	111	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009165_nucleotide_biosynthetic_process	91	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009199_ribonucleoside_triphosphate_metabolic_process	101	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009205_purine_ribonucleoside_triphosphate_metabolic_p	101	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009259_ribonucleotide_metabolic_process	116	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009260_ribonucleotide_biosynthetic_process	71	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009266_response_to_temperature_stimulus	93	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009793_embryo_development_ending_in_seed_dormanc	101	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0009888_tissue_development	78	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0010038_response_to_metal_ion	123	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0010154_fruit_development	121	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0015031_protein_transport	197	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0016049_cell_growth	89	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0016051_carbohydrate_biosynthetic_process	80	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0019941_modification-dependent_protein_catabolic_proces	90	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0022403_cell_cycle_phase	77	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0023034_intracellular_signaling_pathway	156	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0030163_protein_catabolic_process	106	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0032535_regulation_of_cellular_component_size	92	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0034404_nucleobase__nucleoside_and_nucleotide_biosyn	96	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0034613_cellular_protein_localization	144	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0034654_nucleobase__nucleoside__nucleotide_and_nucle	96	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0034660_ncRNA_metabolic_process	101	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0035556_intracellular_signal_transduction	108	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0043632_modification-dependent_macromolecule_catabolic	90	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0044257_cellular_protein_catabolic_process	96	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0044262_cellular_carbohydrate_metabolic_process	202	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0044265_cellular_macromolecule_catabolic_process	106	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0045184_establishment_of_protein_localization	199	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0046686_response_to_cadmium_ion	92	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0046907_intracellular_transport	193	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0048316_seed_development	115	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0048589_developmental_growth	88	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0050790_regulation_of_catalytic_activity	98	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0051186_cofactor_metabolic_process	82	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0051276_chromosome_organization	145	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0051603_proteolysis_involved_in_cellular_protein_catabolic	93	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0051649_establishment_of_localization_in_cell	221	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0060560_developmental_growth_involved_in_morphogene	77	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0065009_regulation_of_molecular_function	101	0	0	0	439	425.11131	487.36	549.60869	1.110159
GO:0090066_regulation_of_anatomical_structure_size	94	0	0	0	439	425.11131	487.36	549.60869	1.110159

GO:0000724_double-strand_break_repair_via_homologous_rec	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0002520_immune_system_development	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0002682_regulation_of_immune_system_process	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0006071_glycerol_metabolic_process	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0006354_transcription_elongation__DNA-dependent	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0006415_translational_termination	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0007062_sister_chromatid_cohesion	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0007163_establishment_or_maintenance_of_cell_polarity	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0009411_response_to_UV	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0010053_root_epidermal_cell_differentiation	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0016138_glycoside_biosynthetic_process	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0019932_second-messenger-mediated_signaling	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0022415_viral_reproductive_process	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0045944_positive_regulation_of_transcription_from_RNA_p	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0048545_response_to_steroid_hormone_stimulus	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0051656_establishment_of_organelle_localization	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0090329_regulation_of_DNA-dependent_DNA_replication	15	0	0	0	456	442.805604	503.49	564.174396	1.104145
GO:0000723_telomere_maintenance	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0006096_glycolysis	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0006875_cellular_metal_ion_homeostasis	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0008033_tRNA_processing	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0008654_phospholipid_biosynthetic_process	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0010646_regulation_of_cell_communication	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0015849_organic_acid_transport	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0021700_developmental_maturation	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0032200_telomere_organization	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0045892_negative_regulation_of_transcription__DNA-depe	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0046942_carboxylic_acid_transport	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0051253_negative_regulation_of_RNA_metabolic_process	22	0	0	0	468	457.424681	516.88	576.335319	1.104444
GO:0000746_conjugation	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0000747_conjugation_with_cellular_fusion	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0001558_regulation_of_cell_growth	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0002252_immune_effector_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006012_galactose_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006213_pyrimidine_nucleoside_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006271_DNA_strand_elongation_involved_in_DNA_replic	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006312_mitotic_recombination	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006368_transcription_elongation_from_RNA_polymerase_	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006541_glutamine_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006635_fatty_acid_beta-oxidation	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006665_sphingolipid_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006949_syncytium_formation	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0007610_behavior	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0008360_regulation_of_cell_shape	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0009606_tropism	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0010054_trichoblast_differentiation	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0015914_phospholipid_transport	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0016128_phytosteroid_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0019362_pyridine_nucleotide_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0022616_DNA_strand_elongation	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0030097_hemopoiesis	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0030243_cellulose_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0032506_cytokinetic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0033205_cell_cycle_cytokinesis	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0042157_lipoprotein_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0043549_regulation_of_kinase_activity	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0045017_glycerolipid_biosynthetic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0048284_organelle_fusion	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0048511_rhythmic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0048534_hemopoietic_or_lymphoid_organ_development	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0051053_negative_regulation_of_DNA_metabolic_process	12	0	0	0	505	497.549766	554.87	612.190234	1.098752

GO:0051130_positive_regulation_of_cellular_component_orgar	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0051320_S_phase	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0051338_regulation_of_transferase_activity	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0065002_intracellular_protein_transmembrane_transport	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0070838_divalent_metal_ion_transport	12	0	0	0	505	497.549766	554.87	612.190234	1.098752
GO:0006261_DNA-dependent_DNA_replication	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0006486_protein_glycosylation	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0009100_glycoprotein_metabolic_process	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0009101_glycoprotein_biosynthetic_process	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0009408_response_to_heat	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0009894_regulation_of_catabolic_process	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0022621_shoot_system_development	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0043413_macromolecule_glycosylation	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0070085_glycosylation	38	0	0	0	514	503.244386	559.91	616.575614	1.089319
GO:0000398_nuclear_mRNA_splicing__via_spliceosome	21	0	0	0	520	512.168672	568.11	624.051328	1.092519
GO:0006367_transcription_initiation_from_RNA_polymerase_II	21	0	0	0	520	512.168672	568.11	624.051328	1.092519
GO:0032318_regulation_of_Ras_GTPase_activity	21	0	0	0	520	512.168672	568.11	624.051328	1.092519
GO:0032879_regulation_of_localization	21	0	0	0	520	512.168672	568.11	624.051328	1.092519
GO:0042446_hormone_biosynthetic_process	21	0	0	0	520	512.168672	568.11	624.051328	1.092519
GO:0046165_alcohol_biosynthetic_process	21	0	0	0	520	512.168672	568.11	624.051328	1.092519
GO:0007169_transmembrane_receptor_protein_tyrosine_kinas	47	0	0	0	523	515.805145	571.4	626.994855	1.092543
GO:0022622_root_system_development	47	0	0	0	523	515.805145	571.4	626.994855	1.092543
GO:0048364_root_development	47	0	0	0	523	515.805145	571.4	626.994855	1.092543
GO:0000082_G1_S_transition_of_mitotic_cell_cycle	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0000154_rRNA_modification	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0000741_karyogamy	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0001666_response_to_hypoxia	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0001944_vasculature_development	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0005982_starch_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0005992_trehalose_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006090_pyruvate_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006221_pyrimidine_nucleotide_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006278_RNA-dependent_DNA_replication	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006383_transcription_from_RNA_polymerase_III_promote	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006563_L-serine_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006623_protein_targeting_to_vacuole	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006739_NADP_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0007051_spindle_organization	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0007281_germ_cell_development	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0007420_brain_development	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0007584_response_to_nutrient	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0007600_sensory_perception	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0007623_circadian_rhythm	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0008284_positive_regulation_of_cell_proliferation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0008643_carbohydrate_transport	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009086_methionine_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009164_nucleoside_catabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009225_nucleotide-sugar_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009396_folic_acid-containing_compound_biosynthetic_pro	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009644_response_to_high_light_intensity	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009832_plant-type_cell_wall_biogenesis	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009845_seed_germination	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009853_photorespiration	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009873_ethylene_mediated_signaling_pathway	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0009933_meristem_structural_organization	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0010332_response_to_gamma_radiation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0010382_cellular_cell_wall_macromolecule_metabolic_pro	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0010675_regulation_of_cellular_carbohydrate_metabolic_p	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0010833_telomere_maintenance_via_telomere_lengthening	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0010948_negative_regulation_of_cell_cycle_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0016036_cellular_response_to_phosphate_starvation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497

GO:0016109_tetraterpenoid_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0016117_carotenoid_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0016131_brassinosteroid_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0016441_posttranscriptional_gene_silencing	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0019226_transmission_of_nerve_impulse	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0022413_reproductive_process_in_single-celled_organism	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0022904_respiratory_electron_transport_chain	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0030174_regulation_of_DNA-dependent_DNA_replication_	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0030244_cellulose_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0031123_RNA_3'-end_processing	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0032568_general_transcription_from_RNA_polymerase_II_	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0032569_gene-specific_transcription_from_RNA_polymera	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0034504_protein_localization_to_nucleus	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0034754_cellular_hormone_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0034968_histone_lysine_methylation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0035194_posttranscriptional_gene_silencing_by_RNA	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0040023_establishment_of_nucleus_localization	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0042023_DNA_endoreduplication	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0042454_ribonucleoside_catabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0043161_proteasomal_ubiquitin-dependent_protein_catabo	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0043255_regulation_of_carbohydrate_biosynthetic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0043543_protein_acylation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0045321_leukocyte_activation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0046087_cytidine_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0046488_phosphatidylinositol_metabolic_process	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0046649_lymphocyte_activation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0048532_anatomical_structure_arrangement	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0048573_photoperiodism__flowering	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0048581_negative_regulation_of_post-embryonic_develop	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0048645_organ_formation	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0048871_multicellular_organismal_homeostasis	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0050657_nucleic_acid_transport	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0050658_RNA_transport	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0050767_regulation_of_neurogenesis	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0051236_establishment_of_RNA_localization	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0051247_positive_regulation_of_protein_metabolic_proces	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0051259_protein_oligomerization	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0051647_nucleus_localization	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0051960_regulation_of_nervous_system_development	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0055074_calcium_ion_homeostasis	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0060429_epithelium_development	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0070192_chromosome_organization_involved_in_meiosis	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0070482_response_to_oxygen_levels	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0071369_cellular_response_to_ethylene_stimulus	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0072507_divalent_inorganic_cation_homeostasis	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0080135_regulation_of_cellular_response_to_stress	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0090351_seedling_development	8	0	0	0	608	602.451662	654.51	706.568338	1.076497
GO:0006140_regulation_of_nucleotide_metabolic_process	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0006184_GTP_catabolic_process	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0006413_translational_initiation	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0006820_anion_transport	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0009827_plant-type_cell_wall_modification	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0055082_cellular_chemical_homeostasis	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0080134_regulation_of_response_to_stress	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:2000241_regulation_of_reproductive_process	30	0	0	0	616	610.561818	661.56	712.558182	1.073961
GO:0000725_recombinational_repair	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0006284_base-excision_repair	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0006342_chromatin_silencing	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0006855_drug_transmembrane_transport	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0009067_aspartate_family_amino_acid_biosynthetic_proce	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0009119_ribonucleoside_metabolic_process	16	0	0	0	634	628.635498	678.48	728.324502	1.070158

GO:0009124_nucleoside_monophosphate_biosynthetic_proces	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0009312_oligosaccharide_biosynthetic_process	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0015995_chlorophyll_biosynthetic_process	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0016571_histone_methylation	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0019400_alditol_metabolic_process	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0030036_actin_cytoskeleton_organization	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0043094_cellular_metabolic_compound_salvage	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0045132_meiotic_chromosome_segregation	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0046274_lignin_catabolic_process	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0048469_cell_maturation	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0048638_regulation_of_developmental_growth	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0051049_regulation_of_transport	16	0	0	0	634	628.635498	678.48	728.324502	1.070158
GO:0009733_response_to_auxin_stimulus	45	0	0	0	639	633.214613	682.16	731.105387	1.067543
GO:0010629_negative_regulation_of_gene_expression	45	0	0	0	639	633.214613	682.16	731.105387	1.067543
GO:0016568_chromatin_modification	45	0	0	0	639	633.214613	682.16	731.105387	1.067543
GO:0048583_regulation_of_response_to_stimulus	45	0	0	0	639	633.214613	682.16	731.105387	1.067543
GO:0048878_chemical_homeostasis	45	0	0	0	639	633.214613	682.16	731.105387	1.067543
GO:0006470_protein_dephosphorylation	37	0	0	0	643	636.154447	684.87	733.585553	1.065117
GO:0006790_sulfur_compound_metabolic_process	37	0	0	0	643	636.154447	684.87	733.585553	1.065117
GO:0008380_RNA_splicing	37	0	0	0	643	636.154447	684.87	733.585553	1.065117
GO:0048367_shoot_development	37	0	0	0	643	636.154447	684.87	733.585553	1.065117
GO:0015672_monovalent_inorganic_cation_transport	68	0	0	0	644	637.687848	686.23	734.772152	1.065575
GO:0006073_cellular_glucan_metabolic_process	51	0	0	0	647	639.931594	688.38	736.828406	1.063957
GO:0006418_tRNA_aminoacylation_for_protein_translation	51	0	0	0	647	639.931594	688.38	736.828406	1.063957
GO:0007018_microtubule-based_movement	51	0	0	0	647	639.931594	688.38	736.828406	1.063957
GO:0000070_mitotic_sister_chromatid_segregation	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0000722_telomere_maintenance_via_recombination	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0001510_RNA_methylation	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0001775_cell_activation	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0005991_trehalose_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006220_pyrimidine_nucleotide_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006298_mismatch_repair	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006403_RNA_localization	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006487_protein_N-linked_glycosylation	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006505_GPI_anchor_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006555_methionine_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006826_iron_ion_transport	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006891_intra-Golgi_vesicle-mediated_transport	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0006997_nucleus_organization	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0007267_cell-cell_signaling	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009081_branched_chain_family_amino_acid_metabolic_p	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009156_ribonucleoside_monophosphate_biosynthetic_pro	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009161_ribonucleoside_monophosphate_metabolic_proce	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009561_megagametogenesis	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009624_response_to_nematode	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009636_response_to_toxin	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009648_photoperiodism	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009746_response_to_hexose_stimulus	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0009749_response_to_glucose_stimulus	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0010498_proteasomal_protein_catabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0010565_regulation_of_cellular_ketone_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0010639_negative_regulation_of_organelle_organization	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0010769_regulation_of_cell_morphogenesis_involved_in_d	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0010927_cellular_component_assembly_involved_in_morp	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0016090_prenol_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0016093_polyprenol_metabolic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0018205_peptidyl-lysine_modification	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0019722_calcium-mediated_signaling	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0030010_establishment_of_cell_polarity	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0031399_regulation_of_protein_modification_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0032507_maintenance_of_protein_location_in_cell	9	0	0	0	698	690.270135	737.07	783.869865	1.055974

GO:0034284_response_to_monosaccharide_stimulus	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0043065_positive_regulation_of_apoptosis	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0045036_protein_targeting_to_chloroplast	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0045185_maintenance_of_protein_location	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0046364_monosaccharide_biosynthetic_process	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0048440_carpel_development	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0048527_lateral_root_development	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0048528_post-embryonic_root_development	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0048598_embryonic_morphogenesis	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0048732_gland_development	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0051651_maintenance_of_location_in_cell	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0061245_establishment_or_maintenance_of_bipolar_cell_p	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0070972_protein_localization_in_endoplasmic_reticulum	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0090305_nucleic_acid_phosphodiester_bond_hydrolysis	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:2000104_negative_regulation_of_DNA-dependent_DNA_re	9	0	0	0	698	690.270135	737.07	783.869865	1.055974
GO:0000012_single_strand_break_repair	2	0							
GO:0000022_mitotic_spindle_elongation	2	0							
GO:0000080_G1_phase_of_mitotic_cell_cycle	2	0							
GO:0000147_actin_cortical_patch_assembly	2	0							
GO:0000184_nuclear-transcribed_mRNA_catabolic_process__	2	0							
GO:0000212_meiotic_spindle_organization	2	0							
GO:0000273_lipoic_acid_metabolic_process	2	0							
GO:0000282_cellular_bud_site_selection	2	0							
GO:0000289_nuclear-transcribed_mRNA_poly(A)_tail_shorteni	2	0							
GO:0000321_re-entry_into_mitotic_cell_cycle_after_pheromone	2	0							
GO:0000387_spliceosomal_snRNP_assembly	2	0							
GO:0000422_mitochondrion_degradation	2	0							
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GO:0042362_fat-soluble_vitamin_biosynthetic_process	2	0							
GO:0042371_vitamin_K_biosynthetic_process	2	0							
GO:0042373_vitamin_K_metabolic_process	2	0							
GO:0042391_regulation_of_membrane_potential	2	0							
GO:0042402_cellular_biogenic_amine_catabolic_process	2	0							
GO:0042439_ethanolamine-containing_compound_metabolic_	2	0							
GO:0042455_ribonucleoside_biosynthetic_process	2	0							
GO:0042632_cholesterol_homeostasis	2	0							
GO:0042710_biofilm_formation	2	0							
GO:0042787_protein_ubiquitination_involved_in_ubiquitin-depe	2	0							
GO:0042822_pyridoxal_phosphate_metabolic_process	2	0							
GO:0042823_pyridoxal_phosphate_biosynthetic_process	2	0							
GO:0042886_amide_transport	2	0							
GO:0043062_extracellular_structure_organization	2	0							
GO:0043111_replication_fork_arrest	2	0							
GO:0043112_receptor_metabolic_process	2	0							
GO:0043154_negative_regulation_of_caspase_activity	2	0							
GO:0043173_nucleotide_salvage	2	0							
GO:0043266_regulation_of_potassium_ion_transport	2	0							
GO:0043268_positive_regulation_of_potassium_ion_transport	2	0							
GO:0043289_apocarotenoid_biosynthetic_process	2	0							
GO:0043297_apical_junction_assembly	2	0							
GO:0043462_regulation_of_ATPase_activity	2	0							
GO:0043486_histone_exchange	2	0							
GO:0043487_regulation_of_RNA_stability	2	0							
GO:0043488_regulation_of_mRNA_stability	2	0							
GO:0043491_protein_kinase_B_signaling_cascade	2	0							
GO:0043542_endothelial_cell_migration	2	0							
GO:0043570_maintenance_of_DNA_repeat_elements	2	0							
GO:0043620_regulation_of_transcription_in_response_to_stres	2	0							
GO:0044000_movement_in_host	2	0							
GO:0044110_growth_involved_in_symbiotic_interaction	2	0							
GO:0044116_growth_of_symbiont_involved_in_interaction_with	2	0							
GO:0044117_growth_of_symbiont_in_host	2	0							
GO:0044409_entry_into_host	2	0							

GO:0045023_G0_to_G1_transition	2	0								
GO:0045038_protein_import_into_chloroplast_thylakoid_memb	2	0								
GO:0045337_farnesyl_diphosphate_biosynthetic_process	2	0								
GO:0045444_fat_cell_differentiation	2	0								
GO:0045453_bone_resorption	2	0								
GO:0045471_response_to_ethanol	2	0								
GO:0045719_negative_regulation_of_glycogen_biosynthetic_pr	2	0								
GO:0045727_positive_regulation_of_translation	2	0								
GO:0045730_respiratory_burst	2	0								
GO:0045732_positive_regulation_of_protein_catabolic_process	2	0								
GO:0045736_negative_regulation_of_cyclin-dependent_protein	2	0								
GO:0045739_positive_regulation_of_DNA_repair	2	0								
GO:0045740_positive_regulation_of_DNA_replication	2	0								
GO:0045766_positive_regulation_of_angiogenesis	2	0								
GO:0045785_positive_regulation_of_cell_adhesion	2	0								
GO:0045787_positive_regulation_of_cell_cycle	2	0								
GO:0045792_negative_regulation_of_cell_size	2	0								
GO:0045807_positive_regulation_of_endocytosis	2	0								
GO:0045833_negative_regulation_of_lipid_metabolic_process	2	0								
GO:0045834_positive_regulation_of_lipid_metabolic_process	2	0								
GO:0045835_negative_regulation_of_meiosis	2	0								
GO:0045876_positive_regulation_of_sister_chromatid_cohesio	2	0								
GO:0045896_regulation_of_transcription_during_mitosis	2	0								
GO:0045910_negative_regulation_of_DNA_recombination	2	0								
GO:0045913_positive_regulation_of_carbohydrate_metabolic_p	2	0								
GO:0045937_positive_regulation_of_phosphate_metabolic_pro	2	0								
GO:0046036_CTP_metabolic_process	2	0								
GO:0046037_GMP_metabolic_process	2	0								
GO:0046051_UTP_metabolic_process	2	0								
GO:0046149_pigment_catabolic_process	2	0								
GO:0046168_glycerol-3-phosphate_catabolic_process	2	0								
GO:0046209_nitric_oxide_metabolic_process	2	0								
GO:0046218_indolalkylamine_catabolic_process	2	0								
GO:0046390_ribose_phosphate_biosynthetic_process	2	0								
GO:0046391_5-phosphoribose_1-diphosphate_metabolic_proce	2	0								
GO:0046460_neutral_lipid_biosynthetic_process	2	0								
GO:0046463_acylglycerol_biosynthetic_process	2	0								
GO:0046470_phosphatidylcholine_metabolic_process	2	0								
GO:0046471_phosphatidylglycerol_metabolic_process	2	0								
GO:0046497_nicotinate_nucleotide_metabolic_process	2	0								
GO:0046504_glycerol_ether_biosynthetic_process	2	0								
GO:0046651_lymphocyte_proliferation	2	0								
GO:0046653_tetrahydrofolate_metabolic_process	2	0								
GO:0046739_spread_of_virus_in_host	2	0								
GO:0046740_spread_of_virus_in_host__cell_to_cell	2	0								
GO:0046785_microtubule_polymerization	2	0								
GO:0046849_bone_remodeling	2	0								
GO:0046885_regulation_of_hormone_biosynthetic_process	2	0								
GO:0046889_positive_regulation_of_lipid_biosynthetic_process	2	0								
GO:0048015_phosphoinositide-mediated_signaling	2	0								
GO:0048168_regulation_of_neuronal_synaptic_plasticity	2	0								
GO:0048169_regulation_of_long-term_neuronal_synaptic_plast	2	0								
GO:0048260_positive_regulation_of_receptor-mediated_endocy	2	0								
GO:0048308_organelle_inheritance	2	0								
GO:0048546_digestive_tract_morphogenesis	2	0								
GO:0048599_oocyte_development	2	0								
GO:0048619_embryonic_hindgut_morphogenesis	2	0								
GO:0048639_positive_regulation_of_developmental_growth	2	0								
GO:0048663_neuron_fate_commitment	2	0								
GO:0048675_axon_extension	2	0								
GO:0048741_skeletal_muscle_fiber_development	2	0								

GO:0048747_muscle_fiber_development	2	0								
GO:0048814_regulation_of_dendrite_morphogenesis	2	0								
GO:0048829_root_cap_development	2	0								
GO:0048831_regulation_of_shoot_development	2	0								
GO:0048838_release_of_seed_from_dormancy	2	0								
GO:0048859_formation_of_anatomical_boundary	2	0								
GO:0050679_positive_regulation_of_epithelial_cell_proliferatio	2	0								
GO:0050688_regulation_of_defense_response_to_virus	2	0								
GO:0050728_negative_regulation_of_inflammatory_response	2	0								
GO:0050774_negative_regulation_of_dendrite_morphogenesis	2	0								
GO:0050777_negative_regulation_of_immune_response	2	0								
GO:0050792_regulation_of_viral_reproduction	2	0								
GO:0050803_regulation_of_synapse_structure_and_activity	2	0								
GO:0050808_synapse_organization	2	0								
GO:0050810_regulation_of_steroid_biosynthetic_process	2	0								
GO:0050821_protein_stabilization	2	0								
GO:0050826_response_to_freezing	2	0								
GO:0050848_regulation_of_calcium-mediated_signaling	2	0								
GO:0050850_positive_regulation_of_calcium-mediated_signali	2	0								
GO:0050865_regulation_of_cell_activation	2	0								
GO:0050866_negative_regulation_of_cell_activation	2	0								
GO:0050880_regulation_of_blood_vessel_size	2	0								
GO:0050926_regulation_of_positive_chemotaxis	2	0								
GO:0050927_positive_regulation_of_positive_chemotaxis	2	0								
GO:0051026_chiasma_assembly	2	0								
GO:0051046_regulation_of_secretion	2	0								
GO:0051055_negative_regulation_of_lipid_biosynthetic_proces	2	0								
GO:0051103_DNA_ligation_involved_in_DNA_repair	2	0								
GO:0051225_spindle_assembly	2	0								
GO:0051231_spindle_elongation	2	0								
GO:0051249_regulation_of_lymphocyte_activation	2	0								
GO:0051250_negative_regulation_of_lymphocyte_activation	2	0								
GO:0051278_fungal-type_cell_wall_polysaccharide_biosyntheti	2	0								
GO:0051318_G1_phase	2	0								
GO:0051322_anaphase	2	0								
GO:0051340_regulation_of_ligase_activity	2	0								
GO:0051350_negative_regulation_of_lyase_activity	2	0								
GO:0051351_positive_regulation_of_ligase_activity	2	0								
GO:0051384_response_to_glucocorticoid_stimulus	2	0								
GO:0051598_meiotic_recombination_checkpoint	2	0								
GO:0051646_mitochondrion_localization	2	0								
GO:0051648_vesicle_localization	2	0								
GO:0051650_establishment_of_vesicle_localization	2	0								
GO:0051705_behavioral_interaction_between_organisms	2	0								
GO:0051782_negative_regulation_of_cell_division	2	0								
GO:0051814_movement_in_other_organism_involved_in_symb	2	0								
GO:0051828_entry_into_other_organism_involved_in_symbioti	2	0								
GO:0051924_regulation_of_calcium_ion_transport	2	0								
GO:0051928_positive_regulation_of_calcium_ion_transport	2	0								
GO:0051983_regulation_of_chromosome_segregation	2	0								
GO:0052031_modulation_by_symbiont_of_host_defense_resp	2	0								
GO:0052255_modulation_by_organism_of_defense_response_	2	0								
GO:0055001_muscle_cell_development	2	0								
GO:0055002_striated_muscle_cell_development	2	0								
GO:0055046_microgametogenesis	2	0								
GO:0055081_anion_homeostasis	2	0								
GO:0055088_lipid_homeostasis	2	0								
GO:0055092_sterol_homeostasis	2	0								
GO:0060047_heart_contraction	2	0								
GO:0060193_positive_regulation_of_lipase_activity	2	0								
GO:0060562_epithelial_tube_morphogenesis	2	0								

GO:0060917_regulation_of_1_6-beta-glucan_biosynthetic_proc	2	0							
GO:0061008_hepaticobiliary_system_development	2	0							
GO:0061077_chaperone-mediated_protein_folding	2	0							
GO:0061136_regulation_of_proteasomal_protein_catabolic_pro	2	0							
GO:0061326_renal_tubule_development	2	0							
GO:0061333_renal_tubule_morphogenesis	2	0							
GO:0061351_neural_precursor_cell_proliferation	2	0							
GO:0070086_ubiquitin-dependent_endocytosis	2	0							
GO:0070193_synaptonemal_complex_organization	2	0							
GO:0070316_regulation_of_G0_to_G1_transition	2	0							
GO:0070317_negative_regulation_of_G0_to_G1_transition	2	0							
GO:0070592_cell_wall_polysaccharide_biosynthetic_process	2	0							
GO:0070816_phosphorylation_of_RNA_polymerase_II_C-termi	2	0							
GO:0070873_regulation_of_glycogen_metabolic_process	2	0							
GO:0070874_negative_regulation_of_glycogen_metabolic_proc	2	0							
GO:0070988_demethylation	2	0							
GO:0071248_cellular_response_to_metal_ion	2	0							
GO:0071324_cellular_response_to_disaccharide_stimulus	2	0							
GO:0071329_cellular_response_to_sucrose_stimulus	2	0							
GO:0071543_diphosphoinositol_polyphosphate_metabolic_proc	2	0							
GO:0071544_diphosphoinositol_polyphosphate_catabolic_proc	2	0							
GO:0071545_inositol_phosphate_catabolic_process	2	0							
GO:0071695_anatomical_structure_maturation	2	0							
GO:0071775_regulation_of_cell_cycle_cytokinesis	2	0							
GO:0071779_G1_S_transition_checkpoint	2	0							
GO:0071901_negative_regulation_of_protein_serine_threonine_	2	0							
GO:0071966_fungal-type_cell_wall_polysaccharide_metabolic_	2	0							
GO:0072001_renal_system_development	2	0							
GO:0072002_Malpighian_tubule_development	2	0							
GO:0080026_response_to_indolebutyric_acid_stimulus	2	0							
GO:0080119_ER_body_organization	2	0							
GO:0090030_regulation_of_steroid_hormone_biosynthetic_proc	2	0							
GO:0090092_regulation_of_transmembrane_receptor_protein_	2	0							
GO:0090224_regulation_of_spindle_organization	2	0							
GO:2000024_regulation_of_leaf_development	2	0							
GO:2000030_regulation_of_response_to_red_or_far_red_light	2	0							
GO:2000045_regulation_of_G1_S_transition_of_mitotic_cell_cy	2	0							
GO:2000105_positive_regulation_of_DNA-dependent_DNA_rep	2	0							
GO:0006479_protein_methylation	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0006650_glycerophospholipid_metabolic_process	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0006694_steroid_biosynthetic_process	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0007276_gamete_generation	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0007346_regulation_of_mitotic_cell_cycle	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0008213_protein_alkylation	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0009311_oligosaccharide_metabolic_process	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0009553_embryo_sac_development	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0009825_multidimensional_cell_growth	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0017038_protein_import	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0022603_regulation_of_anatomical_structure_morphogene	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0051325_interphase	24	0	0	0	710	701.845116	747.25	792.654884	1.052465
GO:0006195_purine_nucleotide_catabolic_process	46	0	0	0	714	704.463846	749.48	794.496154	1.049692
GO:0006732_coenzyme_metabolic_process	46	0	0	0	714	704.463846	749.48	794.496154	1.049692
GO:0019637_organophosphate_metabolic_process	46	0	0	0	714	704.463846	749.48	794.496154	1.049692
GO:0032259_methylation	46	0	0	0	714	704.463846	749.48	794.496154	1.049692
GO:0000280_nuclear_division	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0009250_glucan_biosynthetic_process	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0009657_plastid_organization	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0010015_root_morphogenesis	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0019439_aromatic_compound_catabolic_process	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0030003_cellular_cation_homeostasis	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0032940_secretion_by_cell	26	0	0	0	724	714.914964	759.06	803.205036	1.048425

GO:0048580_regulation_of_post-embryonic_development	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0051056_regulation_of_small_GTPase_mediated_signal_tr	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0060249_anatomical_structure_homeostasis	26	0	0	0	724	714.914964	759.06	803.205036	1.048425
GO:0006352_transcription_initiation__DNA-dependent	32	0	0	0	729	720.751489	764.29	807.828511	1.048409
GO:0009414_response_to_water_deprivation	32	0	0	0	729	720.751489	764.29	807.828511	1.048409
GO:0018193_peptidyl-amino_acid_modification	32	0	0	0	729	720.751489	764.29	807.828511	1.048409
GO:0046039_GTP_metabolic_process	32	0	0	0	729	720.751489	764.29	807.828511	1.048409
GO:0046365_monosaccharide_catabolic_process	32	0	0	0	729	720.751489	764.29	807.828511	1.048409
GO:0006644_phospholipid_metabolic_process	44	0	0	0	733	724.080366	766.95	809.819634	1.046317
GO:0009143_nucleoside_triphosphate_catabolic_process	44	0	0	0	733	724.080366	766.95	809.819634	1.046317
GO:0009261_ribonucleotide_catabolic_process	44	0	0	0	733	724.080366	766.95	809.819634	1.046317
GO:0051128_regulation_of_cellular_component_organization	44	0	0	0	733	724.080366	766.95	809.819634	1.046317
GO:0043038_amino_acid_activation	54	0	0	0	735	725.020075	767.97	810.919925	1.044857
GO:0043039_tRNA_aminoacylation	54	0	0	0	735	725.020075	767.97	810.919925	1.044857
GO:0006007_glucose_catabolic_process	29	0	0	0	741	730.254963	772.71	815.165037	1.042794
GO:0006779_porphyrin_biosynthetic_process	29	0	0	0	741	730.254963	772.71	815.165037	1.042794
GO:0033014_tetrapyrrole_biosynthetic_process	29	0	0	0	741	730.254963	772.71	815.165037	1.042794
GO:0051052_regulation_of_DNA_metabolic_process	29	0	0	0	741	730.254963	772.71	815.165037	1.042794
GO:0055080_cation_homeostasis	29	0	0	0	741	730.254963	772.71	815.165037	1.042794
GO:0071365_cellular_response_to_auxin_stimulus	29	0	0	0	741	730.254963	772.71	815.165037	1.042794
GO:0006200_ATP_catabolic_process	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0006643_membrane_lipid_metabolic_process	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0006888_ER_to_Golgi_vesicle-mediated_transport	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0007131_reciprocal_meiotic_recombination	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0009738_abscisic_acid_mediated_signaling_pathway	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0016477_cell_migration	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0019058_viral_infectious_cycle	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0035468_positive_regulation_of_signaling_pathway	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0042127_regulation_of_cell_proliferation	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0042558_pteridine-containing_compound_metabolic_proce	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0043069_negative_regulation_of_programmed_cell_death	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0044087_regulation_of_cellular_component_biogenesis	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0046351_disaccharide_biosynthetic_process	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0051129_negative_regulation_of_cellular_component_orga	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0060284_regulation_of_cell_development	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0060548_negative_regulation_of_cell_death	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0071806_protein_transmembrane_transport	13	0	0	0	758	750.947929	791.77	832.592071	1.044551
GO:0007167_enzyme_linked_receptor_protein_signaling_pathw	49	0	0	0	763	755.10967	795.3	835.49033	1.042333
GO:0009166_nucleotide_catabolic_process	49	0	0	0	763	755.10967	795.3	835.49033	1.042333
GO:0009451_RNA_modification	49	0	0	0	763	755.10967	795.3	835.49033	1.042333
GO:0043086_negative_regulation_of_catalytic_activity	49	0	0	0	763	755.10967	795.3	835.49033	1.042333
GO:0051172_negative_regulation_of_nitrogen_compound_meta	49	0	0	0	763	755.10967	795.3	835.49033	1.042333
GO:0006302_double-strand_break_repair	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0007186_G-protein_coupled_receptor_protein_signaling_pa	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0007265_Ras_protein_signal_transduction	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0009108_coenzyme_biosynthetic_process	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0009860_pollen_tube_growth	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0009913_epidermal_cell_differentiation	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0010941_regulation_of_cell_death	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0019684_photosynthesis__light_reaction	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0040008_regulation_of_growth	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0043067_regulation_of_programmed_cell_death	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0045595_regulation_of_cell_differentiation	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0045893_positive_regulation_of_transcription__DNA-deper	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0046578_regulation_of_Ras_protein_signal_transduction	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0055065_metal_ion_homeostasis	23	0	0	0	777	771.914587	810.22	848.525413	1.042754
GO:0006334_nucleosome_assembly	50	0	0	0	782	775.002034	812.94	850.877966	1.039565
GO:0006397_mRNA_processing	50	0	0	0	782	775.002034	812.94	850.877966	1.039565
GO:0006605_protein_targeting	50	0	0	0	782	775.002034	812.94	850.877966	1.039565
GO:0031497_chromatin_assembly	50	0	0	0	782	775.002034	812.94	850.877966	1.039565
GO:0044092_negative_regulation_of_molecular_function	50	0	0	0	782	775.002034	812.94	850.877966	1.039565

GO:0000278_mitotic_cell_cycle	53	0	0	0	786	777.921762	815.28	852.638238	1.037252
GO:0010558_negative_regulation_of_macromolecule_biosynth	53	0	0	0	786	777.921762	815.28	852.638238	1.037252
GO:0034637_cellular_carbohydrate_biosynthetic_process	53	0	0	0	786	777.921762	815.28	852.638238	1.037252
GO:0034728_nucleosome_organization	53	0	0	0	786	777.921762	815.28	852.638238	1.037252
GO:0009142_nucleoside_triphosphate_biosynthetic_process	59	0	0	0	789	779.690112	816.9	854.109888	1.035361
GO:0009409_response_to_cold	59	0	0	0	789	779.690112	816.9	854.109888	1.035361
GO:0051301_cell_division	59	0	0	0	789	779.690112	816.9	854.109888	1.035361
GO:0000096_sulfur_amino_acid_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0000160_two-component_signal_transduction_system_(ph	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0006014_D-ribose_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0006305_DNA_alkylation	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0006306_DNA_methylation	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0006733_oxidoreduction_coenzyme_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0007034_vacuolar_transport	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0009069_serine_family_amino_acid_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0009744_response_to_sucrose_stimulus	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0009850_auxin_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0010073_meristem_maintenance	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0010647_positive_regulation_of_cell_communication	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0016125_sterol_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0016126_sterol_biosynthetic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0019220_regulation_of_phosphate_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0034285_response_to_disaccharide_stimulus	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0042325_regulation_of_phosphorylation	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0048585_negative_regulation_of_response_to_stimulus	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0048870_cell_motility	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0051174_regulation_of_phosphorus_metabolic_process	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0051258_protein_polymerization	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0051674_localization_of_cell	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0071215_cellular_response_to_abscisic_acid_stimulus	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0072511_divalent_inorganic_cation_transport	14	0	0	0	813	812.562611	847.72	882.877389	1.042706
GO:0000038_very_long-chain_fatty_acid_metabolic_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0000084_S_phase_of_mitotic_cell_cycle	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0000097_sulfur_amino_acid_biosynthetic_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0006338_chromatin_remodeling	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0006497_protein_lipidation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0006760_folic_acid-containing_compound_metabolic_proce	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0006879_cellular_iron_ion_homeostasis	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0006944_cellular_membrane_fusion	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0007292_female_gamete_generation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0007417_central_nervous_system_development	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0008272_sulfate_transport	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0009629_response_to_gravity	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0009741_response_to_brassinosteroid_stimulus	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0009767_photosynthetic_electron_transport_chain	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0010043_response_to_zinc_ion	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0010212_response_to_ionizing_radiation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0015931_nucleobase__nucleoside__nucleotide_and_nucle	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0019216_regulation_of_lipid_metabolic_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0022604_regulation_of_cell_morphogenesis	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0032101_regulation_of_response_to_external_stimulus	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0042158_lipoprotein_biosynthetic_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0043066_negative_regulation_of_apoptosis	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0043900_regulation_of_multi-organism_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0043934_sporulation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0046131_pyrimidine_ribonucleoside_metabolic_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0046496_nicotinamide_nucleotide_metabolic_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0048232_male_gamete_generation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0048467_gynoecium_development	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0048764_trichoblast_maturation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0048765_root_hair_cell_differentiation	11	0	0	0	849	846.285316	879.93	913.574684	1.036431

GO:0050776_regulation_of_immune_response	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0051094_positive_regulation_of_developmental_process	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0051605_protein_maturation_by_peptide_bond_cleavage	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0051606_detection_of_stimulus	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0055072_iron_ion_homeostasis	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0061025_membrane_fusion	11	0	0	0	849	846.285316	879.93	913.574684	1.036431
GO:0006310_DNA_recombination	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0007010_cytoskeleton_organization	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0009664_plant-type_cell_wall_organization	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0015979_photosynthesis	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0034470_ncRNA_processing	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0044275_cellular_carbohydrate_catabolic_process	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0045934_negative_regulation_of_nucleobase__nucleoside_	48	0	0	0	856	851.434765	884.36	917.285235	1.033131
GO:0000226_microtubule_cytoskeleton_organization	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0000375_RNA_splicing__via_transesterification_reactions	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0000377_RNA_splicing__via_transesterification_reactions_	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0006364_rRNA_processing	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0008202_steroid_metabolic_process	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0009828_plant-type_cell_wall_loosening	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0016072_rRNA_metabolic_process	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0019751_polyol_metabolic_process	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0030811_regulation_of_nucleotide_catabolic_process	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0033121_regulation_of_purine_nucleotide_catabolic_proce	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0046486_glycerolipid_metabolic_process	27	0	0	0	867	861.524605	894.04	926.555395	1.031188
GO:0006873_cellular_ion_homeostasis	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0009734_auxin_mediated_signaling_pathway	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0009932_cell_tip_growth	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0015985_energy_coupled_proton_transport__down_electro	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0015986_ATP_synthesis_coupled_proton_transport	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0016569_covalent_chromatin_modification	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0016570_histone_modification	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0022900_electron_transport_chain	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0042445_hormone_metabolic_process	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0046903_secretion	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0048827_phyllome_development	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0048868_pollen_tube_development	28	0	0	0	879	872.939323	904.9	936.860677	1.029465
GO:0009826_unidimensional_cell_growth	69	0	0	0	884	876.08135	907.36	938.63865	1.026425
GO:0009892_negative_regulation_of_metabolic_process	69	0	0	0	884	876.08135	907.36	938.63865	1.026425
GO:0044270_cellular_nitrogen_compound_catabolic_process	69	0	0	0	884	876.08135	907.36	938.63865	1.026425
GO:0046034_ATP_metabolic_process	69	0	0	0	884	876.08135	907.36	938.63865	1.026425
GO:0071103_DNA_conformation_change	69	0	0	0	884	876.08135	907.36	938.63865	1.026425
GO:0006778_porphyrin_metabolic_process	31	0	0	0	890	882.757919	913.29	943.822081	1.026169
GO:0019320_hexose_catabolic_process	31	0	0	0	890	882.757919	913.29	943.822081	1.026169
GO:0033013_tetrapyrrole_metabolic_process	31	0	0	0	890	882.757919	913.29	943.822081	1.026169
GO:0033692_cellular_polysaccharide_biosynthetic_process	31	0	0	0	890	882.757919	913.29	943.822081	1.026169
GO:0046148_pigment_biosynthetic_process	31	0	0	0	890	882.757919	913.29	943.822081	1.026169
GO:0048193_Golgi_vesicle_transport	31	0	0	0	890	882.757919	913.29	943.822081	1.026169
GO:0001522_pseudouridine_synthesis	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0015837_amine_transport	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0030029_actin_filament-based_process	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0032984_macromolecular_complex_disassembly	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0034623_cellular_macromolecular_complex_disassembly	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0043085_positive_regulation_of_catalytic_activity	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0043241_protein_complex_disassembly	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0043624_cellular_protein_complex_disassembly	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0044093_positive_regulation_of_molecular_function	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0050877_neurological_system_process	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0051640_organelle_localization	18	0	0	0	901	893.223443	922.97	952.716557	1.024384
GO:0000279_M_phase	56	0	0	0	904	895.061462	924.6	954.138538	1.022788
GO:0006754_ATP_biosynthetic_process	56	0	0	0	904	895.061462	924.6	954.138538	1.022788
GO:0051188_cofactor_biosynthetic_process	56	0	0	0	904	895.061462	924.6	954.138538	1.022788

GO:0006006_glucose_metabolic_process	39	0	0	0	907	898.407355	927.41	956.412645	1.022503
GO:0040029_regulation_of_gene_expression__epigenetic	39	0	0	0	907	898.407355	927.41	956.412645	1.022503
GO:0051321_meiotic_cell_cycle	39	0	0	0	907	898.407355	927.41	956.412645	1.022503
GO:0035466_regulation_of_signaling_pathway	52	0	0	0	909	900.361001	928.79	957.218999	1.021771
GO:2000113_negative_regulation_of_cellular_macromolecule_	52	0	0	0	909	900.361001	928.79	957.218999	1.021771
GO:0000271_polysaccharide_biosynthetic_process	34	0	0	0	914	907.655687	935.12	962.584313	1.023107
GO:0009415_response_to_water	34	0	0	0	914	907.655687	935.12	962.584313	1.023107
GO:0010817_regulation_of_hormone_levels	34	0	0	0	914	907.655687	935.12	962.584313	1.023107
GO:0031329_regulation_of_cellular_catabolic_process	34	0	0	0	914	907.655687	935.12	962.584313	1.023107
GO:0048285_organelle_fission	34	0	0	0	914	907.655687	935.12	962.584313	1.023107
GO:0006730_one-carbon_metabolic_process	60	0	0	0	917	910.01852	936.86	963.70148	1.021658
GO:0019953_sexual_reproduction	60	0	0	0	917	910.01852	936.86	963.70148	1.021658
GO:0031324_negative_regulation_of_cellular_metabolic_proce	60	0	0	0	917	910.01852	936.86	963.70148	1.021658
GO:0000245_spliceosome_assembly	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0000726_non-recombinational_repair	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0000749_response_to_pheromone_involved_in_conjugatio	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0001525_angiogenesis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0002684_positive_regulation_of_immune_system_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0005977_glycogen_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0005978_glycogen_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006074_1_3-beta-glucan_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006075_1_3-beta-glucan_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006094_gluconeogenesis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006112_energy_reserve_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006144_purine_base_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006308_DNA_catabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006405_RNA_export_from_nucleus	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006525_arginine_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006526_arginine_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006547_histidine_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006553_lysine_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006558_L-phenylalanine_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006613_cotranslational_protein_targeting_to_membrane	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006614_SRP-dependent_cotranslational_protein_targetin	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006662_glycerol_ether_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006836_neurotransmitter_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006892_post-Golgi_vesicle-mediated_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006916_anti-apoptosis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006917_induction_of_apoptosis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0006972_hyperosmotic_response	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007015_actin_filament_organization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007052_mitotic_spindle_organization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007088_regulation_of_mitosis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007204_elevation_of_cytosolic_calcium_ion_concentratio	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007349_cellularization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007431_salivary_gland_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0007517_muscle_organ_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0008216_spermidine_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0008295_spermidine_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0008406_gonad_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009075_histidine_family_amino_acid_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009085_lysine_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009089_lysine_biosynthetic_process_via_diaminopimelat	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009126_purine_nucleoside_monophosphate_metabolic_p	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009127_purine_nucleoside_monophosphate_biosynthetic	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009167_purine_ribonucleoside_monophosphate_metaboli	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009168_purine_ribonucleoside_monophosphate_biosynth	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009190_cyclic_nucleotide_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009292_genetic_transfer	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009294_DNA_mediated_transformation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009735_response_to_cytokinin_stimulus	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807

GO:0009742_brassinosteroid_mediated_signaling_pathway	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009792_embryo_development_ending_in_birth_or_egg_h	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009910_negative_regulation_of_flower_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009914_hormone_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009926_auxin_polar_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009965_leaf_morphogenesis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0009967_positive_regulation_of_signal_transduction	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010026_trichome_differentiation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010075_regulation_of_meristem_growth	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010208_pollen_wall_assembly	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010224_response_to_UV-B	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010374_stomatal_complex_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010588_cotyledon_vascular_tissue_pattern_formation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0010975_regulation_of_neuron_projection_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0016050_vesicle_organization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0016132_brassinosteroid_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0016143_S-glycoside_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0016246_RNA_interference	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0016573_histone_acetylation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0016579_protein_deubiquitination	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0018904_organic_ether_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0019236_response_to_pheromone	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0019319_hexose_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0019757_glycosinolate_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0019760_glucosinolate_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0019954_asexual_reproduction	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0023056_positive_regulation_of_signaling_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0030473_nuclear_migration_along_microtubule	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0030497_fatty_acid_elongation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0030865_cortical_cytoskeleton_organization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0031344_regulation_of_cell_projection_organization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0031348_negative_regulation_of_defense_response	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0031365_N-terminal_protein_amino_acid_modification	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0032878_regulation_of_establishment_or_maintenance_of_	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0035266_meristem_growth	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0035270_endocrine_system_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0035272_exocrine_system_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0040034_regulation_of_development__heterochronic	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0042168_heme_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0043269_regulation_of_ion_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0043401_steroid_hormone_mediated_signaling_pathway	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0043450_alkene_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0043562_cellular_response_to_nitrogen_levels	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0043647_inositol_phosphate_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0045005_maintenance_of_fidelity_involved_in_DNA-depen	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0045047_protein_targeting_to_ER	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0045664_regulation_of_neuron_differentiation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0045860_positive_regulation_of_protein_kinase_activity	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0046451_diaminopimelate_metabolic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0046467_membrane_lipid_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0046685_response_to_arsenic	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0046688_response_to_copper_ion	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0046890_regulation_of_lipid_biosynthetic_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0048508_embryonic_meristem_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0048514_blood_vessel_morphogenesis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0048729_tissue_morphogenesis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0048863_stem_cell_differentiation	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0048872_homeostasis_of_number_of_cells	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0051028_mRNA_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0051050_positive_regulation_of_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0051240_positive_regulation_of_multicellular_organismal_p	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807

GO:0051480_cytosolic_calcium_ion_homeostasis	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0051510_regulation_of_unidimensional_cell_growth	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0051783_regulation_of_nuclear_division	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0060341_regulation_of_cellular_localization	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0060541_respiratory_system_development	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0060918_auxin_transport	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0061246_establishment_or_maintenance_of_bipolar_cell_p	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0071367_cellular_response_to_brassinosteroid_stimulus	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0071383_cellular_response_to_steroid_hormone_stimulus	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0090068_positive_regulation_of_cell_cycle_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:2000099_regulation_of_establishment_or_maintenance_of_	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:2000100_regulation_of_establishment_or_maintenance_of_	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:2000243_positive_regulation_of_reproductive_process	6	0	0	0	1039	1035.290619	1058.54	1081.789381	1.018807
GO:0065004_protein-DNA_complex_assembly	64	0	0	0	1041	1036.739096	1059.76	1082.780904	1.018021
GO:0071824_protein-DNA_complex_subunit_organization	64	0	0	0	1041	1036.739096	1059.76	1082.780904	1.018021
GO:0006323_DNA_packaging	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0009755_hormone-mediated_signaling_pathway	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0009890_negative_regulation_of_biosynthetic_process	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0019318_hexose_metabolic_process	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0031327_negative_regulation_of_cellular_biosynthetic_pro	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0044042_glucan_metabolic_process	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0048646_anatomical_structure_formation_involved_in_mor	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0071669_plant-type_cell_wall_organization_or_biogenesis	55	0	0	0	1049	1041.264179	1063.53	1085.795821	1.013851
GO:0016071_mRNA_metabolic_process	57	0	0	0	1053	1043.367957	1065.24	1087.112043	1.011624
GO:0034655_nucleobase__nucleoside__nucleotide_and_nucle	57	0	0	0	1053	1043.367957	1065.24	1087.112043	1.011624
GO:0034656_nucleobase__nucleoside_and_nucleotide_catabo	57	0	0	0	1053	1043.367957	1065.24	1087.112043	1.011624
GO:0044264_cellular_polysaccharide_metabolic_process	57	0	0	0	1053	1043.367957	1065.24	1087.112043	1.011624
GO:0000819_sister_chromatid_segregation	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0005985_sucrose_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006020_inositol_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006084_acetyl-CoA_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006109_regulation_of_carbohydrate_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006465_signal_peptide_processing	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006612_protein_targeting_to_membrane	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006814_sodium_ion_transport	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006914_autophagy	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0006954_inflammatory_response	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0007031_peroxisome_organization	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0007243_intracellular_protein_kinase_cascade	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0007283_spermatogenesis	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0008156_negative_regulation_of_DNA_replication	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0009566_fertilization	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0009567_double_fertilization_forming_a_zygote_and_endo	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0009630_gravitropism	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0009739_response_to_gibberellin_stimulus	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0009851_auxin_biosynthetic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0010051_xylem_and_phloem_pattern_formation	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0010087_phloem_or_xylem_histogenesis	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0010150_leaf_senescence	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0010260_organ_senescence	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0010942_positive_regulation_of_cell_death	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0016108_tetraterpenoid_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0016116_carotenoid_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0016129_phytosteroid_biosynthetic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0018208_peptidyl-proline_modification	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0018401_peptidyl-proline_hydroxylation_to_4-hydroxy-L-pr	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0019471_4-hydroxyproline_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0019511_peptidyl-proline_hydroxylation	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0023014_signal_transmission_via_phosphorylation_event	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0030435_sporulation_resulting_in_formation_of_a_cellular_	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0031047_gene_silencing_by_RNA	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441

GO:0032392_DNA_geometric_change	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0032505_reproduction_of_a_single-celled_organism	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0032508_DNA_duplex_unwinding	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0033044_regulation_of_chromosome_organization	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0042335_cuticle_development	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0042559_pteridine-containing_compound_biosynthetic_pro	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0043068_positive_regulation_of_programmed_cell_death	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0045596_negative_regulation_of_cell_differentiation	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0045859_regulation_of_protein_kinase_activity	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0046474_glycerophospholipid_biosynthetic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0048477_oogenesis	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0048509_regulation_of_meristem_development	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0051187_cofactor_catabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0051235_maintenance_of_location	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0051273_beta-glucan_metabolic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0051274_beta-glucan_biosynthetic_process	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0051493_regulation_of_cytoskeleton_organization	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0072358_cardiovascular_system_development	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0072359_circulatory_system_development	10	0	0	0	1106	1100.653642	1119.76	1138.866358	1.012441
GO:0043414_macromolecule_methylation	42	0	0	0	1107	1103.346325	1122	1140.653675	1.01355
GO:0000087_M_phase_of_mitotic_cell_cycle	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0000910_cytokinesis	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0006813_potassium_ion_transport	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0006839_mitochondrial_transport	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0006913_nucleocytoplasmic_transport	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0007067_mitosis	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0007127_meiosis_I	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0008544_epidermis_development	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
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GO:0016458_gene_silencing	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0033043_regulation_of_organelle_organization	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
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GO:0033365_protein_localization_to_organelle	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
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GO:0048507_meristem_development	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
GO:0051169_nuclear_transport	25	0	0	0	1125	1122.202665	1138.69	1155.177335	1.012169
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GO:0001541_ovarian_follicle_development	3	0							
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GO:0002208_somatic_diversification_of_immunoglobulins_invo	3	0							
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GO:0006432_phenylalanyl-tRNA_aminoacylation	3	0							
GO:0006433_prolyl-tRNA_aminoacylation	3	0							
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GO:0006857_oligopeptide_transport	3	0							
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GO:0006896_Golgi_to_vacuole_transport	3	0							
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GO:0009969_xyloglucan_biosynthetic_process	3	0								
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GO:0046521_sphingoid_catabolic_process	3	0								
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GO:0046660_female_sex_differentiation	3	0								
GO:0046661_male_sex_differentiation	3	0								
GO:0046822_regulation_of_nucleocytoplasmic_transport	3	0								
GO:0046999_regulation_of_conjugation	3	0								
GO:0048016_inositol_phosphate-mediated_signaling	3	0								
GO:0048017_inositol_lipid-mediated_signaling	3	0								
GO:0048102_autophagic_cell_death	3	0								
GO:0048134_germ-line_cyst_formation	3	0								
GO:0048136_male_germ-line_cyst_formation	3	0								
GO:0048137_spermatocyte_division	3	0								
GO:0048259_regulation_of_receptor-mediated_endocytosis	3	0								
GO:0048441_petal_development	3	0								
GO:0048465_corolla_development	3	0								
GO:0048506_regulation_of_timing_of_meristematic_phase_tra	3	0								
GO:0048510_regulation_of_timing_of_transition_from_vegetati	3	0								
GO:0048520_positive_regulation_of_behavior	3	0								
GO:0048565_digestive_tract_development	3	0								
GO:0048568_embryonic_organ_development	3	0								
GO:0048678_response_to_axon_injury	3	0								
GO:0048768_root_hair_cell_tip_growth	3	0								
GO:0048821_erythrocyte_development	3	0								
GO:0050673_epithelial_cell_proliferation	3	0								
GO:0050678_regulation_of_epithelial_cell_proliferation	3	0								
GO:0050768_negative_regulation_of_neurogenesis	3	0								
GO:0050769_positive_regulation_of_neurogenesis	3	0								
GO:0050770_regulation_of_axonogenesis	3	0								
GO:0050773_regulation_of_dendrite_development	3	0								
GO:0050817_coagulation	3	0								
GO:0050900_leukocyte_migration	3	0								
GO:0050918_positive_chemotaxis	3	0								

GO:0050920_regulation_of_chemotaxis	3	0							
GO:0050921_positive_regulation_of_chemotaxis	3	0							
GO:0050954_sensory_perception_of_mechanical_stimulus	3	0							
GO:0050994_regulation_of_lipid_catabolic_process	3	0							
GO:0051146_striated_muscle_cell_differentiation	3	0							
GO:0051177_meiotic_sister_chromatid_cohesion	3	0							
GO:0051205_protein_insertion_into_membrane	3	0							
GO:0051223_regulation_of_protein_transport	3	0							
GO:0051241_negative_regulation_of_multicellular_organismal_	3	0							
GO:0051261_protein_depolymerization	3	0							
GO:0051270_regulation_of_cellular_component_movement	3	0							
GO:0051272_positive_regulation_of_cellular_component_move	3	0							
GO:0051304_chromosome_separation	3	0							
GO:0051307_meiotic_chromosome_separation	3	0							
GO:0051324_prophase	3	0							
GO:0051339_regulation_of_lyase_activity	3	0							
GO:0051346_negative_regulation_of_hydrolase_activity	3	0							
GO:0051348_negative_regulation_of_transferase_activity	3	0							
GO:0051452_intracellular_pH_reduction	3	0							
GO:0051453_regulation_of_intracellular_pH	3	0							
GO:0051495_positive_regulation_of_cytoskeleton_organization	3	0							
GO:0051567_histone_H3-K9_methylation	3	0							
GO:0051568_histone_H3-K4_methylation	3	0							
GO:0051644_plastid_localization	3	0							
GO:0051667_establishment_of_plastid_localization	3	0							
GO:0051702_interaction_with_symbiont	3	0							
GO:0051865_protein_autoubiquitination	3	0							
GO:0052317_camalexin_metabolic_process	3	0							
GO:0052547_regulation_of_peptidase_activity	3	0							
GO:0052548_regulation_of_endopeptidase_activity	3	0							
GO:0055070_copper_ion_homeostasis	3	0							
GO:0055084_fruiting_body_development_in_response_to_starv	3	0							
GO:0055123_digestive_system_development	3	0							
GO:0060326_cell_chemotaxis	3	0							
GO:0060537_muscle_tissue_development	3	0							
GO:0060538_skeletal_muscle_organ_development	3	0							
GO:0070125_mitochondrial_translational_elongation	3	0							
GO:0070201_regulation_of_establishment_of_protein_localizati	3	0							
GO:0070661_leukocyte_proliferation	3	0							
GO:0071241_cellular_response_to_inorganic_substance	3	0							
GO:0071370_cellular_response_to_gibberellin_stimulus	3	0							
GO:0071446_cellular_response_to_salicylic_acid_stimulus	3	0							
GO:0071478_cellular_response_to_radiation	3	0							
GO:0071482_cellular_response_to_light_stimulus	3	0							
GO:0071489_cellular_response_to_red_or_far_red_light	3	0							
GO:0071514_genetic_imprinting	3	0							
GO:0071956_cellular_component_maintenance_at_cellular_lev	3	0							
GO:2000027_regulation_of_organ_morphogenesis	3	0							
GO:2000067_regulation_of_root_morphogenesis	3	0							
GO:2000145_regulation_of_cell_motility	3	0							
GO:2000147_positive_regulation_of_cell_motility	3	0							
GO:0006357_regulation_of_transcription_from_RNA_polymeras	40	0	0	0	1128	1126.498179	1142.53	1158.561821	1.012881
GO:0016311_dephosphorylation	40	0	0	0	1128	1126.498179	1142.53	1158.561821	1.012881
GO:0046164_alcohol_catabolic_process	40	0	0	0	1128	1126.498179	1142.53	1158.561821	1.012881
GO:0009152_purine_ribonucleotide_biosynthetic_process	67	0	0	0	1129	1127.357782	1143.24	1159.122218	1.012613
GO:0000076_DNA_replication_checkpoint	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0000373_Group_II_intron_splicing	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0001568_blood_vessel_development	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006081_cellular_aldehyde_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006098_pentose-phosphate_shunt	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006099_tricarboxylic_acid_cycle	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698

GO:0006216_cytidine_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006265_DNA_topological_change	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006268_DNA_unwinding_involved_in_replication	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006301_postreplication_repair	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006348_chromatin_silencing_at_telomere	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006473_protein_acetylation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006475_internal_protein_amino_acid_acetylation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006544_glycine_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006595_polyamine_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006596_polyamine_biosynthetic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006606_protein_import_into_nucleus	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006672_ceramide_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006714_sesquiterpenoid_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006740_NADPH_regeneration	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006816_calcium_ion_transport	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0006874_cellular_calcium_ion_homeostasis	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0007033_vacuole_organization	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0007097_nuclear_migration	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0007268_synaptic_transmission	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0007548_sex_differentiation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009070_serine_family_amino_acid_biosynthetic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009074_aromatic_amino_acid_family_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009109_coenzyme_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009112_nucleobase_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009187_cyclic_nucleotide_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009251_glucan_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009306_protein_secretion	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009581_detection_of_external_stimulus	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009582_detection_of_abiotic_stimulus	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0009972_cytidine_deamination	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0010305_leaf_vascular_tissue_pattern_formation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0010383_cell_wall_polysaccharide_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0010638_positive_regulation_of_organelle_organization	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0010648_negative_regulation_of_cell_communication	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0010970_microtubule-based_transport	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0012502_induction_of_programmed_cell_death	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0016091_prenol_biosynthetic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0016094_polyprenol_biosynthetic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0018393_internal_peptidyl-lysine_acetylation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0018394_peptidyl-lysine_acetylation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0019080_viral_genome_expression	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0019083_viral_transcription	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0030705_cytoskeleton-dependent_intracellular_transport	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0031124_mRNA_3'-end_processing	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0032270_positive_regulation_of_cellular_protein_metabolic	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0032297_negative_regulation_of_DNA-dependent_DNA_re	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0032543_mitochondrial_translation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0032844_regulation_of_homeostatic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0032886_regulation_of_microtubule-based_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0033674_positive_regulation_of_kinase_activity	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0043254_regulation_of_protein_complex_assembly	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0043434_response_to_peptide_hormone_stimulus	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0043449_cellular_alkene_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0043523_regulation_of_neuron_apoptosis	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0045088_regulation_of_innate_immune_response	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0045137_development_of_primary_sexual_characteristics	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0045143_homologous_chromosome_segregation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0046133_pyrimidine_ribonucleoside_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0046135_pyrimidine_nucleoside_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0046174_polyol_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0046356_acetyl-CoA_catabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698

GO:0046489_phosphoinositide_biosynthetic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0046519_sphingoid_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0046677_response_to_antibiotic	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0048481_ovule_development	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0048767_root_hair_elongation	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051123_RNA_polymerase_II_transcriptional_preinitiation_	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051168_nuclear_export	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051170_nuclear_import	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051260_protein_homooligomerization	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051302_regulation_of_cell_division	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051347_positive_regulation_of_transferase_activity	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051402_neuron_apoptosis	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0051761_sesquiterpene_metabolic_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0061061_muscle_structure_development	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0070507_regulation_of_microtubule_cytoskeleton_organiza	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0070646_protein_modification_by_small_protein_removal	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0070897_DNA-dependent_transcriptional_preinitiation_com	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0070997_neuron_death	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0072384_organelle_transport_along_microtubule	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0072503_cellular_divalent_inorganic_cation_homeostasis	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:2000242_negative_regulation_of_reproductive_process	7	0	0	0	1217	1216.873598	1230.02	1243.166402	1.010698
GO:0010605_negative_regulation_of_macromolecule_metaboli	65	0	0	0	1218	1217.399672	1230.36	1243.320328	1.010148
GO:0000002_mitochondrial_genome_maintenance	1	0							
GO:0000011_vacuole_inheritance	1	0							
GO:0000027_ribosomal_large_subunit_assembly	1	0							
GO:0000028_ribosomal_small_subunit_assembly	1	0							
GO:0000045_autophagic_vacuole_assembly	1	0							
GO:0000050_urea_cycle	1	0							
GO:0000052_citrulline_metabolic_process	1	0							
GO:0000060_protein_import_into_nucleus__translocation	1	0							
GO:0000090_mitotic_anaphase	1	0							
GO:0000187_activation_of_MAPK_activity	1	0							
GO:0000209_protein_polyubiquitination	1	0							
GO:0000239_pachytene	1	0							
GO:0000281_cytokinesis_after_mitosis	1	0							
GO:0000290_deadenylation-dependent_decapping_of_nuclear-	1	0							
GO:0000291_nuclear-transcribed_mRNA_catabolic_process__	1	0							
GO:0000338_protein_deneddylation	1	0							
GO:0000354_cis_assembly_of_pre-catalytic_spliceosome	1	0							
GO:0000372_Group_I_intron_splicing	1	0							
GO:0000376_RNA_splicing__via_transesterification_reactions_	1	0							
GO:0000380_alternative_nuclear_mRNA_splicing__via_spliceo	1	0							
GO:0000381_regulation_of_alternative_nuclear_mRNA_splicing	1	0							
GO:0000394_RNA_splicing__via_endonucleolytic_cleavage_ar	1	0							
GO:0000395_nuclear_mRNA_5'-splice_site_recognition	1	0							
GO:0000718_nucleotide-excision_repair__DNA_damage_remo	1	0							
GO:0000720_pyrimidine_dimer_repair_by_nucleotide-excision_	1	0							
GO:0000730_DNA_recombinase_assembly	1	0							
GO:0000734_gene_conversion_at_mating-type_locus__DNA_r	1	0							
GO:0000750_pheromone-dependent_signal_transduction_invol	1	0							
GO:0000751_cell_cycle_arrest_in_response_to_pheromone	1	0							
GO:0000753_cell_morphogenesis_involved_in_conjugation_wit	1	0							
GO:0000767_cell_morphogenesis_involved_in_conjugation	1	0							
GO:0000768_syncytium_formation_by_plasma_membrane_fus	1	0							
GO:0000909_sporocarp_development_involved_in_sexual_rep	1	0							
GO:0000915_cytokinesis__actomyosin_contractile_ring_assem	1	0							
GO:0000916_contractile_ring_contraction_involved_in_cell_cyc	1	0							
GO:0001503_ossification	1	0							
GO:0001504_neurotransmitter_uptake	1	0							
GO:0001514_selenocysteine_incorporation	1	0							
GO:0001556_oocyte_maturation	1	0							

GO:0001570_vasculogenesis	1	0								
GO:0001578_microtubule_bundle_formation	1	0								
GO:0001649_osteoblast_differentiation	1	0								
GO:0001660_fever	1	0								
GO:0001661_conditioned_taste_aversion	1	0								
GO:0001662_behavioral_fear_response	1	0								
GO:0001672_regulation_of_chromatin_assembly_or_disassem	1	0								
GO:0001678_cellular_glucose_homeostasis	1	0								
GO:0001702_gastrulation_with_mouth_forming_second	1	0								
GO:0001704_formation_of_primary_germ_layer	1	0								
GO:0001707_mesoderm_formation	1	0								
GO:0001736_establishment_of_planar_polarity	1	0								
GO:0001746_Bolwig's_organ_morphogenesis	1	0								
GO:0001748_optic_lobe_placode_development	1	0								
GO:0001752_compound_eye_photoreceptor_fate_commitment	1	0								
GO:0001763_morphogenesis_of_a_branching_structure	1	0								
GO:0001776_leukocyte_homeostasis	1	0								
GO:0001778_plasma_membrane_repair	1	0								
GO:0001779_natural_killer_cell_differentiation	1	0								
GO:0001818_negative_regulation_of_cytokine_production	1	0								
GO:0001819_positive_regulation_of_cytokine_production	1	0								
GO:0001824_blastocyst_development	1	0								
GO:0001832_blastocyst_growth	1	0								
GO:0001833_inner_cell_mass_cell_proliferation	1	0								
GO:0001836_release_of_cytochrome_c_from_mitochondria	1	0								
GO:0001893_maternal_placenta_development	1	0								
GO:0001897_cytolysis_by_symbiont_of_host_cells	1	0								
GO:0001907_killing_by_symbiont_of_host_cells	1	0								
GO:0001945_lymph_vessel_development	1	0								
GO:0001952_regulation_of_cell-matrix_adhesion	1	0								
GO:0001954_positive_regulation_of_cell-matrix_adhesion	1	0								
GO:0001963_synaptic_transmission__dopaminergic	1	0								
GO:0001964_startle_response	1	0								
GO:0001975_response_to_amphetamine	1	0								
GO:0002053_positive_regulation_of_mesenchymal_cell_prolife	1	0								
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GO:0071345_cellular_response_to_cytokine_stimulus	1	0								
GO:0071352_cellular_response_to_interleukin-2	1	0								
GO:0071366_cellular_response_to_indolebutyric_acid_stimulus	1	0								
GO:0071368_cellular_response_to_cytokinin_stimulus	1	0								
GO:0071371_cellular_response_to_gonadotropin_stimulus	1	0								
GO:0071372_cellular_response_to_follicle-stimulating_hormone	1	0								
GO:0071407_cellular_response_to_organic_cyclic_substance	1	0								
GO:0071415_cellular_response_to_purine	1	0								
GO:0071445_cellular_response_to_protein_stimulus	1	0								
GO:0071452_cellular_response_to_singlet_oxygen	1	0								
GO:0071453_cellular_response_to_oxygen_levels	1	0								
GO:0071456_cellular_response_to_hypoxia	1	0								
GO:0071574_protein_localization_to_medial_cortex	1	0								
GO:0071621_granulocyte_chemotaxis	1	0								
GO:0071622_regulation_of_granulocyte_chemotaxis	1	0								
GO:0071674_mononuclear_cell_migration	1	0								
GO:0071675_regulation_of_mononuclear_cell_migration	1	0								
GO:0071680_response_to_indole-3-methanol	1	0								
GO:0071681_cellular_response_to_indole-3-methanol	1	0								
GO:0071701_regulation_of_MAPK_export_from_nucleus	1	0								
GO:0071706_tumor_necrosis_factor_superfamily_cytokine_pro	1	0								
GO:0071776_negative_regulation_of_cell_cycle_cytokinesis	1	0								
GO:0071887_leukocyte_apoptosis	1	0								
GO:0071894_histone_H2B_conserved_C-terminal_lysine_ubiqu	1	0								
GO:0071902_positive_regulation_of_protein_serine_threonine_	1	0								
GO:0071921_cohesin_localization_to_chromatin	1	0								
GO:0071937_barrier_septum_formation_involved_in_cell_cycle	1	0								
GO:0071940_fungal-type_cell_wall_assembly	1	0								
GO:0072337_modified_amino_acid_transport	1	0								
GO:0075141_maintenance_of_symbiont_tolerance_to_host_en	1	0								
GO:0075260_regulation_of_spore-bearing_organ_development	1	0								
GO:0075306_regulation_of_conidium_formation	1	0								
GO:0080009_mRNA_methylation	1	0								
GO:0080024_indolebutyric_acid_metabolic_process	1	0								
GO:0080050_regulation_of_seed_development	1	0								
GO:0080056_petal_vascular_tissue_pattern_formation	1	0								
GO:0080057_sepal_vascular_tissue_pattern_formation	1	0								
GO:0080058_protein_deglutathionylation	1	0								

GO:0080093_regulation_of_photorespiration	1	0							
GO:0080112_seed_growth	1	0							
GO:0080113_regulation_of_seed_growth	1	0							
GO:0080117_secondary_growth	1	0							
GO:0080151_positive_regulation_of_salicylic_acid_mediated_s	1	0							
GO:0080154_regulation_of_fertilization	1	0							
GO:0080155_regulation_of_double_fertilization_forming_a_zyg	1	0							
GO:0080159_zygote_elongation	1	0							
GO:0080160_selenate_transport	1	0							
GO:0080164_regulation_of_nitric_oxide_metabolic_process	1	0							
GO:0085020_protein_K6-linked_ubiquitination	1	0							
GO:0090031_positive_regulation_of_steroid_hormone_biosynth	1	0							
GO:0090056_regulation_of_chlorophyll_metabolic_process	1	0							
GO:0090069_regulation_of_ribosome_biogenesis	1	0							
GO:0090070_positive_regulation_of_ribosome_biogenesis	1	0							
GO:0090093_regulation_of_fungal-type_cell_wall_beta-glucan_	1	0							
GO:0090100_positive_regulation_of_transmembrane_receptor_	1	0							
GO:0090101_negative_regulation_of_transmembrane_receptor	1	0							
GO:0090109_regulation_of_cell-substrate_junction_assembly	1	0							
GO:0090162_establishment_of_epithelial_cell_polarity	1	0							
GO:0090181_regulation_of_cholesterol_metabolic_process	1	0							
GO:0090195_chemokine_secretion	1	0							
GO:0090196_regulation_of_chemokine_secretion	1	0							
GO:0090197_positive_regulation_of_chemokine_secretion	1	0							
GO:0090205_positive_regulation_of_cholesterol_metabolic_pro	1	0							
GO:0090213_regulation_of_radial_pattern_formation	1	0							
GO:0090264_regulation_of_immune_complex_clearance_by_m	1	0							
GO:0090265_positive_regulation_of_immune_complex_clearan	1	0							
GO:0090307_spindle_assembly_involved_in_mitosis	1	0							
GO:0090322_regulation_of_superoxide_metabolic_process	1	0							
GO:0090334_regulation_of_cell_wall_1_3-beta-glucan_biosynth	1	0							
GO:2000021_regulation_of_ion_homeostasis	1	0							
GO:2000023_regulation_of_lateral_root_development	1	0							
GO:2000025_regulation_of_leaf_formation	1	0							
GO:2000028_regulation_of_photoperiodism__flowering	1	0							
GO:2000031_regulation_of_salicylic_acid_mediated_signaling_	1	0							
GO:2000069_regulation_of_post-embryonic_root_development	1	0							
GO:2000071_regulation_of_defense_response_by_callose_dep	1	0							
GO:2000073_regulation_of_site_selection_involved_in_cell_cyc	1	0							
GO:2000142_regulation_of_transcription_initiation__DNA-depe	1	0							
GO:2000144_positive_regulation_of_transcription_initiation__D	1	0							
GO:2000146_negative_regulation_of_cell_motility	1	0							
GO:0000041_transition_metal_ion_transport	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0005984_disaccharide_metabolic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0006304_DNA_modification	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0006518_peptide_metabolic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0006766_vitamin_metabolic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0006887_exocytosis	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0009110_vitamin_biosynthetic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0009639_response_to_red_or_far_red_light	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0009809_lignin_biosynthetic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0009909_regulation_of_flower_development	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0015698_inorganic_anion_transport	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0019321_pentose_metabolic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0022411_cellular_component_disassembly	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0022610_biological_adhesion	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0042981_regulation_of_apoptosis	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0044272_sulfur_compound_biosynthetic_process	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0051329_interphase_of_mitotic_cell_cycle	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0071845_cellular_component_disassembly_at_cellular_leve	19	0	0	0	1236	1238.236853	1249.82	1261.403147	1.011181
GO:0006333_chromatin_assembly_or_disassembly	61	0	0	0	1239	1240.27658	1251.68	1263.08342	1.010234

GO:0006366_transcription_from_RNA_polymerase_II_promote	61	0	0	0	1239	1240.27658	1251.68	1263.08342	1.010234
GO:0032870_cellular_response_to_hormone_stimulus	61	0	0	0	1239	1240.27658	1251.68	1263.08342	1.010234
GO:0006270_DNA-dependent_DNA_replication_initiation	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0006275_regulation_of_DNA_replication	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0006289_nucleotide-excision_repair	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0006767_water-soluble_vitamin_metabolic_process	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0006865_amino_acid_transport	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0006904_vesicle_docking_involved_in_exocytosis	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0007155_cell_adhesion	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0009066_aspartate_family_amino_acid_metabolic_process	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0009123_nucleoside_monophosphate_metabolic_process	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0009658_chloroplast_organization	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0010016_shoot_morphogenesis	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0010228_vegetative_to_reproductive_phase_transition_of_	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0015893_drug_transport	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0015994_chlorophyll_metabolic_process	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0022406_membrane_docking	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0032313_regulation_of_Rab_GTPase_activity	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0032482_Rab_protein_signal_transduction	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0032483_regulation_of_Rab_protein_signal_transduction	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0042364_water-soluble_vitamin_biosynthetic_process	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0042546_cell_wall_biogenesis	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0045165_cell_fate_commitment	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0045814_negative_regulation_of_gene_expression__epige	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0046271_phenylpropanoid_catabolic_process	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0048278_vesicle_docking	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0048584_positive_regulation_of_response_to_stimulus	17	0	0	0	1264	1263.59267	1273.51	1283.42733	1.007524
GO:0009145_purine_nucleoside_triphosphate_biosynthetic_pro	58	0	0	0	1267	1265.774566	1275.44	1285.105434	1.006661
GO:0009201_ribonucleoside_triphosphate_biosynthetic_proces	58	0	0	0	1267	1265.774566	1275.44	1285.105434	1.006661
GO:0009206_purine_ribonucleoside_triphosphate_biosynthetic_	58	0	0	0	1267	1265.774566	1275.44	1285.105434	1.006661
GO:0009146_purine_nucleoside_triphosphate_catabolic_proce	43	0	0	0	1273	1271.638491	1279.9	1288.161509	1.00542
GO:0009154_purine_ribonucleotide_catabolic_process	43	0	0	0	1273	1271.638491	1279.9	1288.161509	1.00542
GO:0009203_ribonucleoside_triphosphate_catabolic_process	43	0	0	0	1273	1271.638491	1279.9	1288.161509	1.00542
GO:0009207_purine_ribonucleoside_triphosphate_catabolic_pr	43	0	0	0	1273	1271.638491	1279.9	1288.161509	1.00542
GO:0009966_regulation_of_signal_transduction	43	0	0	0	1273	1271.638491	1279.9	1288.161509	1.00542
GO:0023051_regulation_of_signaling_process	43	0	0	0	1273	1271.638491	1279.9	1288.161509	1.00542
GO:0000122_negative_regulation_of_transcription_from_RNA_	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0000165_MAPKKK_cascade	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0000216_M_G1_transition_of_mitotic_cell_cycle	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0000727_double-strand_break_repair_via_break-induced_	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0001654_eye_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0001708_cell_fate_specification	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0001709_cell_fate_determination	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0002009_morphogenesis_of_an_epithelium	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0002253_activation_of_immune_response	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0005986_sucrose_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006108_malate_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006266_DNA_ligation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006282_regulation_of_DNA_repair	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006283_transcription-coupled_nucleotide-excision_repair	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006303_double-strand_break_repair_via_nonhomologous	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006359_regulation_of_transcription_from_RNA_polymera	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006360_transcription_from_RNA_polymerase_I_promoter	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006378_mRNA_polyadenylation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006400_tRNA_modification	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006401_RNA_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006402_mRNA_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006406_mRNA_export_from_nucleus	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006467_protein_thiol-disulfide_exchange	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006506_GPI_anchor_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006534_cysteine_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484

GO:0006559_L-phenylalanine_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006566_threonine_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006570_tyrosine_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006625_protein_targeting_to_peroxisome	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006626_protein_targeting_to_mitochondrion	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006749_glutathione_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006783_heme_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006801_superoxide_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006984_ER-nucleus_signaling_pathway	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0006995_cellular_response_to_nitrogen_starvation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007009_plasma_membrane_organization	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007091_mitotic_metaphase_anaphase_transition	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007129_synapsis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007286_spermatid_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007424_open_tracheal_system_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007435_salivary_gland_morphogenesis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007530_sex_determination	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007531_mating_type_determination	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007611_learning_or_memory	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007612_learning	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0008306_associative_learning	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0008608_attachment_of_spindle_microtubules_to_kinetoch	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009088_threonine_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009262_deoxyribonucleotide_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009452_RNA_capping	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009559_embryo_sac_central_cell_differentiation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009612_response_to_mechanical_stimulus	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009637_response_to_blue_light	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009687_abscisic_acid_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009690_cytokinin_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009692_ethylene_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009693_ethylene_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009756_carbohydrate_mediated_signaling	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009765_photosynthesis__light_harvesting	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009773_photosynthetic_electron_transport_in_photosyste	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009787_regulation_of_abscisic_acid_mediated_signaling_	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009846_pollen_germination	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009911_positive_regulation_of_flower_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0009958_positive_gravitropism	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010014_meristem_initiation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010044_response_to_aluminum_ion	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010090_trichome_morphogenesis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010103_stomatal_complex_morphogenesis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010114_response_to_red_light	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010118_stomatal_movement	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010119_regulation_of_stomatal_movement	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010165_response_to_X-ray	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010182_sugar_mediated_signaling_pathway	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010197_polar_nucleus_fusion	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010259_multicellular_organismal_aging	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010584_pollen_exine_formation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0010962_regulation_of_glucan_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0014070_response_to_organic_cyclic_substance	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0016139_glycoside_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0016197_endosome_transport	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0016444_somatic_cell_DNA_recombination	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0016558_protein_import_into_peroxisome_matrix	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0019310_inositol_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0019827_stem_cell_maintenance	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0019935_cyclic-nucleotide-mediated_signaling	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0022612_gland_morphogenesis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484

GO:0030071_regulation_of_mitotic_metaphase_anaphase_tran	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0030148_sphingolipid_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0030149_sphingolipid_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0030433_ER-associated_protein_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0030437_ascospore_formation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0030707_ovarian_follicle_cell_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0031016_pancreas_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0031018_endocrine_pancreas_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0031167_rRNA_methylation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0031349_positive_regulation_of_defense_response	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0031401_positive_regulation_of_protein_modification_proc	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032011_ARF_protein_signal_transduction	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032012_regulation_of_ARF_protein_signal_transduction	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032102_negative_regulation_of_response_to_external_sti	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032147_activation_of_protein_kinase_activity	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032201_telomere_maintenance_via_semi-conservative_re	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032269_negative_regulation_of_cellular_protein_metaboli	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032583_regulation_of_gene-specific_transcription	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032868_response_to_insulin_stimulus	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032881_regulation_of_polysaccharide_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032885_regulation_of_polysaccharide_biosynthetic_proce	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032950_regulation_of_beta-glucan_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0032951_regulation_of_beta-glucan_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0034101_erythrocyte_homeostasis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0034293_sexual_sporulation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0034453_microtubule_anchoring	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0035239_tube_morphogenesis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0035467_negative_regulation_of_signaling_pathway	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042026_protein_refolding	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042113_B_cell_activation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042176_regulation_of_protein_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042278_purine_nucleoside_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042436_indole-containing_compound_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042538_hyperosmotic_salinity_response	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042777_plasma_membrane_ATP_synthesis_coupled_pro	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042816_vitamin_B6_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0042819_vitamin_B6_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043193_positive_regulation_of_gene-specific_transcriptio	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043288_apocarotenoid_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043467_regulation_of_generation_of_precursor_metabolit	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043574_peroxisomal_transport	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043603_cellular_amide_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043631_RNA_polyadenylation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0043935_sexual_sporulation_resulting_in_formation_of_a_	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0044038_cell_wall_macromolecule_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0045927_positive_regulation_of_growth	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0046128_purine_ribonucleoside_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0046466_membrane_lipid_catabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0048444_floral_organ_morphogenesis	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0048515_spermatid_differentiation	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0048582_positive_regulation_of_post-embryonic_developm	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0048864_stem_cell_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0050778_positive_regulation_of_immune_response	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0050890_cognition	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0051054_positive_regulation_of_DNA_metabolic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0051248_negative_regulation_of_protein_metabolic_proces	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0051313_attachment_of_spindle_microtubules_to_chromos	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0051345_positive_regulation_of_hydrolase_activity	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0051494_negative_regulation_of_cytoskeleton_organizatio	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0051592_response_to_calcium_ion	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0052173_response_to_defenses_of_other_organism_invol	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484

GO:0052200_response_to_host_defenses	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0061160_regulation_of_establishment_of_bipolar_cell_pola	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0061161_positive_regulation_of_establishment_of_bipolar_	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0061171_establishment_of_bipolar_cell_polarity	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0061172_regulation_of_establishment_of_bipolar_cell_pola	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0061173_positive_regulation_of_establishment_of_bipolar_	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0070585_protein_localization_in_mitochondrion	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0070589_cellular_component_macromolecule_biosynthetic	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0071322_cellular_response_to_carbohydrate_stimulus	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0071897_DNA_biosynthetic_process	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0075136_response_to_host	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:2000114_regulation_of_establishment_of_cell_polarity	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:2000280_regulation_of_root_development	5	0	0	0	1433	1432.932607	1436.56	1440.187393	1.002484
GO:0007059_chromosome_segregation	35	0	0	0	1436	1435.799073	1439.09	1442.380927	1.002152
GO:0009808_lignin_metabolic_process	35	0	0	0	1436	1435.799073	1439.09	1442.380927	1.002152
GO:0051336_regulation_of_hydrolase_activity	35	0	0	0	1436	1435.799073	1439.09	1442.380927	1.002152
GO:0000018_regulation_of_DNA_recombination	4	0							
GO:0000103_sulfate_assimilation	4	0							
GO:0000105_histidine_biosynthetic_process	4	0							
GO:0000270_peptidoglycan_metabolic_process	4	0							
GO:0000303_response_to_superoxide	4	0							
GO:0000305_response_to_oxygen_radical	4	0							
GO:0000320_re-entry_into_mitotic_cell_cycle	4	0							
GO:0000743_nuclear_migration_involved_in_conjugation_with_	4	0							
GO:0000754_adaptation_of_signaling_pathway_by_response_t	4	0							
GO:0000920_cytokinetic_cell_separation	4	0							
GO:0000956_nuclear-transcribed_mRNA_catabolic_process	4	0							
GO:0001101_response_to_acid	4	0							
GO:0001505_regulation_of_neurotransmitter_levels	4	0							
GO:0001659_temperature_homeostasis	4	0							
GO:0001745_compound_eye_morphogenesis	4	0							
GO:0001751_compound_eye_photoreceptor_cell_differentiatio	4	0							
GO:0001754_eye_photoreceptor_cell_differentiation	4	0							
GO:0001816_cytokine_production	4	0							
GO:0001817_regulation_of_cytokine_production	4	0							
GO:0001894_tissue_homeostasis	4	0							
GO:0001906_cell_killing	4	0							
GO:0002200_somatic_diversification_of_immune_receptors	4	0							
GO:0002218_activation_of_innate_immune_response	4	0							
GO:0002250_adaptive_immune_response	4	0							
GO:0002263_cell_activation_involved_in_immune_response	4	0							
GO:0002285_lymphocyte_activation_involved_in_immune_resp	4	0							
GO:0002366_leukocyte_activation_involved_in_immune_respo	4	0							
GO:0002443_leukocyte_mediated_immunity	4	0							
GO:0002449_lymphocyte_mediated_immunity	4	0							
GO:0002460_adaptive_immune_response_based_on_somatic_	4	0							
GO:0002521_leukocyte_differentiation	4	0							
GO:0002562_somatic_diversification_of_immune_receptors_via	4	0							
GO:0002683_negative_regulation_of_immune_system_process	4	0							
GO:0002831_regulation_of_response_to_biotic_stimulus	4	0							
GO:0003013_circulatory_system_process	4	0							
GO:0006119_oxidative_phosphorylation	4	0							
GO:0006171_cAMP_biosynthetic_process	4	0							
GO:0006267_pre-replicative_complex_assembly	4	0							
GO:0006272_leading_strand_elongation	4	0							
GO:0006297_nucleotide-excision_repair__DNA_gap_filling	4	0							
GO:0006435_threonyl-tRNA_aminoacylation	4	0							
GO:0006446_regulation_of_translational_initiation	4	0							
GO:0006542_glutamine_biosynthetic_process	4	0							
GO:0006551_leucine_metabolic_process	4	0							
GO:0006664_glycolipid_metabolic_process	4	0							

GO:0006696_ergosterol_biosynthetic_process	4	0								
GO:0006771_riboflavin_metabolic_process	4	0								
GO:0006825_copper_ion_transport	4	0								
GO:0006828_manganese_ion_transport	4	0								
GO:0006835_dicarboxylic_acid_transport	4	0								
GO:0006885_regulation_of_pH	4	0								
GO:0007004_telomere_maintenance_via_telomerase	4	0								
GO:0007093_mitotic_cell_cycle_checkpoint	4	0								
GO:0007140_male_meiosis	4	0								
GO:0007143_female_meiosis	4	0								
GO:0007173_epidermal_growth_factor_receptor_signaling_pat	4	0								
GO:0007187_G-protein_signaling__coupled_to_cyclic_nucleoti	4	0								
GO:0007205_activation_of_protein_kinase_C_activity_by_G-pr	4	0								
GO:0007369_gastrulation	4	0								
GO:0007559_histolysis	4	0								
GO:0007601_visual_perception	4	0								
GO:0007602_phototransduction	4	0								
GO:0008015_blood_circulation	4	0								
GO:0008204_ergosterol_metabolic_process	4	0								
GO:0008340_determination_of_adult_lifespan	4	0								
GO:0008614_pyridoxine_metabolic_process	4	0								
GO:0008615_pyridoxine_biosynthetic_process	4	0								
GO:0008629_induction_of_apoptosis_by_intracellular_signals	4	0								
GO:0008653_lipopolysaccharide_metabolic_process	4	0								
GO:0009076_histidine_family_amino_acid_biosynthetic_proces	4	0								
GO:0009082_branched_chain_family_amino_acid_biosynthetic	4	0								
GO:0009103_lipopolysaccharide_biosynthetic_process	4	0								
GO:0009231_riboflavin_biosynthetic_process	4	0								
GO:0009272_fungal-type_cell_wall_biogenesis	4	0								
GO:0009432_SOS_response	4	0								
GO:0009556_microsporogenesis	4	0								
GO:0009583_detection_of_light_stimulus	4	0								
GO:0009593_detection_of_chemical_stimulus	4	0								
GO:0009640_photomorphogenesis	4	0								
GO:0009691_cytokinin_biosynthetic_process	4	0								
GO:0009696_salicylic_acid_metabolic_process	4	0								
GO:0009700_indole_phytoalexin_biosynthetic_process	4	0								
GO:0009750_response_to_fructose_stimulus	4	0								
GO:0009772_photosynthetic_electron_transport_in_photosyste	4	0								
GO:0009870_defense_response_signaling_pathway__resistan	4	0								
GO:0009960_endosperm_development	4	0								
GO:0010074_maintenance_of_meristem_identity	4	0								
GO:0010109_regulation_of_photosynthesis	4	0								
GO:0010229_inflorescence_development	4	0								
GO:0010268_brassinosteroid_homeostasis	4	0								
GO:0010410_hemicellulose_metabolic_process	4	0								
GO:0010431_seed_maturation	4	0								
GO:0010551_regulation_of_gene-specific_transcription_from_	4	0								
GO:0010552_positive_regulation_of_gene-specific_transcriptio	4	0								
GO:0010627_regulation_of_intracellular_protein_kinase_casca	4	0								
GO:0010740_positive_regulation_of_intracellular_protein_kinas	4	0								
GO:0010959_regulation_of_metal_ion_transport	4	0								
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GO:0015833_peptide_transport	4	0								
GO:0015918_sterol_transport	4	0								
GO:0015976_carbon_utilization	4	0								
GO:0015977_carbon_fixation	4	0								
GO:0016106_sesquiterpenoid_biosynthetic_process	4	0								
GO:0016119_carotene_metabolic_process	4	0								
GO:0016122_xanthophyll_metabolic_process	4	0								
GO:0016145_S-glycoside_catabolic_process	4	0								

GO:0016226_iron-sulfur_cluster_assembly	4	0							
GO:0016236_macroautophagy	4	0							
GO:0016271_tissue_death	4	0							
GO:0016337_cell-cell_adhesion	4	0							
GO:0016539_intein-mediated_protein_splicing	4	0							
GO:0017148_negative_regulation_of_translation	4	0							
GO:0019079_viral_genome_replication	4	0							
GO:0019252_starch_biosynthetic_process	4	0							
GO:0019344_cysteine_biosynthetic_process	4	0							
GO:0019348_dolichol_metabolic_process	4	0							
GO:0019363_pyridine_nucleotide_biosynthetic_process	4	0							
GO:0019408_dolichol_biosynthetic_process	4	0							
GO:0019430_removal_of_superoxide_radicals	4	0							
GO:0019759_glycosinolate_catabolic_process	4	0							
GO:0019762_glucosinolate_catabolic_process	4	0							
GO:0023058_adaptation_of_signaling_pathway	4	0							
GO:0030011_maintenance_of_cell_polarity	4	0							
GO:0030098_lymphocyte_differentiation	4	0							
GO:0030099_myeloid_cell_differentiation	4	0							
GO:0030203_glycosaminoglycan_metabolic_process	4	0							
GO:0030245_cellulose_catabolic_process	4	0							
GO:0030261_chromosome_condensation	4	0							
GO:0030422_production_of_siRNA_involved_in_RNA_interfere	4	0							
GO:0030582_fruiting_body_development	4	0							
GO:0030855_epithelial_cell_differentiation	4	0							
GO:0030908_protein_splicing	4	0							
GO:0031050_dsRNA_fragmentation	4	0							
GO:0031056_regulation_of_histone_modification	4	0							
GO:0031099_regeneration	4	0							
GO:0031109_microtubule_polymerization_or_depolymerization	4	0							
GO:0031110_regulation_of_microtubule_polymerization_or_dep	4	0							
GO:0031111_negative_regulation_of_microtubule_polymerizatio	4	0							
GO:0031122_cytoplasmic_microtubule_organization	4	0							
GO:0031163_metallo-sulfur_cluster_assembly	4	0							
GO:0031334_positive_regulation_of_protein_complex_assembl	4	0							
GO:0031644_regulation_of_neurological_system_process	4	0							
GO:0031929_TOR_signaling_cascade	4	0							
GO:0032271_regulation_of_protein_polymerization	4	0							
GO:0032312_regulation_of_ARF_GTPase_activity	4	0							
GO:0032875_regulation_of_DNA_endoreduplication	4	0							
GO:0032880_regulation_of_protein_localization	4	0							
GO:0032957_inositol_trisphosphate_metabolic_process	4	0							
GO:0033273_response_to_vitamin	4	0							
GO:0034330_cell_junction_organization	4	0							
GO:0034605_cellular_response_to_heat	4	0							
GO:0034724_DNA_replication-independent_nucleosome_orgar	4	0							
GO:0034762_regulation_of_transmembrane_transport	4	0							
GO:0035265_organ_growth	4	0							
GO:0040012_regulation_of_locomotion	4	0							
GO:0040017_positive_regulation_of_locomotion	4	0							
GO:0042060_wound_healing	4	0							
GO:0042343_indole_glucosinolate_metabolic_process	4	0							
GO:0042375_quinone_cofactor_metabolic_process	4	0							
GO:0042698_ovulation_cycle	4	0							
GO:0042726_flavin-containing_compound_metabolic_process	4	0							
GO:0042727_flavin-containing_compound_biosynthetic_proces	4	0							
GO:0043244_regulation_of_protein_complex_disassembly	4	0							
GO:0043279_response_to_alkaloid	4	0							
GO:0043331_response_to_dsRNA	4	0							
GO:0043455_regulation_of_secondary_metabolic_process	4	0							
GO:0043627_response_to_estrogen_stimulus	4	0							

GO:0044057_regulation_of_system_process	4	0							
GO:0044107_cellular_alcohol_metabolic_process	4	0							
GO:0044108_cellular_alcohol_biosynthetic_process	4	0							
GO:0044247_cellular_polysaccharide_catabolic_process	4	0							
GO:0044273_sulfur_compound_catabolic_process	4	0							
GO:0044406_adhesion_to_host	4	0							
GO:0045037_protein_import_into_chloroplast_stroma	4	0							
GO:0045089_positive_regulation_of_innate_immune_response	4	0							
GO:0045338_farnesyl_diphosphate_metabolic_process	4	0							
GO:0045426_quinone_cofactor_biosynthetic_process	4	0							
GO:0045597_positive_regulation_of_cell_differentiation	4	0							
GO:0045930_negative_regulation_of_mitotic_cell_cycle	4	0							
GO:0046058_cAMP_metabolic_process	4	0							
GO:0046112_nucleobase_biosynthetic_process	4	0							
GO:0046173_polyol_biosynthetic_process	4	0							
GO:0046217_indole_phytoalexin_metabolic_process	4	0							
GO:0046487_glyoxylate_metabolic_process	4	0							
GO:0046530_photoreceptor_cell_differentiation	4	0							
GO:0046620_regulation_of_organ_growth	4	0							
GO:0046777_protein_autophosphorylation	4	0							
GO:0048167_regulation_of_synaptic_plasticity	4	0							
GO:0048236_plant-type_spore_development	4	0							
GO:0048449_floral_organ_formation	4	0							
GO:0048478_replication_fork_protection	4	0							
GO:0048592_eye_morphogenesis	4	0							
GO:0048749_compound_eye_development	4	0							
GO:0048771_tissue_remodeling	4	0							
GO:0048825_cotyledon_development	4	0							
GO:0050727_regulation_of_inflammatory_response	4	0							
GO:0050795_regulation_of_behavior	4	0							
GO:0050804_regulation_of_synaptic_transmission	4	0							
GO:0050878_regulation_of_body_fluid_levels	4	0							
GO:0050953_sensory_perception_of_light_stimulus	4	0							
GO:0051181_cofactor_transport	4	0							
GO:0051316_attachment_of_spindle_microtubules_to_kinetoch	4	0							
GO:0051445_regulation_of_meiotic_cell_cycle	4	0							
GO:0051455_attachment_of_spindle_microtubules_to_kinetoch	4	0							
GO:0051607_defense_response_to_virus	4	0							
GO:0051668_localization_within_membrane	4	0							
GO:0051762_sesquiterpene_biosynthetic_process	4	0							
GO:0051789_response_to_protein_stimulus	4	0							
GO:0051817_modification_of_morphology_or_physiology_of_o	4	0							
GO:0051825_adhesion_to_other_organism_involved_in_symbi	4	0							
GO:0051969_regulation_of_transmission_of_nerve_impulse	4	0							
GO:0052126_movement_in_host_environment	4	0							
GO:0052192_movement_in_environment_of_other_organism_i	4	0							
GO:0052314_phytoalexin_metabolic_process	4	0							
GO:0052315_phytoalexin_biosynthetic_process	4	0							
GO:0052564_response_to_immune_response_of_other_organi	4	0							
GO:0052572_response_to_host_immune_response	4	0							
GO:0055067_monovalent_inorganic_cation_homeostasis	4	0							
GO:0060191_regulation_of_lipase_activity	4	0							
GO:0060627_regulation_of_vesicle-mediated_transport	4	0							
GO:0070918_production_of_small_RNA_involved_in_gene_sile	4	0							
GO:0071214_cellular_response_to_abiotic_stimulus	4	0							
GO:0071359_cellular_response_to_dsRNA	4	0							
GO:0071375_cellular_response_to_peptide_hormone_stimulus	4	0							
GO:0071450_cellular_response_to_oxygen_radical	4	0							
GO:0071451_cellular_response_to_superoxide	4	0							
GO:0071704_organic_substance_metabolic_process	4	0							
GO:0071900_regulation_of_protein_serine_threonine_kinase_a	4	0							

GO:0071941_nitrogen_cycle_metabolic_process	4	0							
GO:0075259_spore-bearing_organ_development	4	0							
GO:0080010_regulation_of_oxygen_and_reactive_oxygen_spe	4	0							
GO:0080022_primary_root_development	4	0							
GO:0080092_regulation_of_pollen_tube_growth	4	0							
GO:0003008_system_process	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0009831_plant-type_cell_wall_modification_involved_in_mu	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0016032_viral_reproduction	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0016485_protein_processing	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0030384_phosphoinositide_metabolic_process	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0031347_regulation_of_defense_response	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0042547_cell_wall_modification_involved_in_multidimensio	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0051093_negative_regulation_of_developmental_process	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0051604_protein_maturation	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0071705_nitrogen_compound_transport	20	0	0	0	1446	1446.897862	1449.34	1451.782138	1.00231
GO:0006414_translational_elongation	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0006818_hydrogen_transport	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0007126_meiosis	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0008283_cell_proliferation	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0015992_proton_transport	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0034220_ion_transmembrane_transport	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0035295_tube_development	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0042440_pigment_metabolic_process	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0048588_developmental_cell_growth	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0050801_ion_homeostasis	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0051327_M_phase_of_meiotic_cell_cycle	33	0	0	0	1457	1454.991214	1456.08	1457.168786	0.999369
GO:0016481_negative_regulation_of_transcription	36	0	0	0	1458	1456.548271	1457.25	1457.951729	0.999486