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Proteogenomic mapping of *Gossypium mustelinum* Leaf

By
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ABSTRACT

Cotton, having a production value of $7.2 billion in 2017, is one of the most valuable crops in the United States. While not a fiber-producing species, the wild Brazilian tetraploid *Gossypium mustelinum* may produce a hybrid with exceptionally long fibers if crossed with *G. hirsutum*, one of the most commonly cultivated species. For the first time, presented here is the global proteome profile of the *G. mustelinum* leaf which may be used as a reference in future studies. Proteins were extracted from three individual *G. mustelinum* plants. To maximize protein coverage, two sample preparation techniques were utilized: size-based fractionation by SageELF instrument and complex protein mixture. A total of 3005 proteins were identified by nano-liquid chromatography-tandem mass spectrometry and database search, of which 1550 were unique to SageELF fractionation, 472 were unique to complex mixtures, and 983 were common to both techniques. Functional classification by Gene Ontology (GO) Annotation was performed on the identified proteins. For cellular component categorization, 245 were found in protein-containing complexes and 112 were located in organelles such as plastids and Golgi apparatus. The molecular function GO aspect included 306 oxidoreductases, 80 transferases, 71 hydrolases, and 810 proteins involved in binding. Of the proteins involved in biological processes, 241 pertain to transport, 278 belong to biosynthetic processes, and 121 relate to photosynthesis. A total of 16 GO terms such as extracellular region, nucleoplasm, and vacuoles were assigned to proteins identified in the fractionated samples but not in the complex mixture samples. Additionally, GO terms that were found in both types of samples were more plentiful in the fractionated samples than the complex mixture samples. These findings validate the use of two different sample preparation techniques to obtain a more comprehensive proteome coverage.

Key words: proteogenomic mapping, cotton, mass spectrometry, gene ontology

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Hail State!

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ABBREVIATIONS

2D-PAGE	two-dimensional polyacrylamide gel electrophoresis
ESI	electrospray ionization
HPLC	high-performance liquid chromatography
LCMS	liquid chromatography–mass spectrometry
TCA	trichloroacetic acid

CHAPTER I: INTRODUCTION

Cotton, having a production value of $7.2 billion in 2017, is one of the most valuable crops in the United States.[1] The term refers to any of 50 members of the genus *Gossypium*, which exhibits a great deal of variety. For example, *G. hirsutum* forms small shrubs while *G. arboreum* grows up to six feet tall; furthermore, *G. barbadense* and *G. hirsutum* both have cultivatable fibers while many other species, such as *G. mustelinum*, do not. Phylogenic data suggests the existence of a single natural cotton lineage originating in Africa, a theory that is further supported by the diversity of this region. The seeds from these ancestral plants were carried transoceanically to the Americas and China.[2] The sequences of the A genome and the D genome likely diverged 10-15 million years ago.[2,3] About 1.43 million years ago, tetraploid species containing four sets of chromosomes (versus the standard two sets found in diploid organisms) formed naturally when the Old World "A" genome hybridized with the New World "D" genome.[3,4] The donor of the A genome is likely either *G. arboreum* or *G. herbaceum* (lack of mutational differences make ascertaining the species difficult)[3,5] while that of the D genome is believed to be *G. raimondii*.[5] Further speciation has resulted in 43 diploid species containing genomes A-G and 7 tetraploid species with AD genomes belonging to the genus *Gossypium*.[6] Figure 1 illustrates this process.

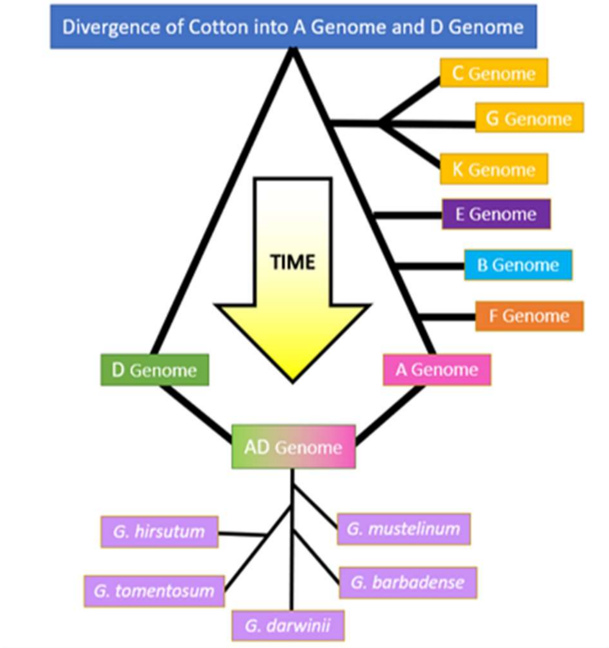

Figure 1: Formation of the AD genome from the A genome and the D genome.

While tetraploid species *G. hirsutum* and *G. barbadense* are most common in agriculture, diploid species *G. arboreum* and *G. herbaceum* are also known to be cultivated.[2,4,6,7] Even though the D genome diploid cottons do not produce any spinnable fibers[2], studies show that the D subgenome contributes to more genetic variation in the AD tetraploid cottons than does the A subgenome.[4] Many consider tetraploidy to have a distinct advantage over diploidy in terms of selection response[4]; however, others argue that tetraploidy statistically has no effect on the successful domestication of cotton or any other tetraploid crop.[8] Regardless, human selective breeding has resulted in superior cotton crops with increased yield and improved fiber traits.[4] In fact, many of these traits are the result of hybridization.

Hybridizing *G. hirsutum* with a different cotton species tends to result in better fiber traits (including fineness, length, and strength), as well as increased fiber yield. Crossing species with *G. barbadense* similarly improves fiber quality in the resulting hybrid.[4,6] Hybridization can also be used to transfer pathogen and disease resistance from one species to another. For example, modern cultivated *G. hirsutum* has rust resistance from *G. raimondii* in addition to boll weevil resistance from *G. armourianum*, and *G. hirsutum* hybrids are often resistant to Verticillium wilt[6], a type of fungal infection.

G. mustelinum, one of the uncultivated tetraploid cottons[9] and the earliest divergence within the AD lineage,[10] is one of the rarest and most unexplored cotton species[11]. It is found exclusively in the Caatinga biome of northeastern Brazil. Unfortunately for *G. mustelinum*, this biome contains sporadic sources of water[11–13]; as a result, it must resort to growing alongside riverbeds and ponds to maintain adequate hydration levels.[11,14] Furthermore, much of its habitat is being destroyed by deforestation and agriculture[11–13], resulting in high endogamy within populations.[9,13] Livestock feeds on both young and adult specimens, killing the former and inhibiting the reproduction of the latter.[9,11] These factors are major contributors to the isolation of *G. mustelinum* populations. Since the various populations are so spread out, they display high genetic variation from one another.[9,11,13] As a result, appropriate genetic conservation requires the maintenance of all these populations.[9]

G. mustelinum has been shown to be sexually compatible with tetraploids *G. hirsutum* and *G. barbadense*, the two most commonly cultivated cotton species.[15–17] Since it is susceptible many to diseases, including cotton blue disease, angular leaf spot, ramulose, and mosaic virus,[14] hybridizing *G. mustelinum* with *G. hirsutum* or *G. barbadense* would be unlikely to improve the pathogen resistance of the latter two species. However, QTL analysis does indicate that crossing *G. hirsutum* with *G. mustelinum* has potential to increase the fiber length[16] even though *G. mustelinum* is not a fiber producing cotton.

Proteomics is the study of the proteome, or the complete set of proteins present in a cell, tissue, or organism. Assembling a proteome not only allows annotation of a species' genome, but may also suggest the function of a protein, which is especially valuable if its role is previously unknown. In addition, proteomics gives insight into the degree of protein expression as well as protein-protein interactions. Furthermore, the assembly of a proteome allows, for example, a comparison between the diseased and healthy conditions of an organism. Proteogenomic mapping of cotton species may also allow for the prediction of successful hybrids with improved fiber quality, yield, pathogen resistance, and drought tolerance in addition to providing insight into their susceptibilities and resistances. Presently, proteome mapping of tetraploid cotton species *G. hirsutum*[18–20] and *G. barbadense*[21,22] has been performed. However, to the authors' knowledge, no research regarding the proteome of *G. mustelinum* has yet been conducted. In this study, we present the first known proteogenomic mapping of the *Gossypium mustelinum* leaf obtained by nanoLCMSMS analysis.

CHAPTER II: MATERIALS AND METHODS

2.1. Tissue Collection

Leaf tissue from *G. mustelinum* clone 1408120.09-8121 (the same clone that was used for sequencing) was obtained from Dept. Soil & Crop Sciences, TAMU, TX. During harvesting, leaves were flash frozen in liquid nitrogen and shipped on dry ice. Once received, tissue was stored at -80˚C.

2.2. Protein Extraction Using Phenol-based Methodology

Total leaf protein (whole cell lysate) was extracted from three *G. mustelinum* biological replicate plants using phenol-based protocol with modifications[23]. Tissue was ground in liquid nitrogen into a fine powder and mixed with 4 mL of cold extraction buffer (0.9 M sucrose, 0.5 M Tris-base, 0.05 M Na_2-EDTA, 0.1 M KCl, 2% β-mercaptoethanol, pH 8.7) per gram of tissue. After vortexing and shaking for 10 minutes on ice, an equal volume of Tris-saturated phenol (pH 8.0) was added and mixture was homogenized for additional 15 minutes. The homogenate was then centrifuged at 8000 x *g* for 15 minutes to separate phenol and aqueous phases. The protein-containing phenol phase was collected and an equal volume of cold extraction buffer was added for another run of homogenization. This process was repeated two more times. Protein was precipitated from final phenol phase with five volumes of methanol solution (0.1 M ammonium acetate and 1% β-mercaptoethanol in 100% methanol) at 20˚C overnight. Protein precipitate was collected by centrifugation at 8000 x *g* for 15 minutes and washed three times with ice cold methanol solution, twice with ice cold 80% acetone, and once with ice cold 100% acetone. The protein was air-dried and stored at -20˚C.

2.2. Protein Extraction by TCA/Acetone Precipitation

Liquid nitrogen-ground fine powder of three biological replicates of *G. mustelinum* leaf was produced as described in section 2.2. Protein was extracted by adding 5 mL of 10% TCA/acetone/2mM DTT per gram of tissue and 10 minute-homogenization[24]. Precipitation was carried out overnight at -20˚C. The precipitated protein was washed once with 80% acetone and four times with 100% acetone before being air-dried and stored at -20˚C.

2.3. Protein Quantitation

All protein samples were quantitated using the 2D Quant Kit (GE Healthcare Life Sciences, Piscataway, NJ) according to manufacturer instruction. Absorbance was measured using at 96-well plate with the BioTek Synergy HTX multi-mode reader (Biotek, Winooski, VT) at 480 nm.

2.4. Two-dimensional polyacrylamide gel electrophoresis (2D PAGE)

For 2D PAGE[25], protein pellet was dissolved in sample buffer containing 9 M urea, 4% CHAPS, 1% DTT, and 0.2% ampholytes pH 3-10. Isoelectric focusing was carried out in PROTEAN IEF Cell (BioRad, Hercules, CA). Three hundred micrograms of protein were loaded on 11 cm IPG with immobilized non-linear 3-10 pH gradient (Bio-Rad) and actively rehydrated at 23˚C for 12 hours, which was followed by isoelectric focusing for a total of 35,000 Volt-hours. Focused strips were then equilibrated for 15 minutes in 4 mL of equilibration buffer I (6 M urea, 0.375 M Tris-HCL pH 6.8, 2% SDS, 20% glycerol, 2% (w/v) DTT). They were subsequently equilibrated for 15 minutes in equilibration buffer II (6 M urea, 0.375 M Tris-HCL pH 6.8, 2% SDS, 20% glycerol, 2.5% (w/v) IAA, and trace of bromophenol blue). For second dimension, equilibrated strips were loaded on Criterion TGX 8-16% (w/v) gradient polyacrylamide precast gel and covered with a layer of 1% agarose. Electrophoresis was carried out in Criterion (BioRad) electrophoretic apparatus at 150 Volts. Running buffer was composed of 25 mM Tris, 250 mM glycine, 0.1 % SDS. Proteins were visualized using Coomassie Brilliant Blue R-250 and gel was imaged by the Proteome Works Spot Cutter/Imager (BioRad).

2.5. Protein Fractionation by SageELF

For fractionation by mass, protein pellets were dissolved in 1xSDS sample buffer (50 mM Tris-HCl pH 6.8, 2% SDS, 10% glycerol, 1% DTT) and obtained complex protein mixture was fractionated according to molecular weight (MW) by SageELF instrument (Sage Science, Beverly, MA). Three hundred and fifty micrograms of protein were prepared following the manufactures' protocol and separated on 3% SDS/agarose cassette. Resulting twelve MW fractions (15 kDa, 19 kDa, 23 kDa, 30 kDa, 38 kDa, 51 kDa, 66 kDa, 88 kDa, 115 kDa, 149 kDa, 230 kDa, and 263 kDa) were collected and desalted (SDS removal) using HiPPR Detergent Removal Resin Column Kit (Thermo Scientific, Rockford, IL).

2.6. In-solution digestion of protein fractions

Prior to mass spectrometry (MS), desalted protein fractions were subjected to in-solution digestion with trypsin[26]. First, they were reduced by adding 1/10 volume of 100mM DTT/100 mM NH_4HCO_3 pH 8.0 to each sample (fraction) and incubated at 65˚C for 15 minutes. After the samples had cooled, they were alkylated by adding a 1/10 volume of 100mM IAA/100 mM NH_4HCO_3 pH 8.0 to each sample and incubated for 45 minutes at room temperature in the dark. Each sample was then complemented with acetonitrile to a final concentration 5%. Mass spectrometry grade Trypsin/Lys-C (20 ug; Promega, Madison, WI) was re-suspended in 20 uL of 5% acetonitrile/100 mM NH_4HCO_3 pH 8.0 (final concentration 1 ug/uL). Mass-dependent distribution of leaf proteins on 2-D gel was used as guide for amount of trypsin used per each fraction. They are depicted in chart below:

Fraction (kDa)	15	19	23	30	38	51	66	86	115	149	230	263
Trypsin (ug)	1.5	1.5	1.5	2.0	2.0	2.0	2.0	2.0	1.0	1.0	1.0	1.0

Table 1: Protein fractions resulting SageELF fractionation.

After the Trypsin/Lys-C Mix was added, the samples were incubated at 37˚C overnight. After digestion, 1% FA was added to a final concentration of 0.1% to stop the enzymatic reaction and to protonize the resulting peptides. The samples, tryptic peptide mixtures, were then freeze-dried (Labconco, Kansas City, MO) and stored at -80˚C. Immediately prior mass spectrometry, lyophilized peptides were resuspended in 2% acetonitrile/0.1% formic acid and transferred to MS vials.

2.7. In-solution digestion of complex protein mixture

For mass spectrometry of leaf complex protein mix, 50 ug of protein was precipitated from protein sample previously dissolved in 1x SDS buffer (50 mM Tris-HCl pH 6.8, 2% SDS, 10% glycerol, 1% DTT). Precipitation was carried out by adding five volumes of 100% acetone to the volume of protein corresponding to 50 ug (1:5 ratio protein:acetone) and incubating at -20˚C overnight. After thorough washing with 100% acetone, precipitated protein was dissolved in 100 ul of 5% acetonitrile/100 mM NH_4HCO_3 pH 8.0. Reduction and alkylation were performed as described in 2.6. Six micrograms of Trypsin/Lys-C were added to the protein sample (enzyme:protein ratio 6:50) and digested overnight at 37˚C. After 1% formic acid was supplemented to 0.1% final concentration, tryptic peptide mixtures were freeze-dried (Labconco) and stored at -80˚C. Immediately prior mass spectrometry, they were resuspended in 2% acetonitrile/0.1% formic acid and transferred to MS vials.

2.8. Nano-liquid chromatography-tandem mass spectrometry analysis (nLC-MSMS)

Two micrograms of protein tryptic digest were subjected to nLC-MSMS analysis as published previously[27]. Briefly, peptides were separated using reversed phase C18 75 µm x 150 mm column and Ultimate 3000 HPLC system (both Thermo Fisher Scientific).

Complex mixtures were analyzed via 170 minutes long, nonlinear, constant flow (0.3 µl.min^{-1}) gradient of acetonitrile (in 0.1% formic acid) as follows: 2%-55% for 125 min, 95% for 15 min, 2% for 30 min. Fractionated samples were subjected to 1 hour nonlinear, constant flow (0.3 µl.min^{-1}) gradient of acetonitrile (in 0.1% formic acid) as follows: 2%-55% for 35 min, 95% for 10 min, 2% for 15 min.

Mass spectra were collected by nano-electro spray ionization LTQ-Orbitrap Velos mass spectrometer (Thermo Fisher Scientific) directly linked to the nLC system. The mass spectrometer operated in the result dependent acquisition (RDA) mode of 18 scan events: one MS scan (m/z range: 300–1700) followed by 17 MSMS scans for the 17 most intense ions detected in MS scan, with dynamics exclusion allowed.

2.9. Protein identification

The raw data files were searched using the SEQUEST algorithm of the Proteome Discoverer software versions 1.1 and 2.1 (Thermo Fisher Scientific), as described previously[28]. Variable modifications were considered for: cysteine carbamidomethylation (+57.021), methionine oxidation (+15.995), and methionine dioxidation (+31.990). To allow for calculation of false discovery rates (FDR), experimental MS and MSMS data were matched against target and decoy databases. *Gossypium mustelinum* protein database was obtained from HudsonAlpha Institute for Biotechnology (Huntsville, AL, USA) and served as the target database, while its reversed copy (created automatically by the software) served as a decoy database. To obtain high confidence protein identifications, the search results were filtered by FDR < 1%.

2.10. Gene Ontology

The GO annotations for proteins found in leaf tissue were retrieved from the functional annotations provided by HudsonAlpha. These GO annotations were reduced to the Generic GO subset using the AgBase GOSlimViewer tool[29].

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CHAPTER III: RESULTS AND DISCUSSION

3.1. Protein Extraction

Figure 2: Leaf from *Gossypium mustelinum*. Picture courtesy of Robert Vaughn, Dept. Soil and Crop Sciences, TAMU.

Protein samples were extracted from *G. mustelinum leaves* (Fig. 2). Trichloroacetic acid (TCA) extraction is relatively simple and time-efficient, however many of the cellular components (with the exception of salts and lipid-soluble components) remain in the sample along with the desired protein. Because of this, the TCA method was used only for two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) where these additional non-protein components do not have as much of an effect on the procedure outcome.

Liquid chromatography–mass spectrometry (LCMS) requires the extracted protein to be very clean to ensure good results and to avoid column clogging and contamination of the instruments. For samples intended for LCMS, the phenol extraction method was used. While more arduous and significantly more time-consuming than TCA extraction, the phenol method produces very clean protein that is generally free of any other cellular components, such as the lipids and polysaccharides that are prominent in many plant tissues.

3.2. 2D-PAGE

Two-dimensional polyacrylamide gel electrophoresis[24,25,30] (2D-PAGE) separates protein into a first dimension based on isoelectric point (pI - the pH at which the protein contains a neutral charge) via isoelectric focusing and then into a second dimension based on molecular weight via electrophoresis. The result is a gel containing spots of proteins mapped into a two-dimension grid with pI on the horizontal axis and molecular weight on the vertical axis. Unlike fractionation, which resolves proteins based solely on molecular weight where each fraction contains multiple proteins of similar size, 2D-PAGE offers much higher resolving power with each protein present in the gel matrix as a single spot. After the proteins are separated, they can be excised from the gel and subjected to in-gel digestion. Subsequently, each protein spot can be identified using MALDI-TOF mass spectrometry. For the purposes of this study, 2D-PAGE was performed mainly for protein visualization. The spot-protein identification will be performed in follow-up study.

2D-PAGE was performed using TCA-extracted protein from leaf replicate 2. This resulted in many spots indicative of the presence of a variety of abundant protein species in this sample (Figure 3). The molecular weight marker/ladder acts as a reference point for the molecular weights (marked). The isoelectric points (pI) range between 3 (left) and 10 (right). In this gel, the pI range is nonlinear, so the intermediate points between 3 and 10 do not necessarily occur at regular intervals.

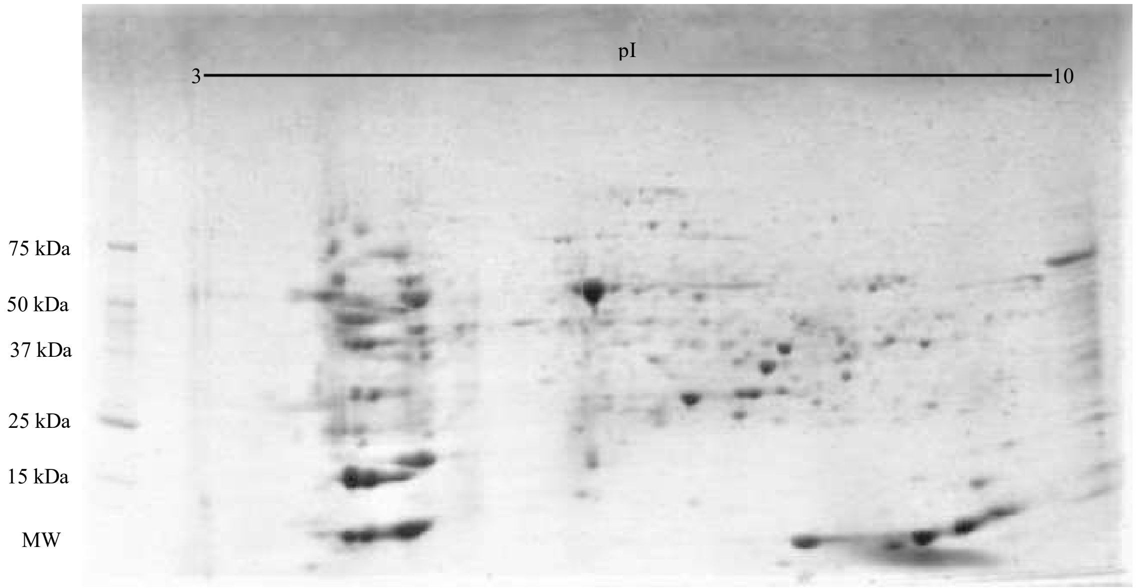


Figure 3: 2D-PAGE gel of TCA-extracted leaf protein from *Gossypium mustelinum*. 1st dimension performed on an 11 cm Bio-Rad 3-10 nonlinear IPG strip. 2nd dimension completed on a Bio-Rad Criterion TGC 8-16% precast polyacrylamide gel.

3.3. SageELF Fractionation

Fractionation resolves the proteins into mass groups by using an electrophoretic system, where they move according to their size. The benefits of this procedure can be seen in Figure 4. The SageELF system (see Figure 5) divides complex mixtures into 12 approximate mass groups, which may be subsequently treated as individual samples. These fractionated samples each contain a significantly smaller number of proteins than the unfractionated complex mixture

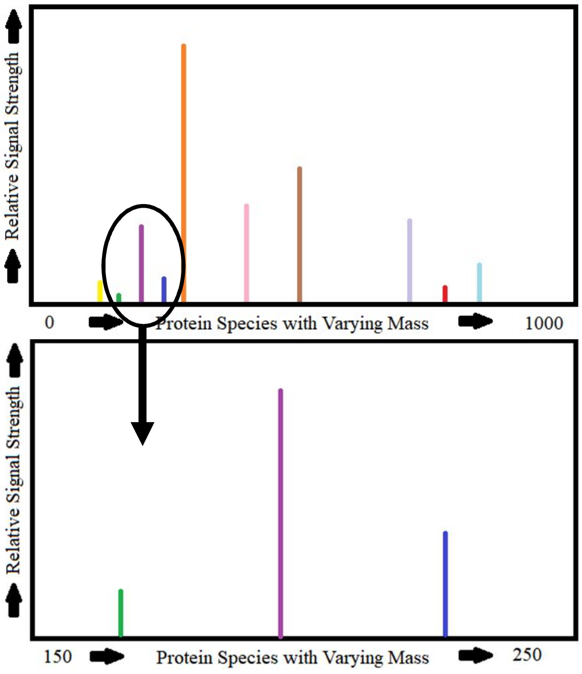


Figure 4: Comparison of complex mixture (top) and fractionated (bottom) LCMS signals. The green signal present in the complex mixture is eclipsed by the stronger signals from more abundant peptides. However, fractionation sorts the overshadowing signals into different samples, increasing the visibility of the formerly obscure green signal.

samples. At any point during analysis, the signals that are recognized by the LCMS are the strongest signals at that time. Thus, if many signals of varying size are present, the smallest of them may not be recognized. Sorting the proteins into smaller samples, or fractions, significantly increases the chance that these low-signal proteins are detected since there are fewer of the high-signal proteins present to obscure them.

Figure 5: Sage Science SageELF electrophoretic system for whole sample fractionation of DNA or protein.

As shown in the Venn diagram (Figure 6), not many proteins are found in both the fractions and the complex mixtures. In fact, only 38.8% of the fractionated proteins and 67.6% of the complex mixture proteins are common to both groups. The reason why so many more proteins are found in the fractionated samples is that the species with smaller signals are more likely to be detected versus in the complex mixtures, as described previously in this section. However, there is also a significant number of protein species that are seen only in the complex mixtures. Every procedure performed on a sample results in some loss of protein due to biases in the procedures themselves as well as human error. Thus, no procedure will have 100% protein recovery. Consequently, some proteins are lost from the sample with each additional procedure performed. Fractionated samples must be freed of SDS in order to be compatible with LCMS analysis. It is highly possible that some proteins were during the desalting procedure, which is why additional proteins were identified in the complex mixtures but not the fractions. Our results clearly show that the combined analysis of both fractions and complex mixtures produces a more comprehensive proteome coverage.

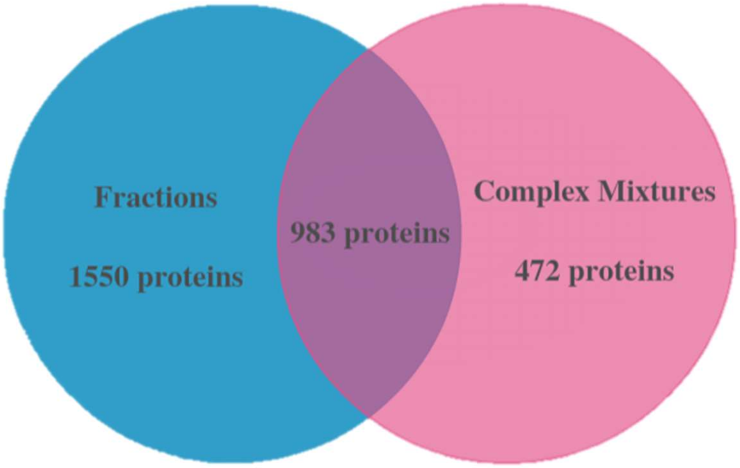


Figure 6: Venn diagram comparing number of proteins found in fractions only, in complex mixtures only, and in both methods.

3.4. In-Solution Digestion

The SDS detergent used in the SageELF fractionation contains many salts that are not compatible with the mass spectrometry equipment. As a result, these salts must be removed from the fractionated samples. It is important to note that doings so may result in a small loss of protein species; however, it is necessary in order to continue sample processing.

Digesting the protein, or cutting it into small peptides, allows for protein identification via mass spectrometry analysis (see section 3.5). All digestion was performed using trypsin/Lys-C mix. Trypsin, which is most active at a pH of about 8, cleaves proteins at the arginine (R) and lysine (K) residues (unless either of these is followed by proline, P). This process is illustrated in Figure 7. Introducing Lys-C to the digestion theoretically further improves the process.

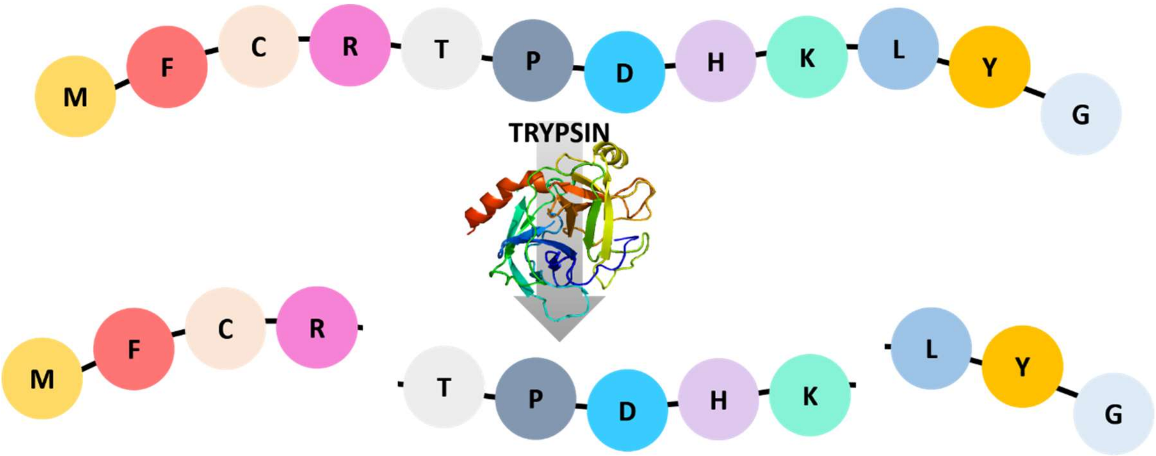


Figure 7: Illustration of trypsin activity. Here, trypsin cleaves a theoretical protein at the C-terminus of the arginine (R) and lysine (K) residues, resulting in three peptides.

3.5. Protein Identification via Liquid Chromatography-Mass Spectrometry.

Liquid chromatography–mass spectrometry (LCMS) is comprised of two separate but connected processes: liquid chromatography and mass spectrometry. Liquid chromatography is a process in which variety of chemical components in a solution are separated into individual components. The type of HPLC implemented here is reverse phase HPLC, which is more common than normal phase HPLC due to a wider application range and an increased level of user control over the system. While traditional chromatography involves a nonpolar mobile phase and a polar stationary phase, reverse-phased chromatography uses a polar mobile phase and a nonpolar stationary phase. As a result, the polar molecules in the samples will pass through the nonpolar stationary phase more quickly than the polar molecules and will consequently exit the system faster.

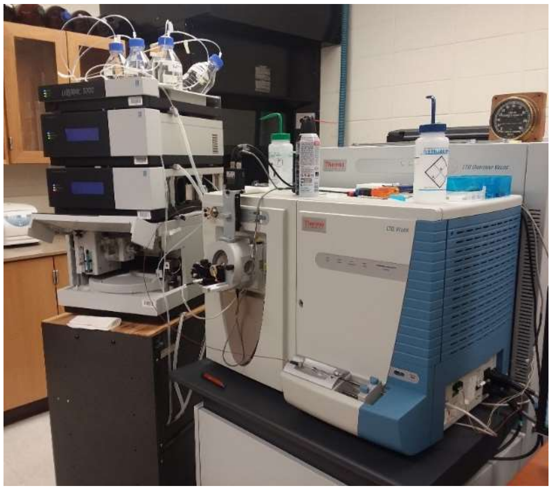


Figure 8: Nano-electro spay ionization LTQ-Orbitrap Velos mass spectrometer with an upstream Ultimate 3000 HPLC system, both from Thermo Fisher Scientific.

In the LCMS system used in this study (see Figure 8), the peptides enter the MS system via electrospray ionization (ESI)[31]. During the ESI process (Fig. 9)[32], positively charged peptides (via excess of protons provided by formic acid) are freed from the solvent and carried from the spray needle to the inlet of the MS system due to high voltage gradient.

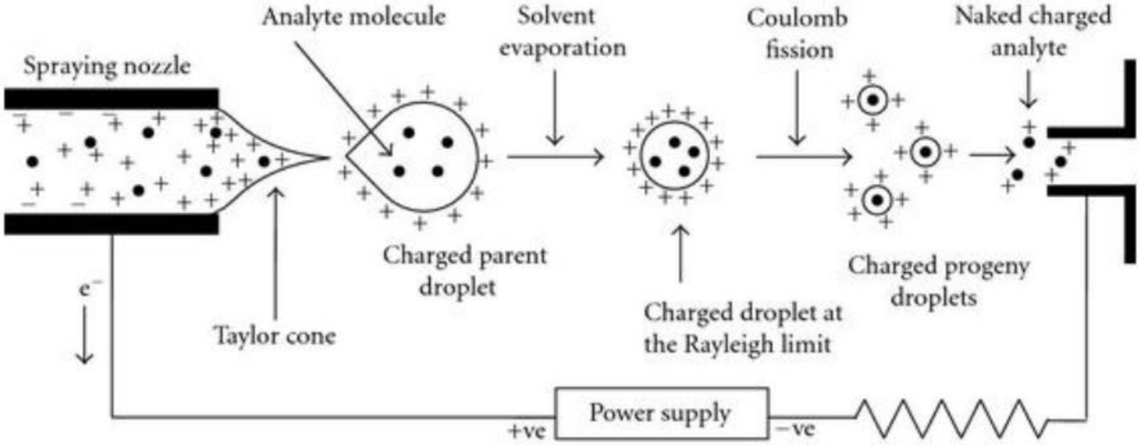


Figure 9: Electrospray Ionization Mass Spectrometry. Image retrieved from the Scientific Figure on Research Gate, based on license CC BY 3.0 (https://creativecommons.org/licenses/by/3.0/)

Within the mass spectrometer, the analyzer (in our case the linear ion trap) works in cycles of MS and MSMS scans. First, the molecular mass of intact peptide precursors is measured (MS) via trapping and consequent ejections of ions, depending on their mass to charge ratio (*m/z*). During the MSMS scans, selected parent ion-peptides are fragmented, and the product ions' m/z values are measured. The fragmentation results in peptide-specific spectrum of several different kinds of ions (*a, b, c, x, y, z*) which are dependent on amino-acid sequence of particular peptides (Fig. 10)[33]. The m/z values of fragment ions are utilized for peptide/protein identification by matching the experimental data to data in properly processed (*in silico*) proteome/genome databases.

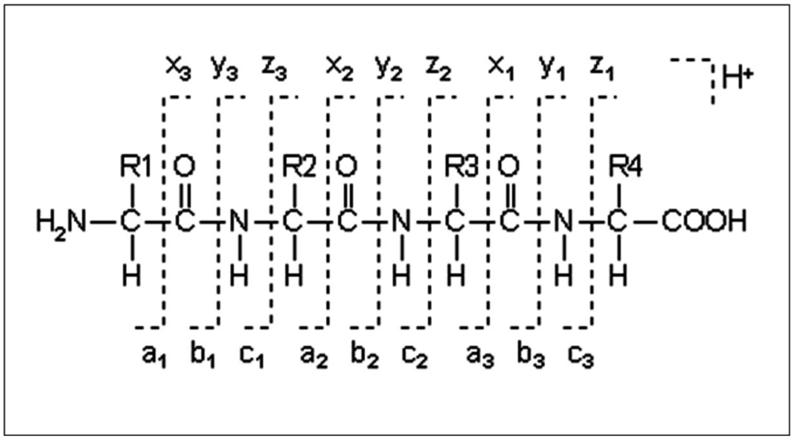


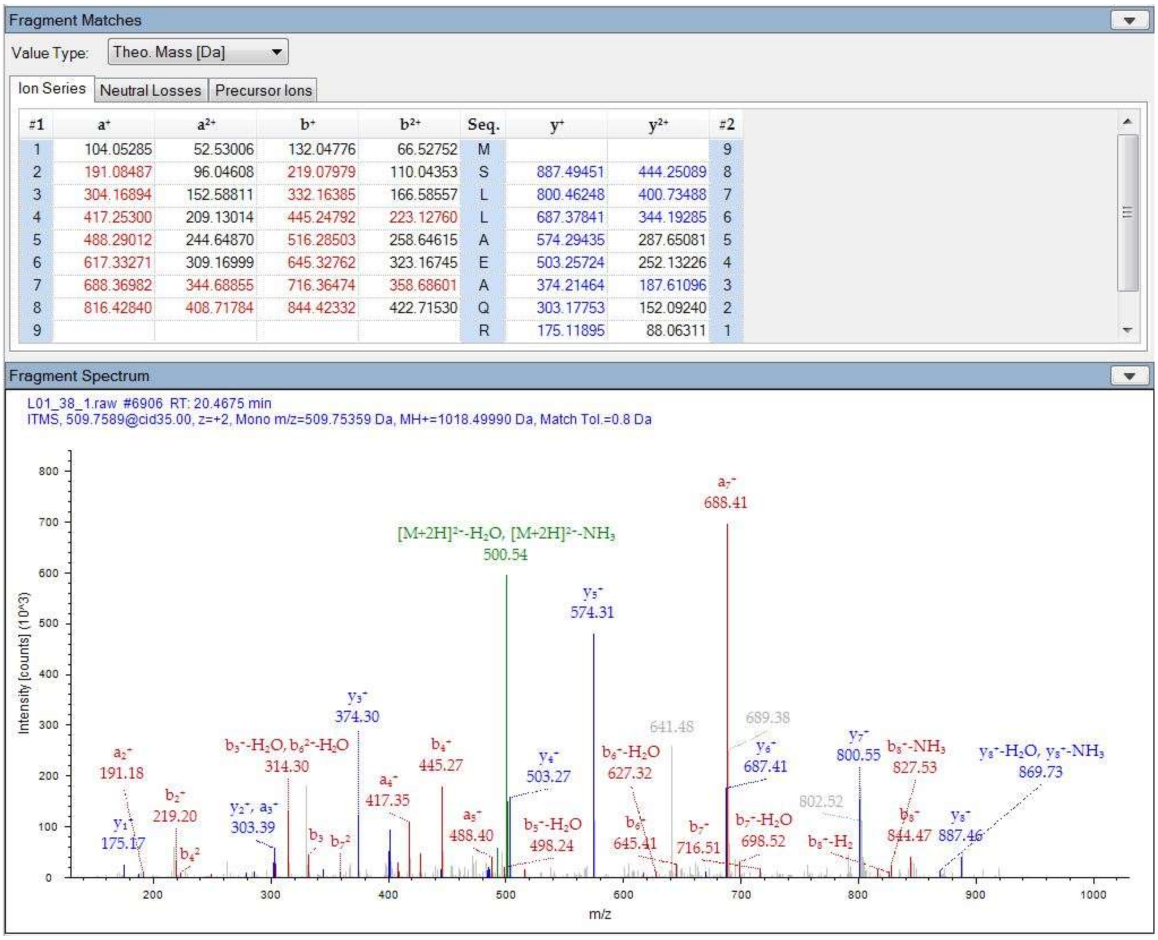
Figure 10: The nomenclature of ions generated by MSMS fragmentation of a generic peptide. (Image courtesy of THERMO)

A total of 3005 proteins from all three replicates of the leaf tissue were identified using nLC-MSMS. Due to space limitation, list of all identified proteins is not given in the text, but the top 10 proteins (in regards of confidence of identification) are shown in Table 2. The complete list of the identified proteins may be found in the Table 3 in the appendix.

ID #	Description	Score	% Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	Ribulose bisphosphate carboxylase large chain	7637.38	53.80	27	2776	487	54.0	6.43
2	26S proteasome regulatory complex	3542.75	67.81	22	1121	438	48.0	5.59
3	F0F1-type ATP synthase	3199.87	79.12	25	1062	498	53.6	5.33
4	TCP-1/cpn60 chaperonin	2375.26	73.04	28	715	586	62.0	5.2
5	Photosystem II protein	2148.73	27.36	9	659	508	56.1	6.77
6	Phosphoglycerate kinase	1610.82	60.25	21	544	488	50.9	8.5
7	Transketolase, C-terminal domain	1383.29	40.27	17	453	745	80.5	6.8
8	Ribulose bisphosphate carboxylase, small chain	1352.88	46.15	9	453	182	20.6	8.51
9	Heat shock 70kDa protein	1332.13	53.09	25	431	648	71.0	5.21
10	Manganese-stabilising protein / photosystem II polypeptide	1307.69	51.81	13	429	332	35.0	5.96

Table 2. Top 10 proteins identified in *G. mustelinum* leaves. [PSMs – Peptide Spectral Matches; AA – amino acids]

Figure 11 shows an example of peptide identification by Proteome Discoverer (Thermo) software.


Fragment Matches

Value Type: Theo. Mass [Da]

#1	a^+	a^{2+}	b^+	b^{2+}	Seq.	y^+	y^{2+}	#2
1	104.05285	52.53006	132.04776	66.52752	M			9
2	191.08487	96.04608	219.07979	110.04353	S	887.49451	444.25089	8
3	304.16894	152.58811	332.16385	166.58557	L	800.46248	400.73488	7
4	417.25300	209.13014	445.24792	223.12760	L	687.37841	344.19285	6
5	488.29012	244.64870	516.28503	258.64615	A	574.29435	287.65081	5
6	617.33271	309.16999	645.32762	323.16745	E	503.25724	252.13226	4
7	688.36982	344.68855	716.36474	358.68601	A	374.21464	187.61096	3
8	816.42840	408.71784	844.42332	422.71530	Q	303.17753	152.09240	2
9					R	175.11895	88.06311	1

Fragment Spectrum

L01_38_1.raw #6906 RT: 20.4675 min
ITMS, 509.7589@cid35.00, z=+2, Mono m/z=509.75359 Da, MH+=1018.49990 Da, Match Tol.=0.8 Da

Figure 11: Identification of MSLLAEAQR peptide in fractionated sample of *G. mustelinum* leaf. Color-highlighted peaks in experimental MSMS spectra, and m/z values of respective ions were matched to theoretical data using Proteome Discover (Thermo) software and *G. mustelinum* protein database.

3.6. Gene Ontology

Gene Ontology[34] is a computational method of functionally classifying sets of genes or proteins in order to better comprehend large groups. The three major classifications in gene ontology are (1) cellular components, (2) molecular functions, and (3) biological processes. Each of these major groups is broken into subcategories, which then may be further subdivided. These relations can be visualized in an ancestor chart, which is similar in appearance to the classic ancestry family tree (Figure 12).

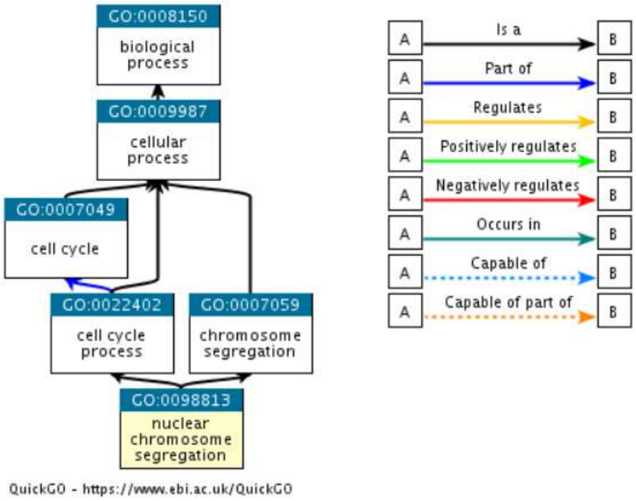


Figure 12: Ancestor chart for GO:0098813 from QuickGO Gene Ontology and GO Annotations developed by the European Molecular Biology Laboratory. https://www.ebi.ac.uk/QuickGO/

The protein species found using nLC-MSMS were functionally characterized using Gene Ontology (GO) annotations. A total of 9607 GO terms were assigned, 609 of which were unique. GO Slim was used to group these terms into broad categories according to relation so that they could be formed into pie charts. The advantage of fractionation is further evidenced by examining the GO terms of proteins that were found in the fractionated samples versus the complex mixture samples. A total of 16 GO terms were assigned to proteins identified in the fractions but not the complex mixtures. These terms include extracellular region, extracellular space, nucleoplasm, vacuole, peroxisome, and cytosol. Additionally, GO terms that were found in both types of samples were more plentiful in the fractionated samples than in the complex mixture samples. For example, the GO term "intracellular" was assigned to 186 proteins from the fractionated samples as opposed to

70 proteins from complex mixture samples, and 118 fractionated proteins versus 39 complex mixture proteins were labelled as “protein-containing complex” proteins.

Distribution of *G. mustelinum* proteins among cellular components was determined and 628 proteins (29.5%) were assigned total of 2388 cellular component GO terms, 83 of which were unique. These were grouped into 25 terms using GO Slim, which were then fused into 17 GO categories in order to make them more manageable (see Figure 13 below). 18.3% of cellular component terms were unknown. The most abundant terms were “intracellular” at 20.0% and “cell” at 13.8%. “Protein-containing complex”, “ribosome”, and “cytoplasm/cytosol” were also prevalent at 12.7%, 8.8%, and 7.6%, respectively. Other terms present were mitochondrion (1.0%), nucleus (4.2%), plastid (3.9%), and endoplasmic reticulum (0.6%). The following terms each composed less than 1% of the total: extracellular region, vacuole, peroxisome, Golgi apparatus, cytoskeleton, plasma membrane, and organelle.

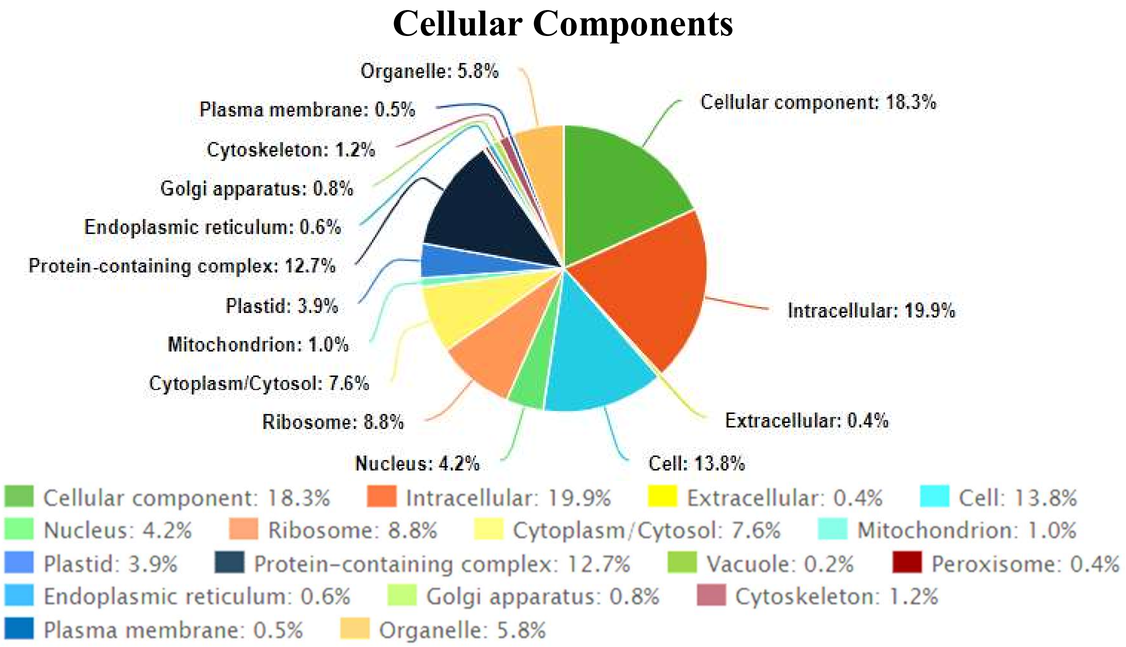


Figure 13: Classification of *G. mustelinum* leaf proteins based on GO terms for cellular components. Pie chart created using meta-chart.com.

3367 GO terms from 304 different molecular functions were assigned to 1808 of the proteins (85.0%). Slim GO resulted in 38 GO categories that were then fused into 16 larger groups (see Figure 14 below). The molecular function was unknown for 35.2% of these proteins. The most abundant terms were “binding activity” at 27.6%, “oxidoreductase activity” at 10.4%, and “structural constituent of ribosome” at 5.7%. Other terms that composed relatively small portions of the population included GTPase activity (2.8%), transferase activity (2.7%), peptidase activity (2.5%), hydrolase activity (2.4%), isomerase activity (2.3%), lyase activity (2.2%), kinase activity (1.8%), ligase activity (1.6%), and transmembrane transporter activity (1.5%). Seen at less than 1% were phosphatase activity, protein transporter activity, and enzyme regulator activity. Several GO terms pertaining to the molecular functions of the citric acid cycle present, including the following: acetyl-CoA carboxylase activity, isocitrate dehydrogenase activity, oxoglutarate dehydrogenase (succinyl-transferring) activity, adenylosuccinate synthase activity, fumarate hydratase activity, and malate dehydrogenase (decarboxylating) (NAD+) activity. GO terms from the pentose phosphate pathway were also seen, including glucose-6-phosphate dehydrogenase activity, phosphogluconate dehydrogenase (decarboxylating) activity, and phosphogluconate dehydrogenase (decarboxylating) activity.

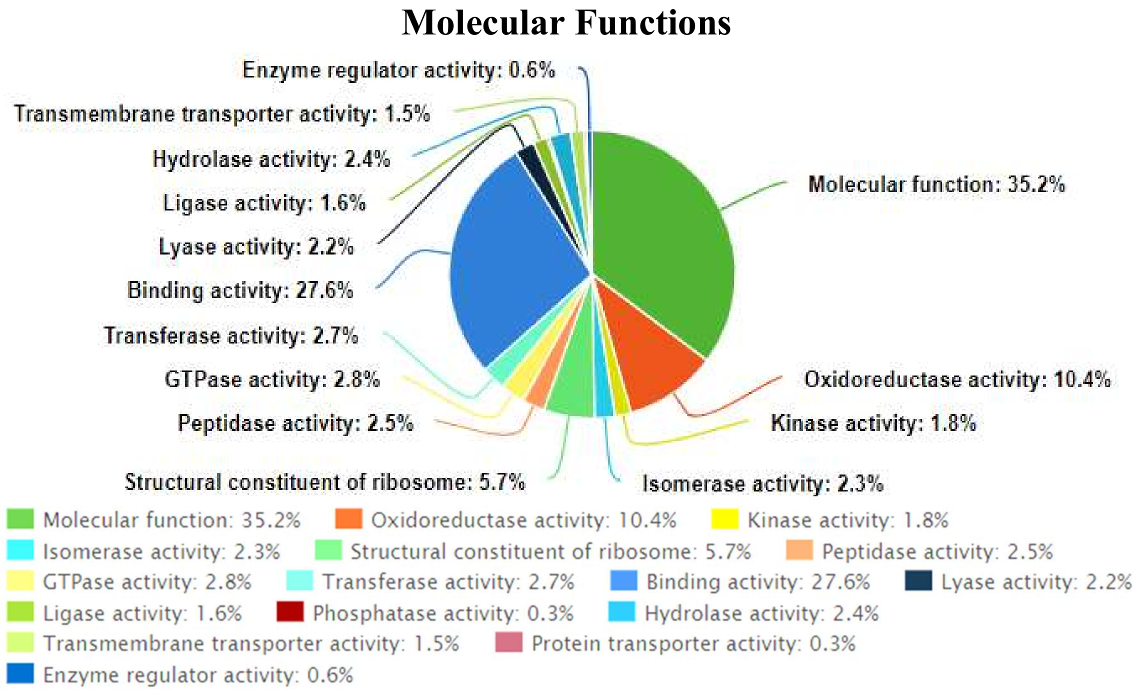


Figure 14: Classification of *G. mustelinum* leaf proteins based on GO terms for molecular functions. Pie chart created using meta-chart.com.

The leaf proteins were also classified by their involvement in various biological processes. 3852 GO terms from 222 biological processes were assigned to 1491 proteins (70.0%). These were categorized into 49 groups using GO Slim, which were further fused into 20 GO categories (see Figure 15 below). 31.0% of the proteins related to an unknown biological process. All of the fundamental metabolic processes were present, which included the metabolism of carbohydrates (3.0%), lipids (1.0%), proteins (10.3), amino acids (0.02%), nucleic acids (2.3%), and other small molecules (7.0%). The most abundant GO categories consisted of "protein metabolic process" at 10.4%, small molecule "metabolic process" at 9.3%, "biosynthetic process" at 9.3%, "cellular nitrogen compound metabolic process" at 7.3%, and "transport" at 7.2%. Other less prevalent biological process groups include catabolic process (4.4%), photosynthesis (3.6%), generation of precursor metabolites and energy (3.3%), response to stress (2.4%), cofactor metabolic process (2.3%), cellular component organization (1.5%), assembly (1.1%), and homeostatic process (1.1%). Present at less than 1% are Signal transduction, reproduction/cell cycle, and other metabolic processes (sulfur compound and nitrogen cycle). A few GO terms pertaining to the citric acid cycle were present, including acetyl-CoA biosynthetic process from pyruvate, isocitrate metabolic process, fumarate metabolic process, and malate metabolic process.

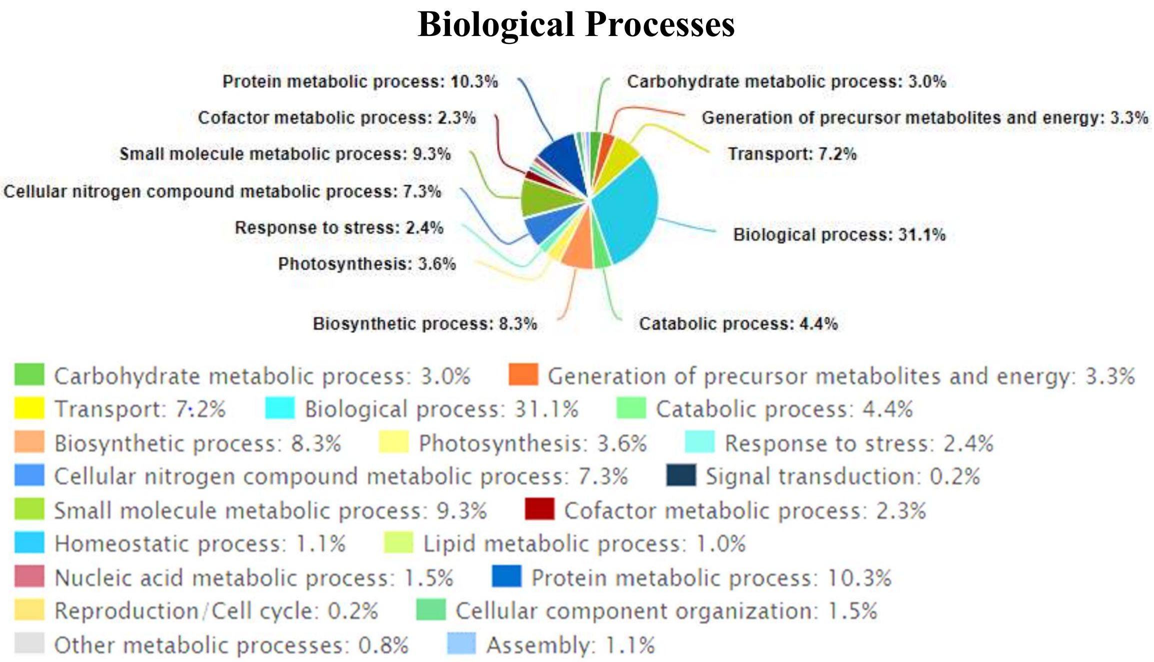


Figure 15: Classification of *G. mustelinum* leaf proteins based on GO terms for biological processes. Pie chart created using meta-chart.com.

CHAPTER IV: SUMMARY AND CONCLUSION

Presented here is the first proteogenomic mapping of the leaf of cotton species *Gossypium mustelinum*, a wild tetraploid cotton from the Caatinga biome of northeastern Brazil. In this study, protein was extracted from *G. mustelinum* leaf tissue to form three biological replicates. Portions of the extracted protein samples were fractionated, and the samples were subsequently analyzed by nano-liquid chromatography-tandem mass spectrometry. Subsequent database search yielded a total of 3005 proteins, of which 1550 were unique to SageELF, 472 were unique to complex mixtures, and 983 were common to both techniques. Gene Ontology (GO) annotations were then used to classify these proteins species. 2388 cellular components GO terms, 3367 molecular functions GO terms, and 3852 biological processes GO terms were assigned to 29.5%, 85.0%, and 70.0% or the proteins, respectively.

Chapter V: Significance

Cotton, having a production value of $7.2 billion in 2017, is one of the most valuable crops in the United States. It has been cultivated for thousands of years, historically used primarily as a textile material. In modern times, cotton contributes to many other products including "paper" currency such as dollar bills, cottonseed oil, book bindings, cattle feed, and many more every-day items. Current research in cotton agriculture is attempting to advance the cultivated cotton species (usually *G. hirsutum* or *G. barbadense*) by improving the quality of the cotton fibers or by increasing the plant's resistance to pathogens and environmental conditions. Desirable traits include increased fiber quantity and length as well as resistances to bacteria, fungi, insects, drought, and frost.

Hybridization is a common method of modifying cotton to exhibit the above traits. In this technique, two or more species of cotton are crossed in order to produce a superior hybrid species. For example, if Cotton A has good fiber quality but is susceptible to bacterial blight and Cotton B has poor fiber quality but is resistant to blight, the two species could be crossed to form Cotton AB that has good fibers and blight resistance. In this way, the wild Brazilian tetraploid *Gossypium mustelinum* may produce a hybrid with exceptionally long fibers if crossed with *G. hirsutum*, one of the most commonly cultivated species.

In the past, hybridization was performed by repeatedly breeding different varieties of cotton until a plant exhibited the desired traits. Now, with advances in molecular biology, species can be genetically analyzed to evaluate their potential for producing a superior hybrid. However, not everything that is written in the DNA of the species will be produced as a functional protein. There are some DNA sequences called “pseudogenes” that appear to be functional genes but are incomplete genes that have lost their ability to be translated into protein. Because of this, it is necessary to determine what proteins are present in the species in order to properly annotate the genome. This is referred to as “proteogenomic mapping”.

In this study, nano-liquid chromatography tandem mass spectrometry (nLC-MSMS) combined with the SEQUEST algorithm of the Proteome Discoverer software was used to identify 3005 proteins from the leaf of cotton species *Gossypium mustelinum*. Sample fractionation prior nLC-MSMS was shown to increase the total number of proteins identified. In the future, additional protein identification from additional *G. mustelinum* tissues as well as technological advances will significantly increase this count. Once the proteogenomic “map” is completed, it can be used as a reference for hybridizing cotton species and for comparing healthy and diseased states of *G. mustelinum*.

CHAPTER VI: RECOMMENDATIONS FOR FUTURE WORK

In the future, this work should be replicated for other *Gossypium mustelinum* tissues such as stems and roots, and possibly even blooms and fibers. In addition, more protein species may be found from cutting spots from 2D-PAGE gels run from the samples, performing in-gel digestion on the protein spots, and running the resulting peptide samples on the LCMS system. Once assembled, the cumulation of this work can be used as a reference proteogenomic map for hybridization between *G. mustelinum* and another cotton species.

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APPENDIX

Table 3: Complete list of proteins identified in *Gossypium mustelinum* leaf using SageELF fractions and complex mixtures. Proteins were identified by nLC-MSMS mass spectrometry and database search.

Accession	Protein name	MW [kDa]	Calc. pI	Peptide count	Score
Gomus.A07G181300.1	Ribulose-bisphosphate carboxylase large chain	54.00	6.43	42	3048.71
Gomus.A01G101500.1	Phosphoglycerate kinase	51.20	8.68	21	1608.21
Gomus.1Z025400.1	Ribulose-bisphosphate carboxylase	47.60	6.96	7	1594.45
Gomus.D05G113500.1	Mitochondrial chaperonin, Cpn60/Hsp60p	61.50	5.29	20	1255.57
Gomus.A10G246600.1	26S proteasome regulatory complex, ATPase RPT4	48.00	5.59	34	1242.95
Gomus.A01G242600.1	Heat shock 70kDa protein 1/8	71.20	5.19	21	1237.28
Gomus.D05G103300.1	Heat shock 70kDa protein 1/8	71.10	5.25	24	1208.86
Gomus.D06G202000.1	26S proteasome regulatory complex, ATPase RPT4	51.50	5.35	30	1204.47
Gomus.A06G181000.1	26S proteasome regulatory complex, ATPase RPT4	51.70	5.53	27	1162.59
Gomus.D10G272000.1	26S proteasome regulatory complex, ATPase RPT4	48.00	5.95	32	1064.30
Gomus.A09G139800.1	F-type H+-transporting ATPase subunit beta	62.60	5.47	11	1051.85
Gomus.D11G090900.1	Transketolase	80.40	6.92	12	935.56
Gomus.A08G032800.1	Molecular chaperone HtpG	80.00	5.10	25	875.90
Gomus.D13G155700.1	Molecular chaperone HtpG	80.10	5.10	25	873.96
Gomus.A05G411700.1	Photosystem II oxygen-evolving enhancer protein 2	27.90	7.85	13	863.56
Gomus.A12G247800.1	F-type H+-transporting ATPase subunit beta	53.60	5.33	29	836.87
Gomus.D08G033800.1	Molecular chaperone HtpG	80.00	5.11	26	819.07
Gomus.A01G209300.1	Glutamate synthase (ferredoxin)	177.40	6.65	37	819.03
Gomus.D13G276800.1	Mitochondrial chaperonin, Cpn60/Hsp60p	62.00	5.20	33	780.97
Gomus.A13G266500.1	Mitochondrial chaperonin, Cpn60/Hsp60p	61.90	5.29	31	748.74
Gomus.D05G141200.1	Chaperonin GroEL	64.90	6.13	8	699.64
Gomus.A01G226700.1	Enolase	47.60	5.82	12	686.37
Gomus.A01G097800.1	Molecular chaperone HtpG	80.00	5.10	20	672.63
Gomus.D10G229700.1	Chaperonin GroEL	64.40	5.88	33	662.74
Gomus.D04G040700.2	Photosystem II oxygen-evolving enhancer protein 2	28.00	8.21	11	626.18
Gomus.A10G211100.2	Chaperonin GroEL	64.40	5.88	30	623.90
Gomus.A05G139400.1	Mitochondrial chaperonin, Cpn60/Hsp60p	50.70	7.46	7	604.99
Gomus.D07G271300.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	43.10	8.44	12	551.43
Gomus.A05G190900.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	48.40	7.20	16	532.02
Gomus.A13G121000.1	Ribulose-bisphosphate carboxylase	42.30	7.28	13	523.32
Gomus.A05G195300.1	Plastocyanin	17.00	5.25	6	511.39
Gomus.D04G144300.1	26S proteasome regulatory complex, ATPase RPT4	51.90	7.64	12	502.62
Gomus.D11G211500.1	Photosystem II oxygen-evolving enhancer protein 1	35.10	5.67	18	500.07
Gomus.A07G247800.1	Predicted carbonic anhydrase involved in protection against oxidative damage	35.20	8.53	12	481.87
Gomus.D12G289300.1	Molecular chaperone HtpG	80.80	5.12	18	465.08
Gomus.A11G203100.1	Photosystem II oxygen-evolving enhancer protein 1	35.00	5.96	17	462.49
Gomus.D01G106400.1	Phosphoglycerate kinase	42.30	6.23	15	456.93
Gomus.A11G333400.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.60	6.40	16	452.15
Gomus.D13G195500.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.80	6.51	20	444.13
Gomus.D07G203300.1	Ribulose-bisphosphate carboxylase small chain	20.60	8.51	13	439.61
Gomus.A07G198000.1	Ribulose-bisphosphate carboxylase small chain	20.50	8.43	13	439.27
Gomus.A04G110700.1	26S proteasome regulatory complex, ATPase RPT4	52.00	6.92	11	437.92
Gomus.A01G101500.2	Phosphoglycerate kinase	50.90	8.50	25	435.54
Gomus.D01G106500.1	Phosphoglycerate kinase	50.90	8.50	25	433.96
Gomus.D01G037800.1	(S)-2-hydroxy-acid oxidase	40.60	9.10	12	429.69
Gomus.D12G066400.1	Fructose-bisphosphate aldolase, class I	42.80	8.44	8	429.27
Gomus.A11G255200.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.60	7.15	14	417.95
Gomus.D11G182800.1	Ribulose-bisphosphate carboxylase small chain	20.10	8.53	12	417.80
Gomus.A11G176500.1	Ribulose-bisphosphate carboxylase small chain	20.10	8.31	11	390.82
Gomus.D07G168300.1	Transketolase	80.50	6.80	18	384.51
Gomus.D05G046200.1	Glycine dehydrogenase	114.00	7.09	22	384.27
Gomus.D11G235100.1	Glycine hydroxymethyltransferase	57.20	8.47	15	383.05
Gomus.D13G241700.1	Photosystem II P680 reaction center D1 protein	34.60	5.17	5	376.52
Gomus.A07G160900.1	Transketolase	80.40	6.76	17	360.15
Gomus.D05G159400.2	(S)-2-hydroxy-acid oxidase	40.40	9.23	10	359.53
Gomus.A13G115900.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.70	7.31	12	359.03
Gomus.D07G263600.1	Glyceraldehyde 3-phosphate dehydrogenase	36.40	7.52	6	353.93
Gomus.D01G193800.1	Peptidylprolyl isomerase	18.20	8.35	8	352.91
Gomus.D05G370400.1	Elongation factor EF-2	94.00	6.18	19	349.92
Gomus.D07G133100.1	Elongation factor EF-1 alpha subunit	49.30	9.06	8	335.67
Gomus.A10G124800.1	Malate dehydrogenase	35.50	6.79	10	335.50
Gomus.A01G204600.1	Photosystem II 22kDa protein	29.20	8.78	6	334.01
Gomus.D09G099200.1	Heat shock 70kDa protein 4	94.50	5.44	15	333.44
Gomus.A05G111900.1	Mitochondrial chaperonin, Cpn60/Hsp60p	61.80	5.29	14	329.08
Gomus.D06G003100.1	Heat shock protein 90kDa beta	91.90	5.01	17	326.53
Gomus.A12G246300.1	Photosystem II CP47 chlorophyll apoprotein	56.10	6.77	14	320.32
Gomus.A08G120700.1	Heat shock 70kDa protein 5	73.20	5.31	9	319.93
Gomus.A11G194800.1	F-type H+-transporting ATPase subunit alpha	46.10	5.06	10	311.69
Gomus.D07G017200.1	Chaperonin GroES	27.20	8.44	9	307.96
Gomus.D07G241400.1	Uncharacterized protein	44.10	4.82	15	304.58
Gomus.A10G211100.1	Chaperonin GroEL	64.43	5.88	25	302.48
Gomus.A05G036000.1	Cupin	26.00	7.33	2	294.11
Gomus.A05G096700.1	Tubulin beta	50.10	4.83	12	294.06
Gomus.A11G241400.2	Actin, other eukaryote	41.70	5.49	9	291.62
Gomus.A05G102100.1	Heat shock 70kDa protein 1/8	71.10	5.25	21	290.79
Gomus.D06G104000.1	Glycine dehydrogenase	113.80	6.98	19	285.55
Gomus.A10G042300.1	Light-harvesting complex II chlorophyll a/b binding protein 1	28.20	5.26	7	276.87
Gomus.A09G030200.1	Carbonic anhydrase	36.70	7.71	12	271.73
Gomus.A03G072900.1	Elongation factor EF-Tu	52.70	6.68	13	271.08
Gomus.A03G028900.1	Tubulin beta	50.10	4.86	10	270.17
Gomus.A11G089600.1	Transketolase	80.50	7.01	11	270.12
Gomus.D13G032800.1	Fructose-bisphosphate aldolase, class I	42.90	8.25	17	268.17
Gomus.D08G033700.1	Molecular chaperone HtpG	79.97	5.10	32	266.82
Gomus.A08G032900.1	Molecular chaperone HtpG	79.96	5.07	33	266.72
Gomus.A13G031100.1	Fructose-bisphosphate aldolase, class I	42.90	8.25	16	265.22
Gomus.D01G102600.1	Molecular chaperone HtpG	79.97	5.10	30	260.45
Gomus.A10G018700.1	Photosystem II oxygen-evolving enhancer protein 3	24.70	9.52	10	260.43
Gomus.D13G032900.1	Fructose-bisphosphate aldolase, class I	42.90	7.96	17	257.59
Gomus.D09G031700.1	Carbonic anhydrase	36.80	7.71	11	257.45
Gomus.D09G224300.1	Chaperonin GroEL	61.40	6.04	13	254.22
Gomus.D10G019300.1	Photosystem II oxygen-evolving enhancer protein 3	24.80	9.54	9	253.77
Gomus.A06G182400.1	Heat shock 70kDa protein 1/8	71.00	5.21	19	248.39
Gomus.D01G198600.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	42.20	7.01	10	245.91

Gomus.A05G159700.1	Light-harvesting complex II chlorophyll a/b binding protein 1	28.10	5.64	7	244.28
Gomus.D06G203500.1	Heat shock 70kDa protein 1/8	71.00	5.21	19	242.77
Gomus.D08G132100.2	Actin, other eukaryote	41.50	5.49	8	241.16
Gomus.D12G034900.1	Peptidylprolyl isomerase	18.10	8.35	6	240.63
Gomus.D04G190900.1	Triosephosphate isomerase (TIM)	33.10	7.33	13	238.92
Gomus.D11G151700.1	Chaperonin GroEL	61.00	5.74	14	237.60
Gomus.D04G040700.1	Photosystem II oxygen-evolving enhancer protein 2	27.96	8.21	14	234.15
Gomus.A02G008600.1	Heat shock 70kDa protein 1/8	75.40	5.39	14	233.76
Gomus.A11G112300.1	H(+)-transporting two-sector ATPase.	25.80	5.17	7	232.05
Gomus.A10G160800.1	Heat shock 70kDa protein 1/8	75.70	5.39	15	230.99
Gomus.D11G182700.1	Ribulose-bisphosphate carboxylase small chain	20.12	8.53	19	228.50
Gomus.A12G064700.1	Fructose-bisphosphate aldolase, class I	42.80	8.03	10	227.78
Gomus.A13G268700.1	Heat shock 70kDa protein 1/8	71.40	5.22	19	227.15
Gomus.A04G150300.1	Tubulin alpha	49.50	5.06	9	226.47
Gomus.A12G018300.1	Molecular chaperone DnaK	72.30	5.77	11	220.80
Gomus.D05G056500.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP)	53.20	7.78	10	219.03
Gomus.D01G226800.1	Glutamate synthase (ferredoxin)	177.42	6.60	21	218.20
Gomus.A07G232800.1	Uncharacterized protein	42.70	4.84	12	214.94
Gomus.D01G012700.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.30	4.83	10	211.77
Gomus.D12G065000.1	Ferredoxin--NADP+ reductase	40.60	8.21	5	210.98
Gomus.D11G366600.1	Tubulin beta	50.30	4.86	9	200.26
Gomus.D10G137200.1	Heat shock 70kDa protein 1/8	75.69	5.44	32	199.31
Gomus.A04G128300.1	F-type H+-transporting ATPase subunit beta	59.80	6.29	15	197.68
Gomus.D04G162700.1	F-type H+-transporting ATPase subunit beta	59.80	6.29	15	196.12
Gomus.D07G110800.1	Histone H2B	16.60	10.02	3	195.07
Gomus.A10G239200.1	Heat shock 70kDa protein 1/8	71.12	5.38	23	193.57
Gomus.A03G055100.1	Heat shock 70kDa protein 1/8	70.79	5.27	28	192.37
Gomus.D05G188800.1	PAP_fibrillin	35.40	5.22	13	187.04
Gomus.D02G230100.1	Light-harvesting complex II chlorophyll a/b binding protein 6	27.30	8.07	6	186.68
Gomus.D11G029900.1	Glycine cleavage system H protein	17.40	5.17	6	186.44
Gomus.D06G147700.1	Photosystem II oxygen-evolving enhancer protein 3	24.90	9.61	7	181.97
Gomus.A02G031600.1	Glutamine synthetase	47.40	7.44	15	180.39
Gomus.A07G063300.1	Nucleolin	35.50	4.55	9	180.07
Gomus.D03G191600.1	Glycine cleavage system H protein	17.60	5.15	6	179.86
Gomus.A13G076000.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.40	4.89	9	179.78
Gomus.D02G041200.1	Glutamine synthetase	47.40	7.44	15	179.48
Gomus.D01G211600.1	Malate dehydrogenase	37.20	6.90	9	176.89
Gomus.A13G250900.1	Alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	44.10	8.05	9	175.56
Gomus.D05G197200.1	Plastocyanin	16.99	5.25	19	174.28
Gomus.A04G097300.1	Transitional endoplasmic reticulum ATPase	89.40	5.29	11	173.55
Gomus.A05G336000.1	Ribulose-bisphosphate carboxylase	10.40	4.81	6	173.07
Gomus.D11G394400.1	Heat shock 70kDa protein 1/8	70.91	5.25	24	173.05
Gomus.A01G109800.1	Catalase	56.80	7.17	7	172.65
Gomus.A07G143400.1	Ubiquitin C	17.80	9.79	4	172.46
Gomus.A01G193800.1	Malate dehydrogenase	37.20	6.90	9	172.30
Gomus.D11G046700.1	Betaine-aldehyde dehydrogenase	54.70	5.50	12	171.74
Gomus.A01G226800.1	Alkyl hydroperoxide reductase/peroxiredoxin	24.10	8.54	4	168.33
Gomus.D01G244700.1	Enolase	47.60	5.97	11	168.14
Gomus.A11G112100.1	H(+)-transporting two-sector ATPase.	30.00	5.00	6	167.49
Gomus.A12G248900.1	Photosystem II CP43 chlorophyll apoprotein	51.80	7.18	6	167.13
Gomus.D10G156100.1	Adenosylhomocysteinase	53.10	6.01	8	166.95
Gomus.A05G389500.1	Carbonic anhydrase	27.60	6.68	6	166.08
Gomus.D04G078300.1	Clathrin heavy chain	192.60	5.40	21	165.76
Gomus.A13G151100.1	Molecular chaperone HtpG	80.09	5.11	12	164.61
Gomus.D07G257500.2	Predicted carbonic anhydrase involved in protection against oxidative damage	35.10	7.96	10	164.26
Gomus.A04G046700.1	Malate dehydrogenase	35.40	8.78	9	163.55
Gomus.D05G194900.1	AAA+-type ATPase containing the peptidase M41 domain	73.10	8.88	8	163.37
Gomus.A07G031700.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP)	53.80	7.59	8	162.48
Gomus.A03G008000.1	Glycine cleavage system H protein	17.60	5.03	6	161.26
Gomus.A06G040100.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	28.60	4.83	9	160.49
Gomus.A07G078900.1	Translation initiation factor eIF-5A	17.30	5.99	4	158.62
Gomus.D06G184300.1	Aminomethyltransferase	44.20	8.63	7	157.53
Gomus.A03G093300.1	Tubulin beta	50.20	4.84	12	156.94
Gomus.A10G076200.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	43.30	8.27	12	154.82
Gomus.D08G013900.1	Large subunit ribosomal protein L7/L12	19.50	5.96	3	154.75
Gomus.D10G131500.1	Protease inhibitor/seed storage/LTP family	11.70	8.48	6	154.47
Gomus.D11G396700.1	Fructose-1,6-bisphosphatase I	44.60	5.40	9	153.68
Gomus.A03G154600.1	Zinc-binding oxidoreductase	40.90	8.92	8	151.61
Gomus.D07G258300.1	Large subunit ribosomal protein L7/L12	19.90	5.66	3	150.16
Gomus.D13G018300.1	Clathrin heavy chain	192.50	5.47	19	149.69
Gomus.A11G369700.1	Fructose-1,6-bisphosphatase I	44.60	5.39	9	149.59
Gomus.A08G014000.1	Large subunit ribosomal protein L7/L12	19.40	5.96	3	149.27
Gomus.D02G192200.1	Zinc-binding oxidoreductase	40.90	8.79	7	148.49
Gomus.A12G047300.1	Elongation factor EF-1 gamma subunit	47.70	7.66	7	148.31
Gomus.A01G178100.1	Peptidylprolyl isomerase	18.22	8.35	19	147.57
Gomus.A09G229000.1	Heat shock 70kDa protein 1/8	75.70	5.39	10	146.59
Gomus.A11G155900.1	3-demethylubiquinone-9 3-methyltransferase	16.70	4.70	7	145.80
Gomus.A05G100900.1	Triosephosphate isomerase (TIM)	27.20	5.92	9	145.68
Gomus.D13G259400.1	Alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	44.20	8.05	9	145.62
Gomus.D05G186300.1	Aminomethyltransferase	44.30	8.88	7	145.40
Gomus.A09G214500.1	Glutamine synthetase	47.60	7.47	9	145.25
Gomus.D07G200000.1	Catalase	49.10	7.34	6	144.81
Gomus.D07G222400.1	Light-harvesting complex II chlorophyll a/b binding protein 2	32.60	5.47	7	143.48
Gomus.A06G069900.1	Elongation factor EF-Ts	117.79	4.79	3	143.12
Gomus.A02G196900.1	Catalase	60.10	8.06	7	142.94
Gomus.A05G071000.1	Lipoxygenase	103.70	6.24	12	141.69
Gomus.D08G008700.1	Large subunit ribosomal protein LP2	11.40	4.37	5	140.98
Gomus.D07G080500.1	Translation initiation factor eIF-5A	17.30	5.99	4	140.94
Gomus.D02G191200.1	Thioredoxin, nucleoredoxin and related proteins	64.10	4.98	11	140.51
Gomus.D05G097400.1	Tubulin beta	50.20	4.81	12	140.15
Gomus.A11G085300.1	Tubulin alpha	49.70	5.10	6	138.46
Gomus.A09G168500.1	Heat shock 70kDa protein 1/8	70.85	5.21	7	136.79
Gomus.A05G264700.1	Light-harvesting complex II chlorophyll a/b binding protein 5	31.00	5.72	9	136.70
Gomus.A06G161500.1	F-type H+-transporting ATPase subunit gamma	41.29	5.90	19	135.40
Gomus.A02G106900.1	Heat shock 70kDa protein 5	73.30	5.24	11	135.31
Gomus.A06G038000.1	L-ascorbate peroxidase	39.10	7.18	9	135.16
Gomus.D03G106900.1	Malate dehydrogenase	43.30	8.19	7	134.92
Gomus.D13G184400.1	Elongation factor EF-2	94.01	6.25	14	134.71
Gomus.A11G135300.1	Ribosome recycling factor	30.90	9.31	6	134.26
Gomus.A01G101400.1	Phosphoglycerate kinase	42.20	6.35	11	133.46
Gomus.A07G188500.1	Light-harvesting complex II chlorophyll a/b binding protein 2	28.60	5.66	7	133.04
Gomus.A11G226500.1	Glycine hydroxymethyltransferase	57.20	8.47	10	132.97
Gomus.A04G156000.1	Peptidylprolyl isomerase	18.30	8.09	6	132.77
Gomus.A07G063100.1	Nucleolin	34.50	4.70	9	131.50
Gomus.A04G066900.1	Elongation factor EF-2	94.00	6.18	8	131.23
Gomus.A07G017100.1	Chaperonin GroES	27.10	8.44	5	131.06
Gomus.D01G037500.1	F-type H+-transporting ATPase subunit delta	26.00	7.55	6	130.41
Gomus.D11G269700.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.60	7.15	11	130.02
Gomus.A02G064300.1	Dihydrolipoamide dehydrogenase	53.90	7.61	9	129.51
Gomus.A05G080800.1	Calmodulin	16.80	4.27	5	129.20
Gomus.A11G159500.1	Light-harvesting complex I chlorophyll a/b binding protein 3	29.50	8.88	6	128.75
Gomus.D11G358900.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.77	6.37	12	126.66

Gomus.D04G165100.1	Glycyl-tRNA synthetase	82.10	7.11	10	126.63
Gomus.A09G228800.1	Cysteine synthase A	42.40	7.94	9	125.96
Gomus.D03G143200.1	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	68.18	5.53	4	125.29
Gomus.D04G188700.1	Ribosomal RNA large subunit methyltransferase F	121.60	5.59	12	124.60
Gomus.D10G057900.1	20S proteasome subunit alpha 5	26.00	4.75	7	124.01
Gomus.D03G181800.1	Heat shock 70kDa protein 1/8	70.84	5.34	19	123.18
Gomus.D08G095200.1	Peroxidase	37.40	5.00	5	122.77
Gomus.A10G261800.1	Light-harvesting complex II chlorophyll a/b binding protein 4	29.90	6.00	4	121.63
Gomus.D02G188900.1	Alanine aminotransferase	53.50	6.43	8	121.54
Gomus.D05G119300.1	Tubulin beta	50.10	4.84	11	121.21
Gomus.A12G135300.1	Uncharacterized protein	13.40	4.96	3	120.68
Gomus.D07G137500.1	Photosystem II P680 reaction center D2 protein	39.50	5.55	4	119.72
Gomus.D02G009000.1	Heat shock 70kDa protein 1/8	75.49	5.40	6	118.46
Gomus.D03G124600.1	Elongation factor EF-Tu	52.55	6.81	7	118.46
Gomus.D05G073300.1	Lipoxygenase	103.10	6.28	13	117.81
Gomus.D11G319300.1	dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	42.50	8.31	7	117.65
Gomus.D11G295000.1	Ribose 5-phosphate isomerase A	29.70	6.93	7	116.51
Gomus.A10G080600.1	Uncharacterized protein	35.60	4.73	12	115.79
Gomus.D06G040100.4	L-ascorbate peroxidase	39.10	6.34	9	114.75
Gomus.D11G159600.1	3-demethylubiquinone-9 3-methyltransferase	16.70	4.79	6	114.48
Gomus.A05G420400.1	Actin, other eukaryote	41.70	5.40	7	113.11
Gomus.A11G244600.1	Photosystem I subunit PsaN	18.30	9.07	5	112.56
Gomus.A03G018800.1	Molecular chaperones HSP70/HSC70, HSP70 superfamily	66.54	5.53	5	111.29
Gomus.A12G278000.1	Molecular chaperone HtpG	80.77	5.12	3	111.09
Gomus.A05G359100.1	Clathrin heavy chain	189.27	5.40	3	110.50
Gomus.A06G131500.1	Photosystem II oxygen-evolving enhancer protein 3	24.70	9.61	6	110.39
Gomus.A08G012000.1	Calmodulin	16.80	4.28	5	110.11
Gomus.A09G148300.1	Large subunit ribosomal protein LP2	11.40	4.45	6	109.93
Gomus.A12G246100.1	Cytochrome b6	23.30	9.54	2	109.58
Gomus.A11G021100.1	Heat shock 70kDa protein 5	73.50	5.27	10	109.40
Gomus.D01G243200.1	Monodehydroascorbate reductase (NADH)	47.20	6.61	8	108.75
Gomus.D11G123200.1	Uncharacterized protein	14.10	5.67	3	108.60
Gomus.A11G301300.1	dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	42.50	8.63	7	108.48
Gomus.D07G064500.1	Nucleolin	34.30	4.67	8	108.08
Gomus.A07G141600.1	Uncharacterized protein	14.10	4.77	2	106.73
Gomus.A09G087100.2	Translation initiation factor eIF-4A	46.90	5.48	6	106.28
Gomus.D01G176500.1	Phosphoglucomutase	63.20	5.92	7	105.66
Gomus.D10G129500.1	Photosystem II oxygen-evolving enhancer protein 2	31.70	8.66	10	103.98
Gomus.D09G237900.1	Heat shock 70kDa protein 1/8	74.55	5.35	4	103.71
Gomus.A01G107400.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	48.40	7.40	10	103.30
Gomus.D06G115800.1	Leucyl aminopeptidase	60.70	7.06	6	103.06
Gomus.D07G055900.1	ATP-dependent Clp protease ATP-binding subunit ClpC	102.20	6.60	10	102.86
Gomus.A11G280200.1	Ribose-5-phosphate isomerase B	33.50	5.33	10	102.71
Gomus.D01G063400.1	Carbamoyl-phosphate synthase large subunit	129.70	5.60	9	102.15
Gomus.D09G159500.1	Large subunit ribosomal protein LP2	11.40	4.45	6	101.73
Gomus.A01G039000.1	(S)-2-hydroxy-acid oxidase	40.60	8.95	8	101.19
Gomus.A02G165900.1	Malate dehydrogenase	38.10	7.65	4	100.49
Gomus.D11G296300.1	Ribose-5-phosphate isomerase B	33.50	5.33	10	100.09
Gomus.A10G166300.1	Protease inhibitor/seed storage/LTP family	11.80	8.65	4	98.56
Gomus.A11G021400.1	Elongation factor EF-G	86.30	5.74	9	98.40
Gomus.A09G030200.2	Carbonic anhydrase	35.22	7.36	5	97.94
Gomus.D05G043400.1	HSP20 family protein	17.50	6.24	5	97.79
Gomus.D07G236900.1	Photosystem I subunit IV	15.80	9.41	3	97.68
Gomus.D08G236800.1	L-ascorbate peroxidase	27.50	5.94	7	97.61
Gomus.A01G038500.1	F-type H+-transporting ATPase subunit delta	26.00	6.81	5	97.43
Gomus.D08G081000.1	UDP-glucose 4-epimerase/UDP-sulfoquinovose synthase	43.40	7.75	6	97.15
Gomus.A05G235300.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	28.50	4.79	5	96.66
Gomus.D02G156600.1	Heat shock protein 90kDa beta	90.07	4.96	2	96.64
Gomus.D02G266000.1	L-ascorbate peroxidase	31.90	7.17	8	96.49
Gomus.D04G089300.1	Glyceraldehyde 3-phosphate dehydrogenase	36.50	7.93	11	95.19
Gomus.D12G235500.1	Phosphoribulokinase	45.40	6.54	7	95.13
Gomus.D10G292300.1	Light-harvesting complex II chlorophyll a/b binding protein 4	29.90	6.00	4	95.01
Gomus.A03G211900.1	Ferredoxin	16.10	5.11	5	94.92
Gomus.A13G202400.1	F-type H+-transporting ATPase subunit alpha	55.60	6.33	7	94.02
Gomus.D01G244800.1	Alkyl hydroperoxide reductase/peroxiredoxin	24.09	8.98	5	93.80
Gomus.A06G003600.1	Tubulin beta	50.70	4.86	9	93.45
Gomus.D09G031700.2	Carbonic anhydrase	35.28	7.36	4	93.38
Gomus.D01G037900.1	(S)-2-hydroxy-acid oxidase	40.60	8.76	7	93.31
Gomus.D09G217500.1	Stress-induced-phosphoprotein 1	65.20	6.64	7	92.56
Gomus.A05G179500.1	Photosystem II oxygen-evolving enhancer protein 3	24.80	9.54	4	92.20
Gomus.D07G198600.2	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.50	4.87	3	91.71
Gomus.A07G261000.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	43.10	8.44	9	91.40
Gomus.D05G076900.2	Alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	44.20	7.74	6	91.28
Gomus.D04G110300.1	Histone H2A	16.60	11.34	7	91.03
Gomus.D04G111600.1	Peroxiredoxin (alkyl hydroperoxide reductase subunit C)	29.00	6.60	4	90.73
Gomus.A09G221800.1	Chaperonin GroES	26.70	8.18	6	90.59
Gomus.A03G062500.1	Tubulin beta	49.97	4.86	5	90.45
Gomus.A01G189800.1	Actin, other eukaryote	41.50	5.49	7	90.43
Gomus.A13G150900.1	Fructose-bisphosphate aldolase, class I	38.30	7.25	8	90.39
Gomus.A08G216800.2	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	82.10	6.29	9	90.36
Gomus.D03G125500.1	ATP-dependent Clp protease ATP-binding subunit ClpC	102.30	6.51	10	89.69
Gomus.D09G105400.1	Cu/Zn superoxide dismutase	22.10	6.51	5	89.51
Gomus.A11G148300.1	Chaperonin GroEL	60.90	6.23	2	89.47
Gomus.A05G042700.1	HSP20 family protein	17.60	6.24	5	89.26
Gomus.A04G087900.1	Peroxiredoxin (alkyl hydroperoxide reductase subunit C)	29.00	6.60	3	88.85
Gomus.A07G034000.1	F-type H+-transporting ATPase subunit b	24.50	8.68	8	88.44
Gomus.D11G020500.1	Heat shock 70kDa protein 5	73.46	5.25	5	88.37
Gomus.A08G215400.1	L-ascorbate peroxidase	27.40	5.97	7	88.17
Gomus.A01G205300.1	Alcohol dehydrogenase, class III	41.60	7.02	7	88.05
Gomus.A05G054900.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP)	53.10	7.58	7	87.45
Gomus.D01G112700.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	48.42	7.40	4	87.36
Gomus.D06G254400.1	Photosystem II protein	53.91	7.43	6	87.32
Gomus.A05G292200.1	Phosphatidylinositol transfer protein SEC14 and related proteins	67.20	4.70	7	87.08
Gomus.D03G099900.1	Heat shock 70kDa protein 5	73.34	5.24	5	86.70
Gomus.D08G292700.1	Alkyl hydroperoxide reductase/peroxiredoxin	17.20	5.91	5	86.56
Gomus.A11G020800.1	Heat shock 70kDa protein 5	73.40	5.25	10	86.52
Gomus.D01G023300.1	Peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	28.10	9.66	6	86.51
Gomus.A06G115100.1	H+-transporting ATPase	105.80	6.86	4	86.30
Gomus.A11G021300.1	Stress-induced-phosphoprotein 1	65.45	6.68	8	86.27
Gomus.D07G035100.1	F-type H+-transporting ATPase subunit b	24.50	8.68	8	86.22
Gomus.A07G111700.1	Predicted dehydrogenase	55.70	6.47	9	86.09
Gomus.A03G085200.1	Small subunit ribosomal protein S2e	29.60	10.32	6	85.60
Gomus.A07G053900.1	ATP-dependent Clp protease ATP-binding subunit ClpC	102.25	6.70	3	85.45
Gomus.A10G063000.1	Translation initiation factor eIF-4A	46.90	5.48	6	85.14
Gomus.A03G072200.1	ATP-dependent Clp protease ATP-binding subunit ClpC	102.20	6.33	10	85.10
Gomus.A09G215700.1	Chaperonin GroEL	61.40	5.88	11	84.96
Gomus.D01G222900.1	Alcohol dehydrogenase, class III	41.60	7.02	7	84.72
Gomus.A03G122300.1	Heat shock protein 90kDa beta	89.90	4.97	12	84.61
Gomus.A04G158800.1	26S proteasome regulatory subunit N10	42.10	4.63	4	84.38
Gomus.D11G020200.1	Heat shock 70kDa protein 5	73.49	5.27	5	83.93
Gomus.D12G116800.1	Transketolase	80.12	6.83	11	83.89
Gomus.A03G033600.1	Molecular chaperone HtpG	81.05	5.10	3	83.34

Gomus.D04G185300.1	Tubulin alpha	49.48	5.06	4	83.20
Gomus.A09G097000.1	Cu/Zn superoxide dismutase	22.10	6.51	5	83.00
Gomus.A09G011300.1	ATP-dependent Clp protease ATP-binding subunit ClpB	110.00	6.16	12	82.99
Gomus.A08G137400.1	S-adenosylmethionine synthetase	43.10	5.82	6	82.88
Gomus.D05G192800.1	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	48.40	7.43	9	82.63
Gomus.A05G106200.1	L-ascorbate peroxidase	27.58	6.38	7	82.58
Gomus.D01G060600.1	Malate dehydrogenase	35.50	8.62	5	81.99
Gomus.A12G192800.1	D-ribulose-5-phosphate 3-epimerase	31.80	7.08	3	81.86
Gomus.A12G091500.1	Photosystem I	9.00	7.08	3	81.71
Gomus.A11G241400.1	Actin, other eukaryote	41.68	5.49	7	81.63
Gomus.A03G154500.1	Predicted carbonic anhydrase involved in protection against oxidative damage	28.00	6.40	8	81.18
Gomus.D02G055800.1	Malate dehydrogenase	35.50	6.54	9	81.17
Gomus.D12G297500.1	Phosphoglucomutase	69.20	7.01	7	80.79
Gomus.D10G087700.1	Phospholipase D	91.50	5.77	5	80.61
Gomus.A04G153600.1	Ribosomal RNA large subunit methyltransferase F	121.54	5.64	4	79.80
Gomus.A01G001200.1	Actin, other eukaryote	41.54	5.40	5	79.29
Gomus.A04G089800.1	Fructose-bisphosphate aldolase, class I	38.60	6.27	3	79.23
Gomus.D07G076800.1	Small subunit ribosomal protein S7e	22.00	9.74	4	78.99
Gomus.D02G123900.1	Tubulin beta	50.11	4.84	6	78.90
Gomus.A01G227300.1	Pyruvate kinase	57.40	7.08	5	78.66
Gomus.A06G226100.1	Lactoylglutathione lyase	32.60	5.47	5	78.34
Gomus.A10G087800.1	Heat shock 70kDa protein 4	94.21	5.48	1	77.66
Gomus.A03G083500.1	Malate dehydrogenase	43.15	7.68	11	77.58
Gomus.A06G104900.1	Leucyl aminopeptidase	60.80	6.80	8	77.33
Gomus.A04G125600.1	Glutathione S-transferase	26.10	6.02	3	77.31
Gomus.D02G046900.1	PsaD	25.20	9.85	5	77.28
Gomus.D10G088300.1	Uncharacterized protein	35.20	4.77	11	76.89
Gomus.D04G039700.1	Ubiquitin-like protein Nedd8	17.20	6.05	3	76.87
Gomus.A05G135900.3	E3 ubiquitin ligase involved in syntaxin degradation	73.98	5.24	3	76.72
Gomus.D09G161100.2	Enolase	47.90	6.02	6	76.05
Gomus.A02G087500.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	28.50	4.79	4	76.00
Gomus.A06G117400.1	Tubulin alpha	49.70	5.06	8	75.97
Gomus.D13G155400.1	Fructose-bisphosphate aldolase, class I	38.40	8.00	8	75.91
Gomus.A07G022000.1	Puromycin-sensitive aminopeptidase	98.73	5.44	7	75.74
Gomus.A11G042500.1	Glyceraldehyde 3-phosphate dehydrogenase	36.93	7.18	10	75.46
Gomus.A07G064800.1	Uncharacterized protein	42.50	9.31	4	75.31
Gomus.A12G018200.1	Molecular chaperone DnaK	72.36	5.77	4	75.15
Gomus.A01G012100.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.31	4.88	6	74.96
Gomus.A12G005000.1	Photosystem I subunit II	22.90	9.64	5	74.41
Gomus.D12G018600.1	Molecular chaperone DnaK	72.30	5.88	3	74.39
Gomus.D02G141300.1	Cytochrome b	18.80	7.87	2	74.02
Gomus.D06G218200.1	Metacaspase involved in regulation of apoptosis	37.00	6.61	9	73.91
Gomus.A13G175900.1	Elongation factor EF-2	94.04	6.25	4	73.82
Gomus.D11G137600.1	Ribosome recycling factor	30.89	9.44	8	72.90
Gomus.A08G229000.1	Histone H2A	15.10	10.43	3	72.63
Gomus.A04G146500.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.14	4.82	6	72.45
Gomus.A13G021900.1	Chalcone isomerase	24.40	5.07	4	72.21
Gomus.A01G142600.1	Small subunit ribosomal protein S5e	23.30	9.70	4	72.16
Gomus.A05G389900.1	Zinc-binding oxidoreductase	34.30	5.41	9	71.92
Gomus.D07G064800.1	Nucleolin	35.44	4.58	6	71.65
Gomus.A12G040700.1	Cyclophilin type peptidyl-prolyl cis-trans isomerase	13.89	7.80	7	71.61
Gomus.D02G129400.1	Phosphoglycerate mutase	61.10	6.00	8	71.49
Gomus.D08G221500.1	Tubulin beta	49.80	4.89	6	71.39
Gomus.A01G233700.1	Elongation factor EF-1 alpha subunit	49.30	9.09	3	71.31
Gomus.A04G089600.1	Fructose-bisphosphate aldolase, class I	38.60	7.37	6	71.17
Gomus.A07G241700.1	Tubulin alpha	49.47	5.10	1	70.88
Gomus.A05G251200.1	Peroxidase	41.70	8.53	8	70.87
Gomus.D12G127200.1	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	60.25	5.64	3	70.72
Gomus.A02G150700.1	Apoptotic chromatin condensation inducer in the nucleus	79.90	4.87	5	70.67
Gomus.D02G247100.1	Polyadenylate-binding protein	70.80	7.81	8	70.62
Gomus.D06G217400.1	Tyrosinase	71.50	6.55	7	70.58
Gomus.D12G065300.1	Naringenin 3-dioxygenase	41.40	5.58	6	70.47
Gomus.A08G124300.1	Actin, other eukaryote	41.53	5.49	6	70.44
Gomus.A05G240400.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	28.83	4.88	7	70.06
Gomus.D04G072000.1	Actin, other eukaryote	41.70	5.49	6	70.04
Gomus.D11G291400.1	Ribulose-bisphosphate carboxylase	52.88	6.29	8	69.41
Gomus.D10G177100.1	Malate dehydrogenase	35.50	7.05	7	69.21
Gomus.D09G237700.1	Cysteine synthase A	42.47	8.16	2	68.81
Gomus.A02G096900.1	Phosphoglycerate mutase	61.10	5.68	8	68.22
Gomus.A03G037400.1	Uncharacterized protein	110.40	5.71	9	68.00
Gomus.D10G081500.1	Heat shock 70kDa protein 4	94.22	5.57	1	67.69
Gomus.A05G436800.1	Chalcone-flavanone isomerase	23.40	4.91	5	67.65
Gomus.D01G115300.1	Catalase	56.80	7.17	6	67.51
Gomus.A01G111900.1	Cell division protease FtsH	74.90	6.34	9	67.41
Gomus.D06G075800.1	Elongation factor EF-Ts	117.46	4.81	3	67.41
Gomus.A01G224800.1	Large subunit ribosomal protein LP2	11.40	4.45	6	67.35
Gomus.A01G248000.1	Light-harvesting complex II chlorophyll a/b binding protein 4	31.10	5.68	5	67.29
Gomus.D06G040100.3	L-ascorbate peroxidase	42.80	8.24	7	67.22
Gomus.D06G234100.1	Metacaspase involved in regulation of apoptosis	41.30	7.80	8	67.20
Gomus.A11G250200.1	Molecular chaperone GrpE	37.70	4.69	2	67.16
Gomus.D01G001500.1	Actin, other eukaryote	41.54	5.40	3	67.02
Gomus.A03G190900.1	Light-harvesting complex II chlorophyll a/b binding protein 6	27.40	8.09	2	66.85
Gomus.A04G102700.1	Large subunit ribosomal protein L4e	44.70	10.33	7	66.58
Gomus.D07G079300.1	ATP-dependent Clp protease ATP-binding subunit ClpB	101.60	6.21	6	66.50
Gomus.A07G128800.1	Elongation factor EF-1 alpha subunit	49.31	9.06	2	66.39
Gomus.D07G105300.1	FK506-binding protein 4/5	63.70	5.11	8	65.99
Gomus.A13G187700.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.62	6.40	2	65.78
Gomus.D07G079300.2	ATP-dependent Clp protease ATP-binding subunit ClpB	101.60	6.21	9	65.40
Gomus.A09G207900.1	Stress-induced-phosphoprotein 1	65.15	6.77	4	64.99
Gomus.D12G108600.1	F-type H+-transporting ATPase oligomycin sensitivity conferral protein	27.50	9.44	4	64.96
Gomus.A12G247500.1	Apocytochrome f	35.20	7.91	6	64.70
Gomus.A10G243900.1	Triosephosphate isomerase (TIM)	27.40	5.48	6	64.63
Gomus.A11G063200.1	Actin, other eukaryote	41.69	5.49	6	64.48
Gomus.A02G046000.1	Malate dehydrogenase	35.60	7.06	9	64.25
Gomus.A10G157800.1	Phage shock protein A	36.70	9.32	6	64.25
Gomus.D07G102000.1	Predicted dehydrogenase	30.70	7.80	6	64.22
Gomus.D01G269600.1	Late embryogenesis abundant protein	36.80	4.98	5	64.05
Gomus.A09G090400.1	Heat shock 70kDa protein 4	94.20	5.43	6	63.67
Gomus.D02G253000.1	Uncharacterized protein	15.10	5.10	5	63.60
Gomus.A05G132200.1	Histone H2A	14.30	10.32	4	63.57
Gomus.D10G268100.1	Triosephosphate isomerase (TIM)	27.20	6.35	6	63.54
Gomus.A06G191600.1	Tyrosinase	70.30	7.23	6	63.49
Gomus.D03G048400.1	Apoptotic chromatin condensation inducer in the nucleus	78.00	4.92	4	63.45
Gomus.A10G220000.1	Pyruvate kinase	57.90	7.11	2	63.33
Gomus.A09G158900.1	Transitional endoplasmic reticulum ATPase	89.38	5.29	1	63.21
Gomus.D10G044000.1	Light-harvesting complex II chlorophyll a/b binding protein 1	28.19	5.43	3	62.92
Gomus.D10G297400.1	Vesicle coat protein clathrin, heavy chain	176.58	5.33	3	62.53
Gomus.D05G308900.1	Uncharacterized protein	30.30	6.40	7	62.46
Gomus.A07G195900.1	Light-harvesting complex II chlorophyll a/b binding protein 2	28.53	5.96	3	62.32
Gomus.A06G038500.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.00	4.75	4	62.29
Gomus.A11G189100.1	Ferredoxin--NADP+ reductase	40.40	8.60	8	62.28
Gomus.A10G081300.1	Phospholipase D	91.50	5.72	5	62.20

Gomus.A02G041700.1	Small subunit ribosomal protein S15e	17.20	10.43	3	61.65
Gomus.D07G193400.1	Light-harvesting complex II chlorophyll a/b binding protein 2	28.59	5.44	2	61.54
Gomus.A01G139300.1	F-type H+-transporting ATPase subunit d	19.60	5.02	5	61.49
Gomus.D06G218400.1	Metacaspase involved in regulation of apoptosis	36.81	6.61	9	61.46
Gomus.A05G186600.1	PAP_fibrillin	35.55	5.24	6	61.20
Gomus.D04G218700.1	Phosphoglucomutase	63.30	5.86	4	61.13
Gomus.A05G370100.1	Glyceraldehyde 3-phosphate dehydrogenase	36.54	7.93	4	60.76
Gomus.D09G040200.1	Glyceraldehyde 3-phosphate dehydrogenase	36.50	7.58	7	60.71
Gomus.D08G237700.1	Eukaryotic translation initiation factor 2C	101.90	8.76	1	60.27
Gomus.D07G257500.1	Predicted carbonic anhydrase involved in protection against oxidative damage	35.13	7.96	3	60.12
Gomus.D13G120600.1	Tubulin alpha	49.64	5.14	1	59.88
Gomus.D04G020800.1	Copper chaperone	12.80	4.78	3	59.53
Gomus.A13G262700.1	Histone H2B	16.20	10.07	3	59.43
Gomus.A04G101800.1	Elongation factor EF-1 alpha subunit	32.85	9.11	2	59.41
Gomus.A10G255700.1	Sedoheptulose-bisphosphatase	42.50	6.04	6	59.24
Gomus.D05G388600.1	Malate dehydrogenase	35.35	8.62	4	59.11
Gomus.A05G198800.1	Ferredoxin--NADP+ reductase	40.39	8.19	7	58.98
Gomus.D07G115500.1	Predicted dehydrogenase	55.66	6.09	3	58.93
Gomus.A07G031700.3	Glyceraldehyde-3-phosphate dehydrogenase (NADP)	53.10	7.37	5	58.87
Gomus.D05G101900.1	Triosephosphate isomerase (TIM)	27.19	5.92	7	58.68
Gomus.1Z015500.1	Metacaspase involved in regulation of apoptosis	36.97	6.61	9	58.50
Gomus.D02G217400.1	Cytochrome b6-f complex iron-sulfur subunit	24.32	8.18	7	58.40
Gomus.D03G170600.1	Tubulin beta	50.10	4.86	2	58.38
Gomus.A04G074600.1	Uncharacterized protein	16.00	4.56	5	58.38
Gomus.D05G107600.1	L-ascorbate peroxidase	27.54	6.11	5	58.38
Gomus.D07G222100.1	Heat shock protein 90kDa beta	90.35	5.40	4	57.98
Gomus.A05G121600.1	V-type H+-transporting ATPase subunit A	68.49	5.52	5	57.92
Gomus.D01G265600.1	Light-harvesting complex II chlorophyll a/b binding protein 4	31.10	5.94	5	57.87
Gomus.D07G255000.1	Uncharacterized protein	20.10	4.81	5	57.78
Gomus.D02G271700.1	Actin, other eukaryote	41.51	5.49	3	57.70
Gomus.A08G233200.1	Histone H2A	14.70	10.21	2	57.61
Gomus.D04G122600.1	Fructose-bisphosphate aldolase, class I	38.80	6.57	5	57.32
Gomus.D13G019700.1	Large subunit ribosomal protein LP0	34.10	5.22	4	57.21
Gomus.A05G334900.1	Aconitate hydratase 1	108.40	7.71	9	57.17
Gomus.D02G141000.1	Photosystem II protein	38.84	8.91	9	57.10
Gomus.D11G393500.1	Large subunit ribosomal protein L4e	44.80	10.33	4	56.97
Gomus.A13G221700.1	20S proteasome subunit alpha 1	27.30	6.32	4	56.87
Gomus.D09G174800.1	Predicted dehydrogenase	35.86	8.79	1	56.70
Gomus.A09G235400.1	Uncharacterized protein	65.80	5.59	7	56.63
Gomus.D04G030500.1	Actin, other eukaryote	20.64	5.41	5	56.54
Gomus.D13G049600.1	F0F1-type ATP synthase, beta subunit	61.18	6.29	10	56.34
Gomus.A12G062800.1	Aconitate hydratase 1	98.10	6.27	7	56.28
Gomus.D05G416300.1	Ubiquitin C	59.68	7.62	3	56.23
Gomus.A05G045300.1	Glycine dehydrogenase	113.91	7.17	1	56.00
Gomus.1Z015700.1	Cu/Zn superoxide dismutase	15.10	6.42	4	55.60
Gomus.D05G157600.1	20S proteasome subunit alpha 2	25.60	5.68	4	55.51
Gomus.A10G072200.1	ATP synthase B/B' CF(0)	18.57	6.15	7	55.45
Gomus.A05G208000.1	dUTP pyrophosphatase	24.40	8.27	4	55.42
Gomus.D11G020800.1	Elongation factor EF-G	86.32	5.81	3	55.30
Gomus.A03G031200.1	Protease M1 zinc metalloprotease	57.10	7.80	3	55.10
Gomus.1Z030300.1	F-type H+-transporting ATPase subunit alpha	49.38	6.32	3	54.84
Gomus.D07G066500.1	Uncharacterized protein	42.40	9.31	5	54.77
Gomus.D06G075800.2	Elongation factor EF-Ts	117.39	4.81	2	54.76
Gomus.A11G046000.1	Transcriptional coactivator p100	108.53	7.09	3	54.56
Gomus.D09G159600.1	Monodehydroascorbate reductase (NADH)	46.80	6.83	4	54.49
Gomus.D09G011500.1	ATP-dependent Clp protease ATP-binding subunit ClpB	110.07	6.35	6	54.48
Gomus.A03G012200.1	Uncharacterized protein	79.90	6.13	7	54.28
Gomus.A12G248300.1	Photosystem I P700 chlorophyll a apoprotein A1	83.10	7.18	1	54.25
Gomus.A11G117700.1	S-adenosylmethionine synthetase	43.01	5.80	3	54.18
Gomus.A03G001600.1	Phosphoribulokinase	45.16	6.42	2	54.17
Gomus.D04G122700.1	Fructose-bisphosphate aldolase, class I	38.63	6.90	3	54.08
Gomus.A02G127400.2	Actin regulatory proteins (gelsolin/villin family)	103.90	5.50	3	53.89
Gomus.D12G023700.1	D-3-phosphoglycerate dehydrogenase	63.70	7.69	8	53.87
Gomus.D07G193100.1	Light-harvesting complex II chlorophyll a/b binding protein 2	28.56	5.44	6	53.49
Gomus.A09G166400.1	Predicted dehydrogenase	35.90	8.95	8	53.19
Gomus.D10G003600.1	V-type H+-transporting ATPase subunit A	68.48	5.52	2	53.16
Gomus.A07G102100.1	FK506-binding protein 4/5	63.68	5.21	8	53.16
Gomus.A13G046200.1	D-3-phosphoglycerate dehydrogenase	63.80	7.52	8	53.15
Gomus.A13G045200.1	Polyadenylate-binding protein	70.60	8.09	6	53.06
Gomus.A08G003700.1	Histone H2A	15.84	10.67	4	52.92
Gomus.A03G206600.1	Polyadenylate-binding protein	70.89	8.10	1	52.84
Gomus.A01G179700.1	Cold shock domain containing proteins	16.80	7.24	4	52.53
Gomus.D06G183000.2	F-type H+-transporting ATPase subunit gamma	41.30	6.20	8	52.46
Gomus.A11G031800.1	Glycine cleavage system H protein	17.39	5.17	5	52.42
Gomus.A04G137900.1	Glutamine synthetase	39.10	5.92	3	52.36
Gomus.A09G220800.1	Adenosylhomocysteinase	53.20	6.28	1	52.19
Gomus.D04G135500.1	Large subunit ribosomal protein L4e	44.68	10.33	1	52.18
Gomus.D05G182000.1	Photosystem II oxygen-evolving enhancer protein 3	24.85	9.45	3	52.10
Gomus.A01G152000.1	Transitional endoplasmic reticulum ATPase	89.50	5.26	5	52.07
Gomus.A07G215500.1	Light-harvesting complex II chlorophyll a/b binding protein 2	28.41	5.43	3	51.90
Gomus.A06G069900.3	Elongation factor EF-Ts	117.80	4.79	7	51.87
Gomus.A09G123500.1	Uncharacterized protein	11.20	9.80	2	51.84
Gomus.A08G194900.1	Uncharacterized protein	36.80	5.02	3	51.42
Gomus.A12G247100.1	Photosystem II cytochrome b559 subunit alpha	22.20	4.79	2	50.90
Gomus.D13G277600.1	Lactoylglutathione lyase	26.60	8.48	3	50.86
Gomus.A08G077200.1	Photosystem I subunit II	22.63	9.58	3	50.62
Gomus.D08G248700.1	Translation initiation factor eIF-3 subunit 10	115.24	9.36	1	50.51
Gomus.D04G172300.1	Glutamine synthetase	39.19	6.13	1	50.40
Gomus.A11G218500.1	Annexin	39.74	8.60	3	50.22
Gomus.A11G301300.2	dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	42.32	8.63	3	50.22
Gomus.D08G152500.1	S-adenosylmethionine synthetase	43.11	5.94	2	50.07
Gomus.D09G161100.1	Enolase	47.91	6.02	3	49.96
Gomus.D05G267400.1	Light-harvesting complex II chlorophyll a/b binding protein 5	30.98	5.72	2	49.72
Gomus.D04G063800.1	Large subunit ribosomal protein L7/L12	20.50	6.05	4	49.63
Gomus.A07G087800.3	Hsp70-interacting protein Hip/Transient component of progesterone receptor complexes and an Hsp70-binding protein	34.40	4.75	3	49.61
Gomus.A05G287700.1	Protein disulfide-isomerase A1	55.40	4.94	6	49.45
Gomus.A03G177800.1	Cytochrome b6-f complex iron-sulfur subunit	24.30	8.38	3	49.42
Gomus.A01G235200.1	Large subunit ribosomal protein L4e	44.71	10.30	2	49.22
Gomus.A07G014900.1	Small subunit ribosomal protein S3e	26.30	9.52	5	49.20
Gomus.A05G223900.1	Adenine phosphoribosyltransferase	27.90	7.71	4	49.00
Gomus.A01G182900.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	42.20	7.42	5	48.99
Gomus.D05G155100.1	Photosystem I subunit III	24.27	9.41	4	48.97
Gomus.A07G181800.1	Apocytochrome f	35.18	7.91	4	48.89
Gomus.D04G072000.2	Actin, other eukaryote	39.73	5.83	2	48.85
Gomus.A11G006300.1	protein phosphatase 2 (formerly 2A), regulatory subunit A	65.50	5.03	8	48.80
Gomus.A08G138400.1	Peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	27.60	7.93	2	48.70
Gomus.A12G047100.1	Elongation factor EF-1 gamma subunit	47.60	7.68	4	48.15
Gomus.D05G200900.1	Tubulin beta	50.49	4.81	2	48.10
Gomus.A08G155700.1	Nucleoside-diphosphate kinase	16.40	6.80	3	48.05
Gomus.A01G201700.1	Acetyl-CoA carboxylase	234.47	6.67	1	48.01
Gomus.A13G139500.1	Phosphatidylinositol transfer protein SEC14 and related proteins	65.70	4.75	3	47.80

Gomus.A11G293900.1	Microtubule-binding protein (translationally controlled tumor protein)	19.10	4.67	4	47.77
Gomus.A05G156900.3	(S)-2-hydroxy-acid oxidase	40.40	9.33	4	47.56
Gomus.D03G002800.1	Catalase	56.92	7.43	1	47.46
Gomus.A06G002700.1	Heat shock protein 90kDa beta	91.90	5.02	5	47.22
Gomus.A04G111700.1	Aldo/keto reductase family proteins	35.00	7.24	6	47.21
Gomus.A01G038900.1	(S)-2-hydroxy-acid oxidase	40.71	9.22	2	47.10
Gomus.A05G188100.1	Uncharacterized protein	32.40	5.87	4	47.01
Gomus.D10G140400.2	Phage shock protein A	36.35	9.32	2	47.00
Gomus.D07G250400.1	Tubulin alpha	49.50	5.10	6	46.95
Gomus.D03G069400.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	164.41	6.87	1	46.77
Gomus.A02G076200.1	Alcohol dehydrogenase, class III	41.00	6.10	3	46.69
Gomus.A02G077100.1	Thioredoxin-like protein	19.50	8.53	4	46.04
Gomus.A03G153800.1	Thioredoxin, nucleoredoxin and related proteins	63.94	5.00	2	45.98
Gomus.A11G288200.1	Uncharacterized	32.30	7.93	5	45.98
Gomus.D06G040100.2	L-ascorbate peroxidase	39.00	6.34	4	45.96
Gomus.A04G007000.1	Chromatin-associated protein Dek and related proteins, contains SAP DNA binding domain	73.39	4.92	1	45.92
Gomus.D11G297100.1	Electron transport oxidoreductase	22.50	7.01	5	45.87
Gomus.A02G048300.2	RNA-binding protein Musashi	46.00	7.06	2	45.80
Gomus.A04G091100.1	Enolase	47.69	6.23	6	45.69
Gomus.A06G002800.1	Heat shock protein 90kDa beta	91.90	5.00	5	45.60
Gomus.A13G163600.1	Histone H2A	13.91	10.05	3	45.39
Gomus.D02G129800.1	Phage shock protein A	36.66	9.16	1	45.32
Gomus.A05G382300.1	Intracellular Cl- channel CLIC, contains GST domain	23.50	7.88	3	45.05
Gomus.D12G146800.1	protein disulfide-isomerase A6	39.30	5.71	3	45.00
Gomus.D04G132100.2	Nucleolin	30.20	6.11	5	44.98
Gomus.A08G091200.1	Peroxidase	36.82	4.91	4	44.93
Gomus.A01G044100.1	Apoptotic ATPase	112.07	6.30	1	44.58
Gomus.A10G229200.1	Elongation factor EF-1 alpha subunit	49.40	9.06	3	44.57
Gomus.A05G269300.1	2-hydroxy-6-oxonona-2,4-dienedioate hydrolase	31.00	5.68	5	44.47
Gomus.A08G235400.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	38.10	6.48	5	44.26
Gomus.A06G096100.1	Glycine dehydrogenase	113.92	7.09	2	44.17
Gomus.D01G118800.1	Cell division protease FtsH	74.88	6.34	2	44.08
Gomus.D05G258100.1	Thioredoxin 1	20.20	7.59	3	44.08
Gomus.A08G027600.1	Histone H2A	13.93	10.05	3	44.08
Gomus.D02G192100.2	Predicted carbonic anhydrase involved in protection against oxidative damage	27.95	6.40	2	44.08
Gomus.D02G096000.1	20S proteasome subunit beta 3	22.90	5.47	5	43.89
Gomus.D09G082700.1	Nuclear protein, contains WD40 repeats	118.67	5.68	1	43.86
Gomus.A08G235200.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	38.00	6.76	5	43.76
Gomus.A13G095300.1	Large subunit ribosomal protein L4e	44.90	10.24	5	43.59
Gomus.D05G082000.1	Nuclear inhibitor of protein phosphatase-1	23.90	6.35	4	43.54
Gomus.A12G220700.1	Phosphoribulokinase	45.16	6.61	2	43.52
Gomus.A10G098500.1	ATP synthase delta/epsilon chain	10.00	4.65	3	43.51
Gomus.A08G211700.1	26S proteasome regulatory subunit T2	49.70	6.33	5	43.50
Gomus.D05G044500.1	Translation initiation factor eIF-4A	46.73	5.57	2	43.36
Gomus.A08G217500.1	Large subunit ribosomal protein L12e	17.90	8.95	2	43.25
Gomus.A05G183900.1	Aminomethyltransferase	44.40	8.88	6	43.13
Gomus.D08G174400.1	Nucleoside-diphosphate kinase	16.40	6.80	4	43.11
Gomus.A10G167900.1	PsbP	17.52	8.40	4	42.99
Gomus.A01G179600.1	Predicted RNA-binding protein containing PIN domain and invovled in translation or RNA processing	17.10	6.74	4	42.96
Gomus.A01G238800.1	Histone H4	11.40	11.47	2	42.92
Gomus.A06G069900.2	Elongation factor EF-Ts	117.72	4.79	1	42.82
Gomus.D02G275000.1	LL-diaminopimelate aminotransferase	50.40	7.85	5	42.78
Gomus.D01G102400.1	Photosystem I P700 chlorophyll a apoprotein A2	82.40	7.24	5	42.78
Gomus.D10G001100.1	Ketol-acid reductoisomerase	63.71	6.48	2	42.63
Gomus.A11G325200.1	Elongation factor EF-2	94.00	6.18	1	42.55
Gomus.A12G063500.1	Naringenin 3-dioxygenase	41.45	5.41	2	42.54
Gomus.A01G150000.1	Pathogenesis-related protein Bet v I family	17.30	5.26	3	42.52
Gomus.D09G167000.1	Transitional endoplasmic reticulum ATPase	89.47	5.26	4	42.52
Gomus.A02G036800.1	Photosystem I subunit II	23.70	9.79	6	42.51
Gomus.D05G159400.1	(S)-2-hydroxy-acid oxidase	40.36	9.23	2	42.48
Gomus.A09G209600.1	Plasminogen activator inhibitor 1 RNA-binding protein	38.33	6.99	1	42.41
Gomus.A08G269400.1	Alkyl hydroperoxide reductase/peroxiredoxin	17.19	5.91	3	42.31
Gomus.A09G231400.1	Elongation factor EF-P	26.20	8.54	4	42.31
Gomus.D11G069300.2	Late embryogenesis abundant (plants) LEA-related	64.81	6.19	1	42.12
Gomus.D06G190600.1	Uncharacterized protein	31.90	5.41	4	42.02
Gomus.A05G135900.1	E3 ubiquitin ligase involved in syntaxin degradation	82.20	5.69	5	41.98
Gomus.A12G194300.1	Translation initiation factor eIF-5A	17.43	5.99	5	41.90
Gomus.A06G104900.2	Leucyl aminopeptidase	52.85	5.40	2	41.82
Gomus.A02G102400.2	Acetyl-CoA carboxylase, biotin carboxylase subunit	58.57	7.46	1	41.81
Gomus.D07G149200.1	S-adenosylmethionine synthetase	43.00	5.81	5	41.73
Gomus.D05G243700.1	Annexin	35.97	6.80	1	41.54
Gomus.D12G304400.1	Guanine nucleotide-binding protein subunit beta-2-like 1 protein	36.00	7.44	6	41.53
Gomus.A01G027000.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	47.50	8.41	6	41.48
Gomus.A09G038600.1	Glyceraldehyde 3-phosphate dehydrogenase	36.52	7.58	2	41.32
Gomus.A03G118600.1	Uncharacterized protein	12.70	7.56	2	41.31
Gomus.A03G157000.1	Pathogenesis-related protein Bet v I family	17.10	5.41	3	41.27
Gomus.D06G173300.1	Photosystem I subunit III	24.30	9.33	3	41.27
Gomus.A05G322000.1	Large subunit ribosomal protein L10	25.30	9.35	1	41.11
Gomus.A13G017400.1	Large subunit ribosomal protein LP0	34.20	5.22	4	41.10
Gomus.A04G163900.1	Inorganic pyrophosphatase	32.80	5.81	4	40.87
Gomus.A01G024900.1	Cell division protease FtsH	75.53	6.67	1	40.83
Gomus.A01G127000.1	Cysteine proteinase Cathepsin L	50.50	5.26	5	40.77
Gomus.A04G156300.1	Triosephosphate isomerase (TIM)	33.10	7.37	5	40.66
Gomus.A02G157500.1	Uncharacterized protein	28.60	9.36	4	40.57
Gomus.D13G063500.1	Endosulfine	14.60	9.26	3	40.54
Gomus.A06G085600.2	Mitochondrial chaperonin	26.39	8.59	3	40.54
Gomus.D01G176500.2	Phosphoglucomutase	63.14	5.92	2	40.46
Gomus.D07G198600.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.51	4.87	3	40.39
Gomus.D11G163500.1	Light-harvesting complex I chlorophyll a/b binding protein 3	29.44	8.88	4	40.36
Gomus.D01G255500.1	Histone H2A	16.30	10.62	3	40.24
Gomus.D05G253100.1	Peroxidase	41.74	8.63	1	40.17
Gomus.D12G044200.1	Inorganic pyrophosphatase	32.90	6.71	4	40.16
Gomus.D06G218500.1	Metacaspase involved in regulation of apoptosis	36.90	5.54	6	40.10
Gomus.A04G133400.1	Pathogenesis-related protein Bet v I family	17.10	5.33	4	40.09
Gomus.A01G058800.1	Malate dehydrogenase	35.49	8.46	3	40.00
Gomus.D12G059500.1	Probable lipid transfer	10.08	8.72	1	39.94
Gomus.D13G136800.1	ADP-ribosylation factor 1	25.10	8.69	5	39.93
Gomus.D04G135000.1	Translation elongation factor EF-1 alpha/Tu	47.10	9.14	3	39.87
Gomus.A04G098800.2	Splicing factor 3b, subunit 4	30.30	6.62	5	39.86
Gomus.A03G056900.1	Triosephosphate isomerase (TIM)	27.10	6.21	5	39.83
Gomus.D08G233800.1	Elongation factor EF-1 beta subunit	24.90	4.59	5	39.81
Gomus.D06G065500.1	U4/U6 small nuclear ribonucleoprotein SNU13	13.90	7.12	2	39.69
Gomus.A04G016700.1	Aconitate hydratase 1	108.62	7.55	3	39.65
Gomus.D04G036400.1	Photosystem I reaction centre subunit N (PSAN or PSI-N)	18.12	9.17	2	39.64
Gomus.A02G012500.1	Phosphoglycerate mutase	60.80	6.05	5	39.57
Gomus.A06G162600.1	Aminomethyltransferase	44.20	8.87	6	39.49
Gomus.A05G199100.1	Tubulin beta	50.50	4.81	5	39.42
Gomus.A02G096300.1	Phage shock protein A	36.54	8.94	1	39.27
Gomus.D04G188700.2	Ribosomal RNA large subunit methyltransferase F	120.47	5.59	6	39.26
Gomus.D07G090600.1	Intracellular Cl- channel CLIC, contains GST domain	29.30	8.46	4	39.17
Gomus.A08G048200.1	ADP-ribosylation factor 1	20.67	6.95	1	39.15
Gomus.D01G243100.1	Large subunit ribosomal protein LP2	11.38	4.45	4	39.08

Gomus.A01G227400.1	Pyruvate kinase	57.35	6.90	2	39.02
Gomus.D05G295400.1	Phosphatidylinositol transfer protein SEC14 and related proteins	66.70	4.74	4	39.01
Gomus.A11G227300.1	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	54.31	4.96	1	38.76
Gomus.A07G215300.1	Heat shock protein 90kDa beta	90.33	5.29	1	38.76
Gomus.A01G088200.1	Trigger factor chaperone and peptidyl-prolyl cis/trans isomerase	61.50	5.47	3	38.75
Gomus.D09G091600.1	20S proteasome, regulatory subunit alpha type PSMA5/PUP2	27.70	5.34	5	38.70
Gomus.D06G042100.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	28.62	4.83	2	38.67
Gomus.D06G104800.1	Far upstream element-binding protein	69.31	6.20	2	38.52
Gomus.A06G109800.1	ATP-dependent Clp protease ATP-binding subunit ClpB	109.00	7.14	4	38.32
Gomus.A09G058900.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	36.60	7.28	3	38.30
Gomus.A10G229100.1	Elongation factor EF-1 alpha subunit	49.29	9.13	1	38.28
Gomus.D06G003000.1	Heat shock protein 90kDa beta	91.86	5.01	2	38.23
Gomus.D01G222200.1	Photosystem II 22kDa protein	29.24	8.78	4	38.10
Gomus.A01G061500.1	Carbamoyl-phosphate synthase large subunit	129.68	5.49	1	37.99
Gomus.A03G233900.2	LL-diaminopimelate aminotransferase	50.40	8.22	5	37.94
Gomus.A08G061900.2	6-phosphogluconate dehydrogenase	53.30	6.27	3	37.88
Gomus.D03G159600.1	Ubiquitin-activating enzyme E1	120.90	5.38	6	37.87
Gomus.A10G082400.2	NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase	13.14	8.35	1	37.86
Gomus.A08G274500.1	Peroxiredoxin Q/BCP	23.87	9.73	5	37.83
Gomus.D06G095800.1	Dimethylaniline monooxygenase (N-oxide forming)	59.97	7.66	1	37.78
Gomus.A04G074400.1	Small subunit ribosomal protein S5e	23.40	9.82	2	37.67
Gomus.A08G194700.1	Leucoanthocyanidin dioxygenase	40.30	5.52	2	37.66
Gomus.A09G063100.1	Small subunit ribosomal protein S3Ae	29.70	9.86	4	37.61
Gomus.A05G355600.1	Fructose-bisphosphate aldolase, class I	42.89	8.69	2	37.58
Gomus.A05G297800.1	Superoxide dismutase, Fe-Mn family	28.00	8.75	3	37.55
Gomus.A03G177900.1	Cytochrome b6-f complex iron-sulfur subunit	24.26	8.38	3	37.53
Gomus.A13G185100.1	Molecular chaperone GrpE	37.80	4.54	3	37.51
Gomus.D13G114200.1	Large subunit ribosomal protein L4e	45.06	10.40	1	37.37
Gomus.A11G151700.1	ATP synthase delta/epsilon chain	11.10	8.68	3	37.30
Gomus.A06G095400.1	Far upstream element-binding protein	69.40	6.38	4	37.25
Gomus.D03G054500.1	Uncharacterized protein	28.70	9.58	4	37.24
Gomus.D01G193100.1	Triosephosphate isomerase (TIM)	33.06	6.54	3	37.09
Gomus.A03G169500.1	WDSAM1 protein	65.82	6.67	1	37.08
Gomus.A03G047300.1	Protein disulfide-isomerase A1	65.70	4.79	5	37.04
Gomus.D07G043700.1	Uncharacterized protein	24.90	5.74	3	37.02
Gomus.D02G152600.1	Uncharacterized protein	12.70	6.95	3	36.88
Gomus.D05G349000.1	Fructose-bisphosphate aldolase, class I	42.95	8.53	2	36.79
Gomus.A13G068900.4	Pyruvate kinase	41.58	7.77	1	36.70
Gomus.D07G054600.1	Calnexin	61.05	4.70	3	36.70
Gomus.D08G203400.1	Plasminogen activator inhibitor 1 RNA-binding protein	38.40	8.47	4	36.64
Gomus.A10G000700.1	Ketol-acid reductoisomerase	76.50	5.97	2	36.56
Gomus.A10G232700.1	Intracellular Cl- channel CLIC, contains GST domain	23.40	6.87	4	36.49
Gomus.D11G334600.1	Cinnamyl-alcohol dehydrogenase	39.11	6.28	2	36.35
Gomus.A02G066400.1	S-adenosylmethionine synthetase	43.00	6.05	4	36.32
Gomus.D04G181500.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.22	4.83	3	36.29
Gomus.A13G187700.2	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.60	6.40	5	36.25
Gomus.D07G117000.1	HSP20 family protein	18.17	6.81	2	36.22
Gomus.A11G313200.1	Apoptotic ATPase	88.46	7.72	1	36.19
Gomus.D05G306200.1	Uncharacterized protein	14.96	5.73	4	36.16
Gomus.A04G026100.1	Histone H2A	14.00	10.05	3	36.14
Gomus.D08G215100.1	Uncharacterized protein	36.78	5.02	2	36.14
Gomus.D11G236000.1	Cinnamyl-alcohol dehydrogenase	39.11	6.28	1	36.12
Gomus.A01G210900.1	Large subunit ribosomal protein L6e	26.10	10.18	3	36.05
Gomus.D05G207400.1	Ornithine carbamoyltransferase	41.10	7.37	3	36.05
Gomus.D07G161100.1	Large subunit ribosomal protein L5	29.70	10.11	4	36.04
Gomus.A11G063000.1	Actin, other eukaryote	28.01	5.66	3	35.99
Gomus.A10G161500.1	T-complex protein 1 subunit alpha	59.12	6.13	1	35.88
Gomus.A13G268400.1	Ubiquitin-activating enzyme E1	113.62	5.25	1	35.80
Gomus.D08G144300.1	Molecular chaperone (HSP90 family)	64.52	5.41	2	35.78
Gomus.A12G131300.1	S-adenosylmethionine synthetase	43.00	5.81	8	35.70
Gomus.A04G130500.1	Transaldolase	47.90	6.05	3	35.57
Gomus.D09G219300.1	Plasminogen activator inhibitor 1 RNA-binding protein	38.70	6.48	5	35.54
Gomus.A02G192400.1	S-phase kinase-associated protein 1	17.60	4.70	2	35.49
Gomus.A11G018900.1	Large subunit ribosomal protein L9e	22.01	9.63	4	35.46
Gomus.A11G245900.1	T-complex protein 1 subunit eta	60.10	6.80	5	35.43
Gomus.A05G124300.2	Uncharacterized protein	33.87	6.57	1	35.41
Gomus.A05G449300.1	Protein phosphatase 2A-associated protein	45.58	5.17	1	35.41
Gomus.D04G153300.1	Pyridoxine biosynthesis protein	33.00	6.80	3	35.40
Gomus.D09G010900.1	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	59.00	6.95	5	35.40
Gomus.D03G135000.1	Proliferating cell nuclear antigen	29.46	4.79	4	35.38
Gomus.A13G122800.1	GDP-D-mannose 3', 5'-epimerase	42.31	6.40	1	35.38
Gomus.A13G255100.1	Calmodulin	16.84	4.27	3	35.37
Gomus.A09G109300.1	DnaJ homolog subfamily A member 2	46.25	6.09	1	35.29
Gomus.A07G119900.1	Large subunit ribosomal protein LP2	11.50	4.37	3	35.24
Gomus.A04G129500.1	Light regulated protein Lir1	19.90	5.30	1	35.19
Gomus.D08G009700.1	Ferredoxin	15.90	5.49	1	35.18
Gomus.D01G023700.1	Cell division protease FtsH	75.47	6.60	1	35.11
Gomus.A03G010800.1	Uncharacterized protein	39.00	6.24	2	35.05
Gomus.A09G070100.1	WD40 repeat-containing protein	124.50	7.20	2	35.04
Gomus.A08G142000.1	Chitinase	52.45	6.44	3	35.03
Gomus.A08G216800.3	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	82.00	6.29	2	34.98
Gomus.A07G130900.1	Large subunit ribosomal protein L7e	28.40	9.88	3	34.97
Gomus.D02G152500.1	Translation initiation factor eIF-5A	17.40	5.99	4	34.97
Gomus.A01G021500.1	26S proteasome regulatory subunit N1	97.39	5.24	1	34.91
Gomus.D13G150500.1	Uncharacterized protein	22.55	9.35	3	34.89
Gomus.D03G084200.1	Actin regulatory proteins (gelsolin/villin family)	103.75	5.43	2	34.84
Gomus.D04G094000.1	ATP synthase D chain, mitochondrial (ATP5H)	15.60	5.68	3	34.82
Gomus.D02G252900.1	Ferredoxin	15.50	4.60	3	34.54
Gomus.D10G090300.1	Chlorophyll A/B binding protein	30.17	5.50	6	34.53
Gomus.A05G003700.1	Large subunit ribosomal protein LP1	11.90	4.36	1	34.46
Gomus.A12G203800.1	Elongation factor EF-1 beta subunit	24.70	4.61	4	34.45
Gomus.A10G189500.1	ATP citrate (pro-S)-lyase	65.90	7.85	5	34.32
Gomus.A05G088000.1	Large subunit ribosomal protein LP2	11.40	4.37	4	34.28
Gomus.A08G270000.1	Lactoylglutathione lyase	40.78	7.80	1	34.26
Gomus.A08G160800.1	Uncharacterized protein	11.00	10.36	1	34.23
Gomus.D13G061200.1	Small subunit ribosomal protein S6e	28.50	10.65	2	33.96
Gomus.A09G178900.1	Pyruvate decarboxylase	65.10	5.90	4	33.89
Gomus.A05G076300.1	Elongation factor EF-1 beta subunit	23.80	4.84	3	33.81
Gomus.A09G117500.1	Large subunit ribosomal protein L7e	28.30	9.94	3	33.81
Gomus.A04G029100.1	Universal stress protein family	24.20	6.02	3	33.81
Gomus.A07G247200.1	Formate dehydrogenase	42.17	7.81	1	33.78
Gomus.A11G213300.1	Glutathione S-transferase	26.10	6.24	2	33.78
Gomus.D12G307900.1	T-complex protein 1 subunit zeta	58.97	6.73	2	33.77
Gomus.D02G071700.1	Karyopherin (importin) alpha	58.16	5.44	5	33.71
Gomus.A12G123700.1	Cytochrome b5	15.50	4.96	3	33.70
Gomus.A09G087100.1	Translation initiation factor eIF-4A	46.86	5.48	3	33.69
Gomus.A07G165500.1	Succinyl-CoA synthetase beta subunit	45.21	6.15	1	33.65
Gomus.D02G075500.1	Dihydrolipoamide dehydrogenase	53.90	7.37	1	33.60
Gomus.D05G209700.1	dUTP pyrophosphatase	24.30	8.73	4	33.56
Gomus.D03G151400.1	Protein disulfide-isomerase A1	65.89	4.73	1	33.53
Gomus.A11G120300.1	ATP-dependent Clp protease, protease subunit	33.00	8.25	3	33.45
Gomus.A09G075200.1	PAP_fibrillin	36.90	5.06	2	33.45

Gomus.A08G157000.1	Chaperonin GroES	14.80	8.66	3	33.34
Gomus.A02G060400.1	Karyopherin (importin) alpha	58.10	5.44	4	33.29
Gomus.A10G000700.2	Ketol-acid reductoisomerase	63.74	6.80	5	33.28
Gomus.A05G326200.1	Photosystem II oxygen-evolving enhancer protein 2	27.60	8.94	4	33.21
Gomus.D07G022400.1	Puromycin-sensitive aminopeptidase	98.64	5.58	1	33.20
Gomus.A05G213300.1	Serpin B	42.66	6.81	2	33.18
Gomus.A11G189900.1	Naringenin 3-dioxygenase	40.72	5.21	1	33.18
Gomus.D07G089500.1	Hsp70-interacting protein Hip/Transient component of progesterone receptor complexes and an Hsp70-binding protein	46.70	6.34	5	33.11
Gomus.A06G179000.1	Chlorophyll A/B binding protein	30.80	6.37	4	33.06
Gomus.D01G136200.1	Cysteine proteinase Cathepsin L	57.20	5.47	4	33.06
Gomus.D13G271000.1	Sorting and assembly machinery (SAM50) protein	88.40	8.69	7	33.06
Gomus.D13G184000.1	Glutathione S-transferase	25.40	5.74	4	33.02
Gomus.D11G252100.1	Glutathione S-transferase	26.10	6.37	2	33.01
Gomus.A05G401300.1	ATP-dependent Clp protease ATP-binding subunit ClpB	109.15	6.65	1	32.99
Gomus.D08G298300.1	Peroxiredoxin Q/BCP	29.30	9.58	4	32.98
Gomus.A12G031800.1	Inorganic pyrophosphatase	33.20	6.71	3	32.91
Gomus.A07G092200.1	E3 ubiquitin ligase involved in syntaxin degradation	154.29	4.67	2	32.89
Gomus.D04G160400.1	Glutathione S-transferase	26.10	6.37	2	32.80
Gomus.D08G112200.1	Leucine rich repeat	48.28	6.29	1	32.76
Gomus.D08G153700.1	Peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	27.51	8.12	3	32.73
Gomus.A03G167100.1	Pyruvate dehydrogenase E1 component subunit beta	39.60	5.83	3	32.71
Gomus.D09G168500.1	Isocitrate dehydrogenase (NAD+)	40.75	6.95	1	32.62
Gomus.A11G348200.1	Apoptotic ATPase	154.76	6.11	1	32.54
Gomus.D03G141500.1	Triosephosphate isomerase (TIM)	27.07	6.54	2	32.54
Gomus.D10G272300.4	Uncharacterized	23.80	8.50	3	32.46
Gomus.D08G257800.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	37.45	6.20	1	32.46
Gomus.A12G297600.1	Aldehyde dehydrogenase (NAD+)	58.78	7.52	2	32.39
Gomus.A05G443700.1	Malate dehydrogenase (NADP+)	47.90	6.73	2	32.37
Gomus.A10G091300.1	T-complex protein 1 subunit gamma	60.33	6.58	2	32.29
Gomus.A08G013400.1	Large subunit ribosomal protein L7e	28.30	9.94	3	32.28
Gomus.A01G183000.1	S-phase kinase-associated protein 1	17.80	4.67	3	32.20
Gomus.D02G194800.1	Pathogenesis-related protein Bet v I family	19.83	5.64	5	32.18
Gomus.A12G164500.1	Histone H1/H5	19.50	10.92	3	32.14
Gomus.A01G228500.1	Adenylosuccinate synthase	53.50	7.01	4	32.12
Gomus.A03G144300.1	Glyceraldehyde 3-phosphate dehydrogenase	37.17	8.18	2	32.03
Gomus.D05G056400.1	Small subunit ribosomal protein S12e	14.70	6.40	3	31.95
Gomus.A11G021500.1	Uncharacterized protein	27.70	5.60	3	31.95
Gomus.A02G075900.1	Alcohol dehydrogenase, class III	41.04	6.39	3	31.90
Gomus.A05G448600.1	Exocyst complex component 4	117.00	5.94	1	31.86
Gomus.D02G166100.2	Nuclear pore complex, Nup155 component (D Nup154, sc Nup157/Nup170)	141.49	5.96	1	31.81
Gomus.D01G154400.1	Small subunit ribosomal protein S5e	23.19	9.73	3	31.74
Gomus.A06G191900.1	Nascent polypeptide-associated complex subunit alpha	22.53	4.60	2	31.67
Gomus.D11G190600.1	UTP--glucose-1-phosphate uridylyltransferase	51.27	5.66	2	31.66
Gomus.A07G167600.1	Photosystem II 13kDa protein	20.40	9.54	1	31.60
Gomus.A06G060000.2	Uncharacterized protein	31.10	4.82	1	31.54
Gomus.A10G210100.1	Nascent polypeptide-associated complex subunit alpha	22.60	4.58	2	31.53
Gomus.D11G087400.1	DnaJ homolog subfamily A member 2	47.38	7.66	2	31.52
Gomus.A05G195600.1	Thioredoxin	33.80	6.74	4	31.50
Gomus.A08G241100.1	Plant protein of unknown function (DUF639)	75.20	6.18	1	31.47
Gomus.D02G192100.1	Carbonic anhydrase	30.40	6.96	4	31.40
Gomus.A01G071400.1	Chlorophyll A/B binding protein	24.30	6.79	2	31.38
Gomus.D08G256900.1	Ser/Thr dehydratase, Trp synthase	26.05	8.84	3	31.31
Gomus.A05G241900.1	Annexin	35.95	6.86	1	31.30
Gomus.A07G073000.2	Ribulose-phosphate 3-epimerase	28.61	7.11	5	31.24
Gomus.D09G047600.1	L-iditol 2-dehydrogenase	39.07	6.58	2	31.24
Gomus.A11G043400.1	Polysaccharide biosynthesis	51.10	8.70	2	31.21
Gomus.A04G050700.1	Uroporphyrinogen decarboxylase	45.60	7.80	2	31.15
Gomus.A09G023700.1	H+-transporting ATPase	105.31	6.79	3	30.95
Gomus.A06G193300.1	Ribonuclease T2	26.30	8.90	5	30.94
Gomus.D12G279000.1	Nascent polypeptide-associated complex subunit alpha	23.80	4.45	3	30.93
Gomus.A09G220700.1	Glycine hydroxymethyltransferase	51.80	7.88	3	30.91
Gomus.A13G010800.1	GTPase, IMAP family member-related	132.13	4.91	1	30.89
Gomus.A09G047000.1	L-iditol 2-dehydrogenase	39.11	6.60	2	30.87
Gomus.D04G165200.1	Transaldolase	47.93	5.85	2	30.86
Gomus.A09G189900.1	Small subunit ribosomal protein S20e	18.50	10.04	1	30.85
Gomus.A05G373400.1	Elongation factor EF-1 alpha subunit	49.40	9.06	3	30.81
Gomus.D11G300200.1	T-complex protein 1 subunit theta	59.25	5.73	1	30.80
Gomus.D10G204000.1	ATP citrate (pro-S)-lyase	65.97	7.66	2	30.79
Gomus.D05G196300.1	T-complex protein 1 subunit beta	57.02	5.88	1	30.79
Gomus.A05G256600.1	Thioredoxin 1	20.02	7.20	2	30.70
Gomus.D11G041400.1	Glyceraldehyde 3-phosphate dehydrogenase	36.93	7.55	2	30.66
Gomus.A04G098800.1	Splicing factor 3b, subunit 4	30.25	6.62	2	30.61
Gomus.D08G003600.1	Histone H2A	15.84	10.58	1	30.59
Gomus.A01G177600.1	Triosephosphate isomerase (TIM)	33.10	6.54	3	30.52
Gomus.D08G226500.1	Pre-mRNA-splicing factor 18	46.70	8.48	1	30.51
Gomus.D09G222900.1	PAP_fibrillin	39.80	4.61	2	30.49
Gomus.A12G038900.1	E3 ubiquitin-protein ligase TRIP12	205.21	6.30	1	30.40
Gomus.A05G097100.1	HSP20 family protein	17.88	6.07	4	30.34
Gomus.D06G037700.1	Glucose-6-phosphate isomerase	67.32	5.31	1	30.34
Gomus.D06G186800.1	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase	61.56	6.61	1	30.34
Gomus.A12G150400.1	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator)	41.10	9.91	2	30.34
Gomus.A09G248900.1	PAP_fibrillin	29.97	9.38	1	30.32
Gomus.D08G080200.1	Photosystem I subunit II	22.58	9.67	4	30.30
Gomus.A01G224900.1	Monodehydroascorbate reductase (NADH)	47.10	6.02	4	30.30
Gomus.D12G064300.2	RNA-binding translational regulator IRP (aconitase superfamily)	92.05	6.35	3	30.25
Gomus.A02G064900.1	HSP20 family protein	17.60	6.07	3	30.20
Gomus.A07G247000.1	Cyclophilin type peptidyl-prolyl cis-trans isomerase	50.00	5.27	5	30.16
Gomus.A01G024500.1	Peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	28.00	9.74	2	30.09
Gomus.A10G141900.1	Glycine hydroxymethyltransferase	51.93	7.69	1	30.06
Gomus.D11G275700.1	Leucyl-tRNA synthetase	123.07	6.46	1	30.05
Gomus.A12G101500.1	F-type H+-transporting ATPase oligomycin sensitivity conferral protein	27.49	9.44	3	30.05
Gomus.A07G130700.1	Beta tubulin	46.54	4.83	1	30.01
Gomus.A08G187500.1	HSP20 family protein	28.60	5.82	2	29.90
Gomus.A11G062100.1	Uncharacterized protein	27.59	9.17	1	29.87
Gomus.D13G037400.1	Alternative splicing factor SRp20/9G8 (RRM superfamily)	17.10	8.13	2	29.83
Gomus.D12G205900.1	Translation initiation factor eIF-5A	17.35	6.20	2	29.79
Gomus.D13G113600.2	Ca2+-binding transmembrane protein LETM1/MRS7	63.46	5.26	1	29.79
Gomus.D07G123400.1	Large subunit ribosomal protein LP2	11.40	4.41	4	29.78
Gomus.D08G238600.1	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	82.17	6.14	2	29.73
Gomus.A06G157400.1	TATA-binding protein-interacting protein	134.36	5.86	1	29.71
Gomus.D07G072900.1	Betaine-aldehyde dehydrogenase	54.70	5.44	5	29.69
Gomus.A06G121100.1	Small subunit ribosomal protein S18e	17.60	10.54	3	29.69
Gomus.D05G287300.1	Cytochrome c oxidase, subunit VIb/COX12	20.30	4.39	1	29.63
Gomus.D03G072100.1	PRONE (Plant-specific Rop nucleotide exchanger)	56.12	5.20	1	29.51
Gomus.A12G063300.1	Ferredoxin--NADP+ reductase	37.76	6.92	1	29.46
Gomus.D05G076900.1	Alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	44.19	7.74	2	29.42
Gomus.A12G214100.2	HSP20 family protein	23.43	5.59	1	29.37
Gomus.D11G062200.1	Uncharacterized protein	27.62	9.17	1	29.32
Gomus.A02G118700.1	p-Nitrophenyl phosphatase	40.74	8.18	1	29.29
Gomus.A05G075000.1	Alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	44.11	7.99	2	29.24
Gomus.D04G198700.1	Inorganic pyrophosphatase	32.90	6.81	2	29.21

Gomus.D06G220700.1	Ribonuclease T2	26.30	8.78	5	29.15
Gomus.A03G001600.2	Uridine kinase	33.29	7.24	2	29.12
Gomus.A05G035200.1	Small subunit ribosomal protein S3e	26.45	9.54	2	29.08
Gomus.A03G224800.1	L-ascorbate peroxidase	31.89	7.17	3	29.06
Gomus.A09G224600.1	Isocitrate lyase	54.50	6.37	2	28.95
Gomus.D07G057100.1	Glutamate-1-semialdehyde 2,1-aminomutase	50.30	6.09	4	28.89
Gomus.A02G061000.1	GTP-binding protein SAR1	22.10	6.95	5	28.86
Gomus.D13G115800.1	Histone H2B	14.71	10.02	1	28.84
Gomus.D01G160800.1	Pathogenesis-related protein Bet v I family	17.30	5.15	5	28.82
Gomus.A05G272200.1	V-type H+-transporting ATPase subunit B	54.40	5.07	6	28.78
Gomus.A12G255000.1	6-phosphogluconate dehydrogenase	54.10	6.30	3	28.70
Gomus.A03G011900.1	Uncharacterized protein	78.32	6.05	1	28.63
Gomus.A11G194900.1	F-type H+-transporting ATPase subunit b	20.90	8.40	2	28.63
Gomus.A08G249300.1	26S proteasome regulatory subunit N12	30.90	5.01	5	28.56
Gomus.D05G039100.1	Sucrose synthase	92.60	6.54	6	28.56
Gomus.D03G171400.1	Thaumatin family	24.33	6.29	2	28.55
Gomus.D12G310800.2	Peroxin-14	57.89	5.83	1	28.53
Gomus.D01G092500.1	Trigger factor chaperone and peptidyl-prolyl cis/trans isomerase	61.57	5.40	1	28.51
Gomus.D05G089900.1	Large subunit ribosomal protein LP2	11.30	4.37	3	28.50
Gomus.A02G016000.1	O-sialoglycoprotein endopeptidase	38.55	5.82	1	28.46
Gomus.A12G264800.1	Large subunit ribosomal protein L9e	22.06	9.63	1	28.45
Gomus.D04G076900.1	Large subunit ribosomal protein LP0	34.00	5.43	5	28.44
Gomus.A10G188200.1	GTP-binding protein SAR1	22.00	8.07	5	28.39
Gomus.D05G125700.1	Uncharacterized protein	33.70	6.90	5	28.38
Gomus.D07G245000.1	Small subunit ribosomal protein S15e	17.16	10.43	4	28.38
Gomus.D12G047700.1	Elongation factor EF-1 gamma subunit	47.56	7.91	2	28.36
Gomus.D08G008800.1	Large subunit ribosomal protein LP2	11.40	4.41	3	28.30
Gomus.A05G107400.1	Eukaryotic translation initiation factor 2C	102.00	9.01	3	28.27
Gomus.A04G065900.1	Glutathione S-transferase	25.69	5.57	1	28.23
Gomus.A11G047900.1	Betaine-aldehyde dehydrogenase	54.70	5.62	2	28.19
Gomus.A13G242900.1	Tubulin alpha	49.70	5.01	3	28.10
Gomus.A02G064100.1	Small subunit ribosomal protein S1	44.56	5.14	1	28.08
Gomus.A03G083600.1	Geranylgeranyl reductase	51.10	8.87	4	28.06
Gomus.D04G014700.1	Chalcone-flavanone isomerase	23.41	4.97	1	28.04
Gomus.A10G266400.1	Ferritin heavy chain	28.10	5.99	5	27.94
Gomus.D10G121000.1	T-complex protein 1 subunit gamma	60.36	6.58	1	27.87
Gomus.D09G098000.3	HGG motif-containing thioesterase	16.71	7.58	2	27.85
Gomus.A06G158200.1	Thiamine biosynthetic enzyme	38.20	6.65	4	27.72
Gomus.D11G077500.1	Serine protease	64.36	6.54	1	27.67
Gomus.A09G232600.1	Glucose-1-phosphate adenylyltransferase	57.82	8.97	1	27.66
Gomus.D05G078200.1	Elongation factor EF-1 beta subunit	23.70	4.84	3	27.62
Gomus.A07G228700.1	Photosystem I subunit IV	15.64	9.41	4	27.54
Gomus.A12G296500.1	Glutamate decarboxylase	56.37	7.40	1	27.53
Gomus.D08G174100.1	Plasminogen activator inhibitor 1 RNA-binding protein	39.11	6.71	1	27.52
Gomus.D09G011200.2	Starch phosphorylase	110.65	6.96	1	27.51
Gomus.D07G158900.1	DYW family of nucleic acid deaminases	106.06	7.30	1	27.45
Gomus.A04G175200.1	HSP20 family protein	27.20	8.92	4	27.42
Gomus.D09G001200.1	Phosphoenolpyruvate carboxylase	110.10	6.29	5	27.37
Gomus.A12G148400.1	Photosystem II Psb27 protein	18.60	10.04	2	27.36
Gomus.A06G220200.1	Magnesium chelatase subunit I	46.30	6.24	3	27.35
Gomus.A07G175000.1	Small subunit ribosomal protein S8e	24.91	10.39	1	27.34
Gomus.D02G121700.1	Acetyl-CoA carboxylase, biotin carboxylase subunit	58.61	7.65	1	27.34
Gomus.A09G265500.1	Predicted haloacid-halidohydrolase and related hydrolases	33.85	6.55	3	27.33
Gomus.D02G029100.1	Leucine-rich repeat protein	116.06	8.27	1	27.32
Gomus.A04G030100.1	Light-harvesting complex II chlorophyll a/b binding protein 3	28.40	5.26	3	27.29
Gomus.A12G001100.1	T-complex protein 1 subunit eta	60.50	6.87	3	27.29
Gomus.A07G247000.2	Cyclophilin type peptidyl-prolyl cis-trans isomerase	49.83	5.27	1	27.27
Gomus.D12G161200.1	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator)	41.16	9.89	2	27.19
Gomus.A05G307800.1	DnaJ homolog subfamily A member 2	46.40	6.48	3	27.17
Gomus.A01G018500.1	Photosystem II Psb27 protein	18.90	9.64	2	27.17
Gomus.D05G137500.3	Myosin	72.95	7.93	1	27.14
Gomus.D06G120100.1	Aspartate aminotransferase	50.37	7.99	1	27.08
Gomus.A02G105400.1	Large subunit ribosomal protein L9e	22.10	9.55	3	27.07
Gomus.A06G168900.1	Uncharacterized protein	31.88	5.67	1	27.07
Gomus.D11G364600.1	Diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	10.01	6.07	1	27.06
Gomus.A13G257500.1	Asparagine synthase (glutamine-hydrolysing)	65.35	6.33	1	27.04
Gomus.D03G107200.1	Geranylgeranyl reductase	51.14	9.00	1	27.00
Gomus.A05G179300.1	Anthocyanidin reductase	36.30	5.76	2	26.96
Gomus.D02G075300.1	Small subunit ribosomal protein S1	44.60	5.14	4	26.96
Gomus.D05G182700.1	Protein involved in thiamine biosynthesis and DNA damage tolerance	30.17	5.14	1	26.96
Gomus.A13G246300.1	ATP-dependent RNA helicase	65.40	8.38	5	26.93
Gomus.A09G104900.1	Uncharacterized protein	12.20	9.45	3	26.93
Gomus.D07G051200.1	NADPH2: quinone reductase	34.60	7.46	2	26.92
Gomus.D10G032900.1	Guanylate-binding protein	120.50	6.61	1	26.89
Gomus.D04G193400.1	26S proteasome regulatory subunit N10	42.20	4.63	3	26.88
Gomus.D02G045000.1	Predicted hydrolase related to dienelactone hydrolase	25.62	5.59	1	26.77
Gomus.D11G160000.1	Serine carboxypeptidases (lysosomal cathepsin A)	55.00	5.10	3	26.70
Gomus.D07G100400.1	Heterogeneous nuclear ribonucleoprotein A1/A3	35.50	8.90	2	26.58
Gomus.A01G075800.1	Large subunit ribosomal protein L24	22.27	9.83	2	26.58
Gomus.D07G078700.1	Heterogeneous nuclear ribonucleoprotein A1/A3	28.30	4.79	3	26.57
Gomus.A06G161900.1	Lactoylglutathione lyase	32.48	5.96	2	26.52
Gomus.A02G072000.1	Small subunit ribosomal protein S18e	17.63	10.54	1	26.51
Gomus.D10G296000.1	Ferritin heavy chain	28.12	5.99	3	26.49
Gomus.A07G071400.2	Aldehyde dehydrogenase	51.92	5.34	1	26.43
Gomus.A09G153500.1	Pyruvate kinase	59.40	6.80	2	26.31
Gomus.D11G010600.1	Tripeptidyl peptidase II	143.99	6.28	1	26.29
Gomus.D06G160000.1	Transcription factor/CCAAT displacement protein CDP1	120.26	6.80	1	26.29
Gomus.A11G021800.1	Suppressor of tumorigenicity protein 13	45.30	5.40	2	26.19
Gomus.D07G031800.1	Outer membrane lipoprotein Blc	20.80	6.80	1	26.18
Gomus.D08G181000.1	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator)	42.50	9.72	2	26.10
Gomus.D03G070500.1	Nuclear pore complex component NPAP60L/NUP50	46.94	4.75	2	26.08
Gomus.D10G235600.1	Copper chaperone	8.70	7.94	2	26.07
Gomus.D09G275600.5	Uncharacterized protein	22.17	8.41	1	25.97
Gomus.A07G188800.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.40	4.75	1	25.95
Gomus.A03G193500.1	Multifunctional chaperone (14-3-3 family)	27.70	4.75	1	25.89
Gomus.D05G431000.1	Molecular chaperone GrpE	34.29	5.50	1	25.88
Gomus.D03G168600.1	Protease M1 zinc metalloprotease	55.20	6.14	6	25.86
Gomus.A08G063500.1	PsbP	27.00	6.65	4	25.83
Gomus.D05G097800.1	HSP20 family protein	17.88	6.07	2	25.82
Gomus.D02G221200.1	Photosynthesis system II assembly factor YCF48	45.41	8.09	3	25.81
Gomus.A11G244700.1	26S proteasome regulatory complex, ATPase RPT2	40.95	5.08	4	25.78
Gomus.D06G183000.1	F-type H+-transporting ATPase subunit gamma	41.29	6.20	3	25.76
Gomus.A06G017800.1	Uncharacterized protein	26.70	8.37	4	25.74
Gomus.A10G135200.1	Acetyl-CoA acyltransferase 1	48.79	7.72	2	25.74
Gomus.A12G284600.1	L-iditol 2-dehydrogenase	38.97	6.83	1	25.71
Gomus.D11G243300.1	Annexin	36.03	6.64	2	25.70
Gomus.A02G072900.1	Large subunit ribosomal protein L3e	44.40	10.14	2	25.68
Gomus.A08G008600.1	Large subunit ribosomal protein LP2	17.50	8.28	3	25.65
Gomus.A12G295800.1	T-complex protein 1 subunit zeta	59.00	6.61	3	25.64
Gomus.D10G238100.3	Pyruvate kinase	54.66	7.08	1	25.62
Gomus.D13G278700.1	Ubiquitin-activating enzyme E1	113.52	5.20	1	25.62
Gomus.A07G067200.1	Ketol-acid reductoisomerase	56.79	6.19	1	25.59

Gomus.D08G289100.1	Histone H3	21.90	10.84	2	25.58
Gomus.A04G013200.1	Molecular chaperone GrpE	34.27	5.85	1	25.53
Gomus.A05G250100.1	Photosystem II 22kDa protein	28.60	8.32	4	25.52
Gomus.A07G200600.1	6-phosphogluconate dehydrogenase	53.55	6.35	2	25.51
Gomus.D13G119900.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	84.82	7.31	2	25.47
Gomus.D12G225300.1	Polyadenylate-binding protein 2	25.98	4.94	1	25.45
Gomus.A02G102400.1	Acetyl-CoA carboxylase, biotin carboxylase subunit	60.20	7.62	2	25.39
Gomus.A08G163800.1	ATP-dependent Clp protease, protease subunit	31.06	6.57	1	25.39
Gomus.A12G187100.1	Zein-binding	60.40	5.71	1	25.39
Gomus.D02G095700.1	WD40-like Beta Propeller Repeat	79.04	6.83	1	25.39
Gomus.A13G059800.1	UV excision repair protein RAD23	40.50	4.84	4	25.38
Gomus.A07G219400.1	Glucose-1-phosphate adenylyltransferase	56.70	7.44	4	25.32
Gomus.D11G244700.1	Glutathione S-transferase	24.60	8.51	2	25.30
Gomus.A10G074700.1	Regulator of chromosome condensation	47.45	6.01	1	25.30
Gomus.A12G006900.1	Elongation factor EF-Tu	49.35	6.64	2	25.25
Gomus.A03G006800.2	Mitochondrial carnitine-acylcarnitine carrier protein	30.60	9.47	2	25.24
Gomus.A06G103900.1	Small subunit ribosomal protein S12e	14.70	6.62	2	25.19
Gomus.A06G013000.1	Small subunit ribosomal protein S9	22.70	10.62	4	25.19
Gomus.A11G260200.1	Leucyl-tRNA synthetase	123.08	6.21	1	25.14
Gomus.D09G031800.2	Oxidative-stress responsive protein 1	75.08	6.42	1	25.06
Gomus.D09G244900.1	Uncharacterized protein	66.18	5.71	1	25.04
Gomus.D12G129100.1	Chitinase	43.80	5.50	3	24.98
Gomus.D09G101700.1	Uncharacterized protein	30.71	4.70	1	24.98
Gomus.A01G113900.1	V-type H+-transporting ATPase subunit B	54.25	5.07	2	24.97
Gomus.A08G111000.2	Suppressor of G2 allele of SKP1	40.87	5.35	3	24.95
Gomus.D12G250600.1	TCP family transcription factor	41.06	8.75	1	24.93
Gomus.D04G069400.1	Prohibitin-like protein	33.00	9.61	4	24.91
Gomus.A07G052400.1	Calnexin	60.72	4.79	1	24.90
Gomus.D05G269500.1	Pyruvate dehydrogenase E2 component	48.32	7.47	1	24.89
Gomus.A10G173200.1	Cyanobacterial and plant NDH-1 subunit O	18.60	9.23	1	24.86
Gomus.A07G182200.1	Photosystem II cytochrome b559 subunit alpha	9.38	4.94	1	24.81
Gomus.A06G165200.1	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase	61.50	6.23	1	24.81
Gomus.A11G260800.1	Acyl carrier protein/NADH-ubiquinone oxidoreductase, NDUFAB1/SDAP subunit	14.60	5.34	2	24.80
Gomus.A05G388900.1	Mitochondrial/chloroplast ribosomal protein L12	17.49	8.35	1	24.78
Gomus.D12G309900.1	Aldehyde dehydrogenase (NAD+)	58.90	7.53	4	24.77
Gomus.A08G017800.2	Enoyl-[acyl-carrier protein] reductase I	41.50	9.04	3	24.77
Gomus.A13G132500.1	Predicted haloacid-halidohydrolase and related hydrolases	117.70	5.91	1	24.68
Gomus.D06G121000.1	Androgen induced inhibitor of proliferation (AS3) / PDS5-related	104.82	6.30	1	24.58
Gomus.A09G183300.1	26S proteasome regulatory subunit T3	44.03	5.83	1	24.52
Gomus.A11G038400.1	Malate dehydrogenase	43.03	8.02	1	24.50
Gomus.D11G256200.1	T-complex protein 1 subunit eta	60.03	7.05	2	24.48
Gomus.D05G181800.1	Anthocyanidin reductase	36.32	5.76	2	24.43
Gomus.D13G238600.1	26S proteasome regulatory subunit T6	47.05	8.90	1	24.41
Gomus.D06G013600.1	Small subunit ribosomal protein S9	22.50	10.54	4	24.37
Gomus.D01G079900.1	Large subunit ribosomal protein L24	22.20	9.77	2	24.32
Gomus.A07G077700.1	ATP-dependent Clp protease ATP-binding subunit ClpB	101.66	6.15	2	24.27
Gomus.A03G040200.1	Ubiquitin-activating enzyme E1	120.88	5.35	1	24.26
Gomus.A07G192100.1	Phosphoserine aminotransferase	46.34	7.91	2	24.25
Gomus.D04G133200.1	V-type H+-transporting ATPase subunit G	12.30	7.50	3	24.25
Gomus.A07G075400.1	40S ribosomal protein S7	20.62	9.39	1	24.23
Gomus.A05G069000.1	Uncharacterized protein	19.00	9.39	3	24.20
Gomus.A04G114800.1	Heme-binding protein-related	22.20	6.87	5	24.19
Gomus.A08G235700.1	GDP-D-mannose 3', 5'-epimerase	42.37	6.34	1	24.19
Gomus.A10G181500.1	Predicted hydrolase related to dienelactone hydrolase	25.70	5.62	1	24.15
Gomus.A03G109000.1	Photosystem II PsbH protein	7.80	6.55	1	24.12
Gomus.A04G002900.2	Stress-induced protein UVI31+	37.50	6.89	1	24.08
Gomus.A07G171200.1	Uncharacterized protein	22.34	8.34	2	24.05
Gomus.A04G130400.1	Glycyl-tRNA synthetase	82.00	7.12	3	24.05
Gomus.D04G211100.1	HSP20 family protein	27.10	8.50	3	24.05
Gomus.D06G256300.1	Uncharacterized protein	29.63	8.31	1	23.93
Gomus.A03G153700.1	ADP-ribosylation factor 1	20.64	6.95	1	23.93
Gomus.D09G227400.1	26S proteasome regulatory subunit N2	109.64	5.43	1	23.91
Gomus.A05G363800.1	V-type H+-transporting ATPase subunit C	42.70	5.77	1	23.90
Gomus.A11G359700.1	Cell division protein FtsZ	50.00	7.03	4	23.88
Gomus.A10G055100.1	20S proteasome subunit alpha 5	25.99	4.75	3	23.80
Gomus.A08G171000.1	Predicted oxidoreductase	32.30	6.28	4	23.79
Gomus.A11G278900.1	Ribose 5-phosphate isomerase A	29.70	6.93	1	23.77
Gomus.D09G277000.1	Adenylate kinase	26.70	8.10	1	23.76
Gomus.A12G245000.1	Glutathione peroxidase	25.55	8.88	1	23.75
Gomus.D09G114100.1	Uncharacterized protein	12.22	9.45	1	23.72
Gomus.D08G178500.1	Large subunit ribosomal protein L1	38.82	9.41	1	23.70
Gomus.D01G018500.1	Photosystem II Psb27 protein	18.94	9.74	1	23.69
Gomus.D07G095500.1	Large subunit ribosomal protein L13e	23.70	10.95	2	23.64
Gomus.A13G253900.1	Elongation factor EF-1 beta subunit	23.67	4.92	1	23.62
Gomus.D12G215600.1	Elongation factor EF-1 beta subunit	24.86	4.63	3	23.62
Gomus.A11G188500.1	20S proteasome subunit alpha 4	27.16	7.94	2	23.58
Gomus.A09G010600.1	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	59.14	6.79	1	23.54
Gomus.A04G049600.1	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis	46.25	7.18	2	23.48
Gomus.A08G115700.1	Photosystem II P680 reaction center D1 protein	39.20	5.24	1	23.46
Gomus.D05G069300.1	Vesicle coat complex COPI, beta subunit	105.70	5.91	1	23.41
Gomus.D05G089500.2	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	42.99	7.72	2	23.40
Gomus.D01G253900.1	Glutathione S-transferase	27.50	5.30	2	23.40
Gomus.D02G251100.1	Peptidyl-prolyl isomerase D (cyclophilin D)	41.44	6.67	1	23.38
Gomus.A12G223300.2	Heat shock protein 90kDa beta	47.31	5.45	1	23.36
Gomus.A01G210100.1	S-formylglutathione hydrolase	31.90	7.53	3	23.34
Gomus.D09G041100.1	Ubiquinol-cytochrome c reductase cytochrome c1 subunit	33.43	6.73	1	23.30
Gomus.A06G033500.2	HVA22-like proteins	46.79	9.23	1	23.30
Gomus.D09G177000.1	Heat shock 70kDa protein 1/8	64.18	5.26	3	23.29
Gomus.D13G218100.1	Membrane-associated progesterone receptor component-related	10.94	5.48	1	23.28
Gomus.D01G242100.4	Cell division protein FtsZ-related	44.60	5.62	1	23.25
Gomus.D08G067100.1	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator)	41.23	9.67	1	23.24
Gomus.D09G096200.2	Lecithin-cholesterol acyltransferase-related	72.23	6.23	1	23.22
Gomus.A07G253000.1	Protein required for fusion of vesicles in vesicular transport, alpha-SNAP	32.60	5.22	1	23.12
Gomus.A12G058300.1	Probable lipid transfer	10.05	8.72	1	23.11
Gomus.A03G039400.1	RNA-binding protein FUS	44.70	8.95	1	23.04
Gomus.D05G047200.1	Far upstream element-binding protein	68.63	6.60	1	23.02
Gomus.D01G094200.1	Small subunit ribosomal protein S8e	24.90	10.55	3	23.00
Gomus.A12G248600.1	Photosystem I P700 chlorophyll a apoprotein A2	82.35	7.24	3	22.99
Gomus.A08G155300.1	Plasminogen activator inhibitor 1 RNA-binding protein	39.00	8.12	5	22.96
Gomus.A08G064300.1	Beta-carotene dioxygenase	45.88	5.74	1	22.94
Gomus.D09G275600.1	Predicted haloacid-halidohydrolase and related hydrolases	36.80	5.76	3	22.91
Gomus.D09G011200.1	Starch phosphorylase	111.00	6.86	5	22.89
Gomus.D13G061100.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.42	4.92	1	22.89
Gomus.A03G061600.1	Universal stress protein family	17.60	6.33	2	22.84
Gomus.D07G172800.1	Oligosaccharyltransferase complex subunit delta (ribophorin II)	75.10	6.55	2	22.76
Gomus.A08G065200.2	Protein transport protein SEC31	120.20	5.49	5	22.72
Gomus.A09G020800.1	Small subunit ribosomal protein S9e	23.10	10.40	2	22.72
Gomus.A12G124800.1	Calcium-responsive transcription coactivator	22.60	6.95	2	22.69
Gomus.A11G223800.1	Kinesin (KAR3 subfamily)	142.30	6.48	3	22.68
Gomus.A04G145600.1	Light-harvesting complex II chlorophyll a/b binding protein 6	27.83	8.88	3	22.63
Gomus.D05G152800.1	Pectinesterase	63.70	8.78	3	22.63
Gomus.D05G251800.1	Photosystem II 22kDa protein	28.37	7.62	2	22.62

Gomus.A05G086400.1	Large subunit ribosomal protein L10Ae	24.52	9.86	1	22.62
Gomus.A03G063200.1	Proliferating cell nuclear antigen	29.49	4.79	2	22.59
Gomus.A03G069700.2	Acetylornithine aminotransferase	49.99	6.30	3	22.57
Gomus.A02G048800.2	RNA-binding protein Musashi	46.20	7.56	2	22.54
Gomus.A03G210200.1	Peptidyl-prolyl isomerase D (cyclophilin D)	41.43	6.74	3	22.54
Gomus.D06G085000.1	Histone-binding protein RBBP4	54.20	6.40	3	22.53
Gomus.A10G228100.2	Chorismate synthase	43.39	9.10	1	22.46
Gomus.A13G260400.1	Reductases with broad range of substrate specificities	32.10	7.77	1	22.45
Gomus.A11G153900.1	FK506-binding protein 4/5	62.73	5.35	3	22.44
Gomus.A03G170400.1	Prohibitin-like protein	32.03	9.55	1	22.41
Gomus.A03G012800.1	Large subunit ribosomal protein L19	26.99	9.70	2	22.37
Gomus.A07G242800.1	Porin/voltage-dependent anion-selective channel protein	29.40	8.76	2	22.36
Gomus.A03G223900.1	Cold shock domain containing proteins	16.20	6.30	1	22.33
Gomus.D06G171700.1	Photosystem II protein	10.56	6.95	4	22.30
Gomus.A09G024800.1	Porin/voltage-dependent anion-selective channel protein	29.50	8.73	2	22.30
Gomus.A09G001400.3	Phosphoenolpyruvate carboxylase	109.23	6.24	1	22.29
Gomus.D08G174000.1	Plasminogen activator inhibitor 1 RNA-binding protein	39.10	7.23	4	22.26
Gomus.D05G222500.1	Uncharacterized protein	16.99	4.70	2	22.26
Gomus.D02G039600.1	26S proteasome regulatory subunit N2	109.80	5.59	3	22.16
Gomus.A05G122000.1	Tyrosyl-tRNA synthetase	43.58	7.55	1	22.15
Gomus.A06G211200.1	Pyruvate dehydrogenase E2 component	58.50	7.90	3	22.14
Gomus.A08G008700.2	Large subunit ribosomal protein LP2	11.30	4.41	3	22.13
Gomus.A02G124300.2	Fructose-1,6-bisphosphatase I	37.30	6.25	3	22.12
Gomus.D08G031800.1	Phytepsin	56.12	5.36	1	22.12
Gomus.A03G130500.1	Photosystem II 10 kDa phosphoprotein	7.94	8.66	2	22.05
Gomus.A05G036100.1	Cupin	26.00	8.56	1	22.05
Gomus.D08G138400.1	Photosystem II protein	49.88	6.84	4	22.01
Gomus.D04G070900.1	2-oxoglutarate dehydrogenase E1 component	115.85	6.79	1	21.97
Gomus.A07G245700.1	Uncharacterized protein	20.02	4.82	1	21.97
Gomus.A07G164600.1	Oligosaccharyltransferase complex subunit delta (ribophorin II)	75.10	7.01	2	21.94
Gomus.A02G058100.1	Large subunit ribosomal protein L19e	24.10	11.50	2	21.93
Gomus.D02G131000.1	40S ribosomal protein S4	26.60	10.02	1	21.93
Gomus.D02G230800.1	Endosulfine	12.60	5.20	3	21.90
Gomus.D10G139600.2	Lysyl-tRNA synthetase, class II	69.09	6.47	1	21.88
Gomus.D08G208300.1	HSP20 family protein	24.71	5.86	2	21.85
Gomus.D06G019000.1	Uncharacterized protein	26.64	8.68	1	21.81
Gomus.A12G012100.1	Lipoyl synthase	17.70	9.09	1	21.80
Gomus.A05G221100.1	Uncharacterized protein	19.80	4.96	1	21.78
Gomus.A11G225300.1	Cinnamyl-alcohol dehydrogenase	39.10	6.15	3	21.77
Gomus.A01G098600.1	Myosin assembly protein/sexual cycle protein and related proteins	74.42	5.25	1	21.77
Gomus.A04G070200.1	Photosystem II 10kDa protein	14.30	9.47	1	21.76
Gomus.D07G009100.1	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	65.20	6.76	3	21.73
Gomus.A12G198800.1	Reversibly glycosylated polypeptide/UDP-arabinopyranose mutase	41.00	6.43	5	21.71
Gomus.A12G114500.1	Acetyl-CoA carboxylase carboxyl transferase subunit alpha	82.57	8.28	1	21.69
Gomus.D04G115400.1	Small subunit ribosomal protein S14e	16.40	10.70	4	21.68
Gomus.A08G053400.1	Histone H2A	14.69	10.43	1	21.60
Gomus.A09G222400.1	FK506-binding protein 4/5	63.19	5.27	2	21.52
Gomus.A06G098800.1	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	63.80	6.18	5	21.52
Gomus.A10G107900.1	Large subunit ribosomal protein L8e	28.10	10.90	1	21.50
Gomus.A07G071400.1	Betaine-aldehyde dehydrogenase	54.70	5.44	4	21.50
Gomus.1Z013400.1	Uncharacterized protein	31.82	5.87	3	21.46
Gomus.D05G348000.1	NADH-cytochrome b-5 reductase	36.10	8.18	3	21.44
Gomus.A05G301000.1	Xylose isomerase	58.30	6.10	3	21.44
Gomus.A03G193900.1	Divalent anion:Na+ symporter, DASS family	60.00	9.47	1	21.40
Gomus.A13G175500.1	Glutathione S-transferase	25.38	5.74	2	21.38
Gomus.A02G081400.1	WD40-like Beta Propeller Repeat	79.03	6.95	1	21.33
Gomus.D06G077900.1	SNW domain-containing protein 1	68.54	8.98	1	21.30
Gomus.A07G059800.1	Serine/threonine protein kinase	83.18	7.43	1	21.28
Gomus.D13G193300.1	Molecular chaperone GrpE	37.80	4.56	2	21.25
Gomus.A05G009700.1	CGTHBA protein (-14 gene protein)	129.69	5.82	1	21.23
Gomus.D07G115000.2	Sorting and assembly machinery (SAM50) protein	86.76	8.60	1	21.18
Gomus.D11G305100.1	Uncharacterized	32.26	8.05	1	21.13
Gomus.A05G090900.1	Small subunit ribosomal protein S2	23.90	9.77	1	21.11
Gomus.A04G156200.1	Translocon-associated protein subunit alpha	27.70	5.25	2	21.10
Gomus.D11G311800.1	Translation initiation factor eIF-3 subunit 10	115.52	9.38	1	21.10
Gomus.A01G176600.1	Light-harvesting complex I chlorophyll a/b binding protein 2	29.00	7.37	1	21.09
Gomus.D11G264200.1	Molecular chaperone GrpE	37.69	4.73	1	21.04
Gomus.D12G072600.1	Serine/threonine protein kinase	69.92	7.17	1	21.04
Gomus.A02G138000.1	Nuclear pore complex component NPAP60L/NUP50	52.30	5.03	2	20.97
Gomus.D13G070500.1	Succinyl-CoA synthetase alpha subunit	35.04	8.75	1	20.95
Gomus.D08G276400.1	Nascent polypeptide-associated complex subunit beta	17.61	8.32	1	20.91
Gomus.A09G196100.1	Nuclear distribution protein NUDC	32.90	5.36	2	20.91
Gomus.A13G036100.1	Alternative splicing factor SRp20/9G8 (RRM superfamily)	16.99	8.13	1	20.89
Gomus.D07G080300.1	Small subunit ribosomal protein S2e	29.60	10.27	4	20.89
Gomus.A05G395700.1	Small subunit ribosomal protein S9e	23.04	10.35	2	20.86
Gomus.A05G309100.1	NifU-like domain-containing proteins	30.31	5.10	2	20.83
Gomus.D11G003100.1	Amidases	64.65	8.40	1	20.83
Gomus.A10G053900.1	26S proteasome regulatory subunit T1	47.70	6.29	3	20.82
Gomus.D09G059900.1	Small subunit ribosomal protein S7e	22.05	9.77	2	20.82
Gomus.D13G125900.1	Uncharacterized protein	49.68	4.98	1	20.80
Gomus.A05G075000.3	Alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	44.10	7.99	3	20.76
Gomus.A08G126400.1	Nascent polypeptide-associated complex subunit alpha	23.90	4.56	1	20.75
Gomus.A09G039400.1	Ubiquinol-cytochrome c reductase cytochrome c1 subunit	33.40	6.62	3	20.73
Gomus.A05G124300.1	Uncharacterized protein	33.90	6.57	2	20.73
Gomus.D03G005500.1	Phospholipase D1	96.70	7.09	1	20.72
Gomus.A05G087800.2	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	43.17	7.33	1	20.71
Gomus.A12G133400.1	Iron-sulfur cluster scaffold protein NFU-related	24.10	6.06	1	20.67
Gomus.A07G042100.1	Uncharacterized protein	24.69	5.74	1	20.65
Gomus.A07G198600.2	Glutamine synthetase	36.35	6.80	1	20.65
Gomus.A13G145800.2	Uncharacterized protein	22.50	9.35	2	20.64
Gomus.D11G018300.1	Large subunit ribosomal protein L11	24.10	9.66	1	20.64
Gomus.A10G196700.1	Superoxide dismutase, Fe-Mn family	25.90	8.50	3	20.62
Gomus.D08G211300.1	Suppressor of tumorigenicity protein 13	42.35	5.31	2	20.61
Gomus.D01G211200.1	Inorganic pyrophosphatase	31.92	8.91	2	20.59
Gomus.A02G066900.2	Novel plant SNARE	30.28	7.25	1	20.58
Gomus.A07G183200.1	Cytochrome b6	22.77	9.29	2	20.57
Gomus.D07G237600.1	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	40.69	7.09	2	20.54
Gomus.D08G215000.1	Leucoanthocyanidin dioxygenase	40.26	5.52	1	20.52
Gomus.A11G166000.1	protein disulfide-isomerase A6	47.10	5.80	3	20.51
Gomus.A12G023400.1	D-3-phosphoglycerate dehydrogenase	63.72	7.97	1	20.51
Gomus.A05G060600.1	Aspartate aminotransferase	50.88	7.50	1	20.48
Gomus.D10G059300.1	Small subunit ribosomal protein SAe	33.05	5.15	1	20.46
Gomus.D02G067000.1	Microtubule-binding protein (translationally controlled tumor protein)	19.13	4.59	1	20.43
Gomus.D12G122400.1	Acetyl-CoA carboxylase carboxyl transferase subunit alpha	82.19	8.51	1	20.42
Gomus.A04G186400.1	Predicted DNA-binding protein, contains SAP domain	125.77	8.07	1	20.42
Gomus.D11G398000.1	Uncharacterized protein	102.19	5.74	1	20.37
Gomus.D02G141500.1	Photosystem II P680 reaction center D1 protein	17.60	5.60	1	20.36
Gomus.D10G113700.1	Uncharacterized protein	22.40	5.14	3	20.31
Gomus.A05G046300.1	Far upstream element-binding protein	69.07	6.20	1	20.28
Gomus.A06G025400.1	Adenine phosphoribosyltransferase	19.97	5.64	1	20.26
Gomus.D02G265100.1	Cold shock domain containing proteins	16.13	6.89	2	20.24
Gomus.A05G017200.1	Uncharacterized protein	33.40	5.15	1	20.21

Gomus.D02G201200.1	Large subunit ribosomal protein L15	28.65	10.89	3	20.19
Gomus.A11G330900.1	Beta-tubulin folding cofactor A	12.86	5.11	1	20.14
Gomus.A02G174500.1	Uncharacterized protein	26.27	6.81	2	20.12
Gomus.A07G177900.1	Photosystem I subunit XI	23.20	9.72	2	20.12
Gomus.D05G409700.1	Protochlorophyllide reductase	28.73	9.28	1	20.10
Gomus.A07G088700.1	Intracellular Cl- channel CLIC, contains GST domain	29.29	7.87	1	20.09
Gomus.A09G149700.3	Cell division protein FtsZ-related	41.65	6.06	1	20.06
Gomus.D05G139400.1	Photosystem I subunit VI	15.28	9.82	1	20.06
Gomus.A13G128700.1	26S proteasome regulatory subunit T5	55.90	5.33	3	20.02
Gomus.A04G152400.1	D-3-phosphoglycerate dehydrogenase, D-isomer-specific 2-hydroxy acid dehydrogenase superfamily	63.57	9.00	1	19.95
Gomus.D11G364500.1	Diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	10.21	5.55	1	19.94
Gomus.A05G433400.1	Formate--tetrahydrofolate ligase	63.76	8.22	1	19.92
Gomus.A10G043200.1	Urease accessory protein	30.60	6.76	5	19.89
Gomus.A08G009600.1	Uncharacterized protein	16.00	5.11	2	19.88
Gomus.D01G047500.1	Apoptotic ATPase	172.89	6.10	1	19.86
Gomus.1Z012200.1	Late embryogenesis abundant protein	35.17	4.77	3	19.86
Gomus.A05G155000.1	20S proteasome subunit alpha 2	25.63	5.68	1	19.84
Gomus.A08G266200.1	U4/U6 small nuclear ribonucleoprotein SNU13	13.85	7.12	2	19.79
Gomus.A13G095800.1	Ca2+-binding transmembrane protein LETM1/MRS7	85.30	6.18	2	19.78
Gomus.A13G128800.1	Microtubule-binding protein (translationally controlled tumor protein)	15.95	5.64	3	19.78
Gomus.A04G095500.1	Aquaporin PIP	25.70	6.02	1	19.77
Gomus.A07G113300.1	HSP20 family protein	18.20	6.61	2	19.73
Gomus.D07G208500.1	Ribulose-bisphosphate carboxylase	9.95	4.75	3	19.70
Gomus.A10G183600.1	Large subunit ribosomal protein L19e	24.10	11.44	2	19.68
Gomus.D13G076100.1	Soluble epoxide hydrolase	35.00	6.27	4	19.66
Gomus.D03G166500.1	40s ribosomal protein s10	20.00	9.67	2	19.64
Gomus.A13G079400.1	Uncharacterized protein	15.00	9.64	1	19.63
Gomus.D09G118800.1	Predicted alkaloid synthase/Surface mucin hemomucin	43.80	6.70	2	19.60
Gomus.A10G048800.1	20S proteasome subunit alpha 2	25.66	5.68	3	19.58
Gomus.D11G360900.1	Apoptotic ATPase	108.82	7.90	1	19.57
Gomus.A04G146400.1	Small subunit ribosomal protein S6e	28.32	10.71	1	19.55
Gomus.A05G145900.1	Pyruvate dehydrogenase E2 component	59.70	7.68	2	19.53
Gomus.A07G154800.1	Large subunit ribosomal protein L5	29.70	10.08	2	19.52
Gomus.A10G230000.3	Ypt/Rab GTPase activating protein	94.37	5.01	1	19.51
Gomus.A11G156300.1	Serine carboxypeptidases (lysosomal cathepsin A)	55.00	5.07	1	19.50
Gomus.A01G027200.1	Large subunit ribosomal protein L14e	15.70	10.15	2	19.49
Gomus.D07G200700.1	Synaptic vesicle protein EHS-1 and related EH domain proteins	133.84	5.58	1	19.48
Gomus.A11G284000.1	T-complex protein 1 subunit theta	59.30	5.73	3	19.46
Gomus.A08G222500.3	Ubiquitin activating enzyme UBA1	86.86	6.40	1	19.44
Gomus.A01G031400.2	Karyopherin (importin) alpha	58.08	5.16	2	19.41
Gomus.D03G192700.1	Mitochondrial carnitine-acylcarnitine carrier protein	30.64	9.47	1	19.31
Gomus.A09G110800.1	Ribulose-bisphosphate carboxylase	33.96	8.18	1	19.31
Gomus.A01G238300.1	Actin depolymerizing factor (cofilin)	16.10	7.24	3	19.31
Gomus.D09G072000.1	Aminoacylase ACY1 and related metalloexopeptidases	51.90	5.52	4	19.29
Gomus.A05G343600.1	Predicted carbonic anhydrase involved in protection against oxidative damage	27.84	5.68	1	19.28
Gomus.A09G131900.1	Magnesium chelatase subunit H	153.36	6.11	1	19.27
Gomus.D07G137400.1	Peptidylprolyl isomerase	35.30	6.60	2	19.27
Gomus.A06G211400.1	Protein interacting with poly(A)-binding protein	69.98	5.16	1	19.22
Gomus.A10G032900.1	Apoptosis inhibitor 5/fibroblast growth factor 2-interacting factor 2, and related proteins	61.52	8.92	2	19.21
Gomus.A10G209000.1	Cystatin family member	26.91	6.39	1	19.18
Gomus.D11G020900.1	Uncharacterized protein	27.60	5.96	2	19.18
Gomus.D13G024200.1	Chalcone isomerase	24.40	4.97	1	19.14
Gomus.D05G420900.1	Serine/threonine protein kinase	104.29	6.65	1	19.12
Gomus.A07G108700.4	NADH dehydrogenase (ubiquinone) flavoprotein 1	51.81	7.77	1	19.10
Gomus.A07G183100.1	Photosystem II PsbH protein	7.77	6.55	4	19.10
Gomus.D04G164200.1	Light regulated protein Lir1	14.44	4.64	1	19.03
Gomus.A07G157500.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	31.30	6.79	2	18.97
Gomus.A08G003800.1	Histone H2A	15.83	10.58	1	18.97
Gomus.A03G185900.1	Lipoyl synthase	17.48	8.56	1	18.97
Gomus.D11G176200.1	Glutathione S-transferase	24.80	5.66	3	18.95
Gomus.D02G058400.1	RNA-binding protein Musashi	46.17	7.06	1	18.88
Gomus.A09G148200.1	Monodehydroascorbate reductase (NADH)	46.90	6.95	3	18.87
Gomus.A07G147600.2	Large subunit ribosomal protein LP1	11.50	4.18	1	18.81
Gomus.D02G146900.1	Calcium-binding protein CML	17.99	4.64	2	18.81
Gomus.D09G240500.2	Elongation factor P	23.25	8.24	3	18.80
Gomus.D12G018800.1	Amidases	66.32	7.18	1	18.78
Gomus.A13G122100.1	Uncharacterized protein	49.80	5.07	2	18.76
Gomus.A01G225000.1	1,4-alpha-glucan branching enzyme	99.56	5.26	1	18.74
Gomus.D07G176200.2	Alcohol dehydrogenase, class III	36.63	8.15	1	18.72
Gomus.A04G118800.1	Uncharacterized protein	36.81	6.62	1	18.71
Gomus.A02G150800.1	Apoptotic chromatin condensation inducer in the nucleus	80.00	4.84	3	18.67
Gomus.A09G160000.1	Adenosine kinase	37.30	5.60	5	18.66
Gomus.D11G197700.1	Naringenin 3-dioxygenase	40.87	5.36	1	18.66
Gomus.A13G184300.1	Large subunit ribosomal protein L3	29.90	10.37	3	18.64
Gomus.D11G187200.1	2-hydroxyacyl-CoA lyase 1	60.37	6.62	1	18.63
Gomus.D02G238700.1	Protein of unknown function (DUF677)	42.96	5.87	1	18.63
Gomus.D10G184900.3	Phosphoenolpyruvate dikinase-related	63.25	5.35	2	18.58
Gomus.D06G107800.1	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	63.70	5.99	3	18.53
Gomus.D05G414100.1	Trp repressor binding protein	21.60	6.18	4	18.52
Gomus.D03G041100.1	Molecular chaperone DnaJ	47.91	9.35	1	18.50
Gomus.D02G178000.1	Plant specific mitochondrial import receptor subunit TOM20	21.91	5.62	1	18.47
Gomus.A01G031800.2	ATP citrate (pro-S)-lyase	66.10	8.25	3	18.43
Gomus.A05G205600.1	Ornithine carbamoyltransferase	41.20	7.40	3	18.40
Gomus.A03G081700.1	1-pyrroline-5-carboxylate dehydrogenase	61.47	7.42	1	18.30
Gomus.D09G091600.2	20S proteasome, regulatory subunit alpha type PSMA5/PUP2	22.08	5.01	2	18.29
Gomus.A13G267200.1	Lactoylglutathione lyase	20.94	5.91	1	18.29
Gomus.D05G034200.1	Glycylpeptide N-tetradecanoyltransferase	49.76	7.27	2	18.27
Gomus.D13G256400.3	Reductases with broad range of substrate specificities	38.73	9.29	1	18.25
Gomus.D13G269100.1	Starch phosphorylase	95.27	6.52	2	18.19
Gomus.A04G122400.1	Importin subunit beta-1	96.30	4.69	3	18.18
Gomus.A05G164400.1	Large subunit ribosomal protein L11e	20.78	9.92	2	18.16
Gomus.A06G074200.1	profilin	14.40	5.68	1	18.15
Gomus.A05G185700.1	UBX domain-containing protein 1	32.75	6.18	1	18.15
Gomus.D02G205900.1	Pyruvate dehydrogenase E1 component subunit beta	39.53	5.83	2	18.07
Gomus.D01G103800.1	Translation initiation factor IF-2	105.98	6.29	1	18.04
Gomus.D13G139700.1	Far upstream element-binding protein	80.60	4.96	4	18.00
Gomus.D07G081900.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.58	4.81	2	17.95
Gomus.A12G267500.1	Nascent polypeptide-associated complex subunit alpha	23.62	4.48	1	17.95
Gomus.D07G061500.1	Adenylate kinase	26.94	7.02	1	17.93
Gomus.D05G300500.1	Superoxide dismutase, Fe-Mn family	25.66	7.74	2	17.93
Gomus.A10G137900.1	Alkyl hydroperoxide reductase/peroxiredoxin	21.40	8.90	3	17.92
Gomus.D08G091800.1	Large subunit ribosomal protein L22e	14.00	9.58	3	17.90
Gomus.D04G062500.1	Zinc-binding oxidoreductase	34.30	5.57	3	17.86
Gomus.A07G199400.1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	80.60	6.73	2	17.83
Gomus.D06G091100.1	20S proteasome subunit alpha 1	27.28	6.32	1	17.82
Gomus.A13G205900.1	Protein of unknown function, DUF538	18.50	6.60	2	17.81
Gomus.A08G155200.1	Plasminogen activator inhibitor 1 RNA-binding protein	38.90	7.39	1	17.81
Gomus.A05G246800.1	Mitogen-activated protein kinase kinase kinase 1, plant	65.76	5.88	1	17.80
Gomus.A08G008700.1	Large subunit ribosomal protein LP2	11.32	4.41	2	17.78
Gomus.A01G155900.1	Phosphoglucomutase	63.10	5.92	2	17.77
Gomus.A03G195000.1	Peptidylprolyl isomerase	12.10	7.12	1	17.74
Gomus.D01G128800.1	20S proteasome subunit alpha 6	29.80	5.16	3	17.73

Gomus.A13G059400.1	UV excision repair protein RAD23	40.66	4.86	1	17.71
Gomus.D13G274500.2	Arsenite-resistance protein 2	77.30	8.41	1	17.65
Gomus.A05G029300.1	Profilin	14.20	5.68	1	17.58
Gomus.A12G120400.1	Chitinase	44.10	6.84	2	17.57
Gomus.A07G083600.1	Putative transcriptional regulator DJ-1	41.84	5.50	1	17.56
Gomus.A07G074600.1	Light-harvesting complex I chlorophyll a/b binding protein 4	27.80	7.44	4	17.52
Gomus.A11G183600.2	UTP--glucose-1-phosphate uridylyltransferase	51.30	6.04	4	17.52
Gomus.D10G272300.3	Uncharacterized	23.43	8.73	1	17.43
Gomus.A13G095200.3	Uncharacterized protein	21.55	9.82	1	17.39
Gomus.D04G130300.1	Transitional endoplasmic reticulum ATPase	89.50	5.29	1	17.37
Gomus.A13G145800.1	Uncharacterized protein	22.50	9.35	1	17.33
Gomus.D03G123000.1	Uncharacterized protein	45.06	9.13	2	17.29
Gomus.A11G146900.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 9	43.90	9.01	2	17.28
Gomus.A13G132200.1	20S proteasome subunit beta 7	27.80	7.53	2	17.25
Gomus.A07G060000.1	Adenylate kinase	26.90	7.42	2	17.24
Gomus.A09G083000.1	20S proteasome subunit alpha 5	25.98	4.79	2	17.24
Gomus.A06G069200.1	Aspartate aminotransferase, cytoplasmic	44.21	7.81	1	17.20
Gomus.A08G094000.2	Glutaredoxin 3	14.40	7.24	1	17.18
Gomus.A09G064000.1	Aminoacylase ACY1 and related metalloexopeptidases	51.71	5.44	1	17.18
Gomus.A02G149500.1	3R-hydroxymyristoyl ACP dehydrase	24.20	9.13	1	17.16
Gomus.D06G238000.1	Pyruvate dehydrogenase E2 component	58.24	7.75	1	17.14
Gomus.D05G334100.1	Aconitate hydratase 1	108.40	7.34	3	17.13
Gomus.D01G076800.3	Universal stress protein family	23.59	6.25	2	17.13
Gomus.A11G326000.1	Glyceraldehyde 3-phosphate dehydrogenase	45.60	8.51	1	17.13
Gomus.A08G082600.1	Histone H2A	14.80	10.48	3	17.07
Gomus.D10G122000.1	Regulator of chromosome condensation	47.80	6.20	1	17.06
Gomus.D10G228300.1	Nascent polypeptide-associated complex subunit alpha	22.90	4.53	3	17.03
Gomus.A02G102000.1	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase	67.38	7.64	1	16.99
Gomus.A05G215400.1	26S proteasome regulatory subunit N11	34.80	6.80	2	16.99
Gomus.D02G058700.1	Large subunit ribosomal protein L23e	15.00	10.39	2	16.97
Gomus.D12G006100.1	Elongation factor EF-Tu	49.50	6.55	1	16.93
Gomus.A12G056100.1	Mitochondrial F1F0-ATP synthase, subunit delta/ATP16	12.60	10.11	2	16.92
Gomus.D13G041500.1	N-acetyl-gamma-glutamyl-phosphate/N-acetyl-gamma-aminoadipyl-phosphate reductase	44.28	8.87	1	16.90
Gomus.A02G092600.2	RNA binding protein pumilio-related	41.74	7.01	1	16.89
Gomus.A06G145000.1	Predicted dehydrogenase	62.60	7.94	3	16.88
Gomus.A11G204200.1	Molybdopterin cofactor sulfurase (MOSC)	105.69	5.90	1	16.87
Gomus.D12G174700.1	Histone H1/H5	19.56	10.92	1	16.85
Gomus.D04G126700.1	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	39.74	6.10	1	16.85
Gomus.D11G042300.1	Polysaccharide biosynthesis	51.15	8.90	1	16.83
Gomus.A03G094500.1	NmrA-like family	81.08	9.52	1	16.81
Gomus.D09G033400.1	Glutaredoxin 3	11.40	7.24	3	16.78
Gomus.A09G203800.1	Small subunit ribosomal protein S10e	19.62	9.64	1	16.73
Gomus.A11G154600.1	Large subunit ribosomal protein L32e	15.60	10.51	1	16.69
Gomus.A11G311800.1	Peptidyl-prolyl cis-trans isomerase	49.89	6.44	1	16.68
Gomus.D13G078200.1	Pyruvate dehydrogenase E2 component	56.29	9.11	1	16.68
Gomus.A07G098900.1	Predicted dehydrogenase	30.90	7.78	2	16.68
Gomus.D10G092200.1	Mitochondrial phosphate carrier protein	40.60	9.29	3	16.66
Gomus.D05G360800.1	Trigger factor chaperone and peptidyl-prolyl cis/trans isomerase	23.60	9.00	3	16.64
Gomus.D13G269300.1	Proliferating cell nuclear antigen	29.45	4.75	2	16.64
Gomus.D08G210300.1	Uncharacterized	30.20	8.43	4	16.63
Gomus.A12G011400.1	Heat shock factor binding protein	9.80	4.36	2	16.62
Gomus.A09G164600.1	Uracil phosphoribosyltransferase	32.20	9.17	1	16.62
Gomus.A07G229500.1	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	40.65	7.09	2	16.62
Gomus.D04G054300.1	Cell division protease FtsH	72.89	5.88	1	16.60
Gomus.D12G010500.1	Glutathione S-transferase	24.00	6.61	2	16.59
Gomus.A05G433600.1	Formate--tetrahydrofolate ligase	68.10	7.50	1	16.58
Gomus.D07G256300.1	Cyclophilin type peptidyl-prolyl cis-trans isomerase	49.57	5.26	1	16.54
Gomus.D02G250600.1	Kinesin family member 15	348.93	5.11	1	16.52
Gomus.A01G227900.1	Large subunit ribosomal protein L24e	18.50	10.71	1	16.50
Gomus.D09G118500.1	DnaJ homolog subfamily A member 2	46.19	5.95	2	16.48
Gomus.D04G150400.1	Acetyl-CoA carboxylase carboxyl transferase subunit alpha	84.94	8.31	2	16.47
Gomus.A09G022900.1	Salt-sensitive 3'-phosphoadenosine-5'-phosphatase HAL2/SAL1	36.90	5.55	2	16.44
Gomus.D13G254800.1	ATP-dependent RNA helicase	65.40	8.38	2	16.39
Gomus.A05G271300.1	Multicopper oxidases	59.81	8.98	1	16.38
Gomus.A06G090600.1	Predicted mechanosensitive ion channel	85.20	8.94	1	16.34
Gomus.A08G280100.2	40S ribosomal protein S12	12.77	7.75	1	16.33
Gomus.A09G234100.1	Heat shock 70kDa protein 4	61.90	5.82	2	16.32
Gomus.A10G158400.1	Chitinase	29.30	7.97	2	16.28
Gomus.D09G241800.2	Glucose-1-phosphate adenylyltransferase	57.92	9.01	2	16.25
Gomus.A12G022800.1	Cinnamyl-alcohol dehydrogenase	38.70	5.55	2	16.24
Gomus.A02G056300.1	Heat shock factor binding protein	9.50	4.26	2	16.22
Gomus.A03G034500.1	Mitochondrial oxoglutarate/malate carrier proteins	31.90	9.28	2	16.20
Gomus.A12G012800.1	Putative serine/threonine protein kinase	111.40	6.86	2	16.20
Gomus.D08G018200.1	Enoyl-[acyl-carrier protein] reductase I	41.44	8.56	1	16.20
Gomus.A09G178100.1	Glutaredoxin-related protein	32.60	6.79	2	16.18
Gomus.D02G058100.1	RNA-binding protein Musashi	45.93	7.06	1	16.16
Gomus.D11G173200.1	Large subunit ribosomal protein L13e	23.70	10.77	2	16.16
Gomus.D09G258000.1	PAP_fibrillin	29.93	9.38	2	16.15
Gomus.D08G295400.1	60S ribosomal protein L31	18.00	9.79	2	16.12
Gomus.A11G295300.1	Large subunit ribosomal protein L18e	20.90	10.86	3	16.12
Gomus.A12G287500.1	Small subunit ribosomal protein S13e	17.10	10.36	1	16.08
Gomus.D11G243300.2	Annexin	33.45	6.74	1	16.05
Gomus.A04G098100.1	Translin family protein	33.70	7.83	2	16.05
Gomus.A09G070100.2	WD40 repeat stress protein/actin interacting protein	119.97	7.44	1	16.04
Gomus.A12G161900.1	Light-harvesting complex I chlorophyll a/b binding protein 2	29.23	7.81	3	16.01
Gomus.A11G331600.1	Leucine-rich repeat-containing protein	127.39	7.69	1	15.96
Gomus.D12G134000.1	Calcium-responsive transcription coactivator	22.30	6.95	1	15.94
Gomus.A08G024700.2	Valyl-tRNA synthetase	114.12	7.66	2	15.93
Gomus.A11G019100.1	Large subunit ribosomal protein L11	24.07	9.73	1	15.88
Gomus.A05G150600.1	Pectinesterase	63.63	8.78	1	15.87
Gomus.A09G237700.1	Small subunit ribosomal protein S3Ae	29.76	9.86	1	15.86
Gomus.D05G115300.1	Ran-binding protein RANBP1 and related RanBD domain proteins	24.50	5.08	1	15.82
Gomus.A07G253700.1	Glyceraldehyde 3-phosphate dehydrogenase	27.54	8.97	1	15.81
Gomus.D05G269400.1	Polyadenylate-binding protein	26.99	9.26	1	15.80
Gomus.D12G296600.1	L-iditol 2-dehydrogenase	38.90	6.46	2	15.80
Gomus.A01G002600.1	Histone-binding protein RBBP4	46.15	4.73	1	15.79
Gomus.A03G211800.1	Ferredoxin	15.46	4.60	1	15.79
Gomus.A13G010700.1	GTPase, IMAP family member-related	137.20	4.73	1	15.76
Gomus.D05G087700.1	Ferredoxin	16.10	5.15	1	15.74
Gomus.A02G136300.1	PRONE (Plant-specific Rop nucleotide exchanger)	56.11	5.16	1	15.72
Gomus.A04G111800.1	Uncharacterized protein	93.61	5.34	1	15.70
Gomus.D06G219200.1	Nascent polypeptide-associated complex subunit alpha	25.73	4.68	1	15.69
Gomus.D03G117800.1	Neoplastic transformation suppressor Pdcd4/MA-3, contains MA3 domain	78.90	5.20	4	15.67
Gomus.D03G165800.1	Mitochondrial oxoglutarate/malate carrier proteins	31.86	9.28	1	15.64
Gomus.D05G240400.1	Cytochrome c oxidase subunit Vib	19.42	4.41	2	15.63
Gomus.A02G164100.1	Glycine/serine hydroxymethyltransferase	38.65	9.26	1	15.63
Gomus.A08G127100.1	Sigma 54 modulation protein / S30EA ribosomal protein	36.02	6.81	1	15.59
Gomus.A11G076300.1	Serine protease	46.08	7.44	1	15.57
Gomus.A08G054900.6	Serine/threonine protein phosphatase	100.01	6.07	1	15.57
Gomus.A12G043500.1	Coatomer	79.24	5.72	1	15.57
Gomus.D04G082800.1	V-type H+-transporting ATPase subunit C	42.44	5.63	2	15.54
Gomus.A09G213900.2	PAP_fibrillin	38.73	4.86	2	15.52

Gomus.A03G087900.1	Uncharacterized protein	14.70	9.51	1	15.52
Gomus.A08G176600.1	Iron/ascorbate family oxidoreductases	33.08	6.73	1	15.51
Gomus.A03G135400.1	Cofactor required for Sp1 transcriptional activation, subunit 3	179.70	6.92	1	15.50
Gomus.D12G225600.1	Peptide-methionine (S)-S-oxide reductase	28.72	8.98	1	15.48
Gomus.A05G033400.1	Glycylpeptide N-tetradecanoyltransferase	49.70	7.27	2	15.48
Gomus.D06G136200.2	ATP-dependent RNA helicase	45.71	7.37	1	15.47
Gomus.D08G175900.1	Chaperonin GroES	14.80	8.68	3	15.45
Gomus.D12G157000.1	HSP20 family protein	18.01	7.50	1	15.43
Gomus.D02G141200.1	Photosystem II PsbH protein	7.83	6.55	1	15.41
Gomus.D11G165700.1	Acetyl-CoA C-acetyltransferase	41.47	6.77	1	15.37
Gomus.A07G160000.1	20S proteasome subunit beta 6	24.60	6.54	2	15.37
Gomus.A02G184200.1	Succinate dehydrogenase (ubiquinone) flavoprotein subunit	69.60	6.95	3	15.36
Gomus.A05G021400.1	26S proteasome regulatory subunit T6	47.08	8.60	1	15.34
Gomus.D05G240600.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	30.22	4.81	1	15.34
Gomus.D03G160400.3	RNA-binding protein FUS	41.66	8.79	1	15.33
Gomus.D05G325200.2	PsbP	27.23	9.36	3	15.31
Gomus.A04G043400.2	Serine/threonine kinase 24	75.69	6.96	1	15.31
Gomus.D10G028300.1	Vesicle coat protein clathrin, light chain	36.71	5.17	1	15.28
Gomus.A11G213200.2	Uncharacterized protein	18.05	9.00	1	15.26
Gomus.D13G145000.1	HSP20 family protein	20.64	5.53	1	15.22
Gomus.D08G176600.1	Protein transport protein SEC31	120.10	5.19	4	15.22
Gomus.D10G244400.1	Phosphoglucomutase/phosphomannomutase	66.50	7.68	2	15.19
Gomus.A06G203000.1	Phospholipase D1	88.23	5.67	1	15.16
Gomus.A05G109100.1	Large subunit ribosomal protein L12e	17.90	8.95	1	15.15
Gomus.D01G135800.1	Uncharacterized protein	16.60	4.58	2	15.15
Gomus.A03G182500.1	Hydroxymethylbilane synthase	40.00	6.99	3	15.14
Gomus.A04G099800.1	V-type H+-transporting ATPase subunit G	12.34	7.50	1	15.13
Gomus.D13G063500.3	Endosulfine	11.81	8.94	1	15.13
Gomus.D12G233600.1	CDK activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, kinase subunit CDK7	49.03	9.35	1	15.12
Gomus.A11G124500.1	Large subunit ribosomal protein L19e	24.43	11.40	1	15.11
Gomus.D01G266400.1	Leucine-rich repeat protein	83.00	8.02	1	15.10
Gomus.A07G077500.1	F-type H+-transporting ATPase subunit gamma	35.48	8.87	1	15.08
Gomus.A10G181500.3	Predicted hydrolase related to dienelactone hydrolase	22.23	6.19	2	15.07
Gomus.A12G031900.1	Peptide-methionine (R)-S-oxide reductase	22.59	8.85	1	15.06
Gomus.A13G206800.1	Uncharacterized protein	15.70	4.69	1	15.06
Gomus.D11G331200.4	Leucine-rich repeat-containing protein	39.54	8.69	1	15.05
Gomus.A01G102700.1	Small subunit ribosomal protein S19e	15.92	10.35	1	15.04
Gomus.A06G139700.1	Uncharacterized protein	16.48	7.72	1	15.00
Gomus.D02G066600.1	Heat shock factor binding protein	9.25	4.16	2	14.99
Gomus.D12G292500.1	CAP160 repeat	46.66	5.29	1	14.97
Gomus.A01G235800.1	Glutathione S-transferase	27.32	5.19	1	14.96
Gomus.D12G048000.1	Ras-related protein Rab-1A	22.45	5.30	3	14.92
Gomus.A05G238800.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	30.20	4.84	1	14.91
Gomus.A13G039700.1	N-acetyl-gamma-glutamyl-phosphate/N-acetyl-gamma-aminoadipyl-phosphate reductase	44.19	8.29	1	14.89
Gomus.A10G232100.1	Splicing factor 3B subunit 3	134.50	5.45	2	14.89
Gomus.D07G164100.2	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	28.00	6.79	1	14.87
Gomus.D09G129700.1	Small subunit ribosomal protein S2e	29.70	10.37	2	14.87
Gomus.D13G270600.1	Tropine dehydrogenase	30.40	6.11	1	14.87
Gomus.D08G067700.1	Carotenoid cleavage dioxygenase	61.90	6.10	3	14.86
Gomus.A06G050000.1	L-ascorbate peroxidase	45.90	7.56	3	14.85
Gomus.A11G030200.1	Ras-related protein Rab-1A	22.50	5.26	2	14.82
Gomus.D09G016100.1	Starch synthase	83.10	5.97	1	14.82
Gomus.A13G215400.1	Small subunit ribosomal protein S12e	14.65	6.62	1	14.82
Gomus.A05G075200.1	Uncharacterized protein	9.20	9.32	1	14.81
Gomus.D10G035300.1	Magnesium chelatase subunit I	46.10	6.04	1	14.76
Gomus.A03G047800.1	RNA-binding protein LARP/SRO9 and related La domain proteins	100.46	7.31	1	14.75
Gomus.A03G035600.1	Protein of unknown function (DUF2488)	24.52	5.73	1	14.72
Gomus.D04G070100.1	Intracellular Cl- channel CLIC, contains GST domain	23.46	7.44	2	14.71
Gomus.D05G166300.1	Ras-related protein Rab-11A	24.10	5.69	1	14.69
Gomus.A10G004100.1	Splicing factor 45	22.25	5.53	1	14.66
Gomus.D05G042400.1	Uncharacterized protein	24.30	5.02	2	14.60
Gomus.D05G323300.1	Large subunit ribosomal protein L10	25.40	9.36	2	14.59
Gomus.A10G117900.1	Pyruvate, orthophosphate dikinase	107.30	5.69	2	14.56
Gomus.D13G272700.2	RRM motif-containing protein	25.30	10.17	2	14.56
Gomus.A13G146200.1	Small subunit ribosomal protein S19e	15.95	10.35	1	14.56
Gomus.A05G032200.1	Histone-binding protein RBBP4	55.60	6.65	3	14.55
Gomus.D04G147400.1	Universal stress protein family	18.30	6.34	4	14.55
Gomus.A03G185500.1	Lipoic acid synthetase	41.97	8.40	1	14.54
Gomus.A06G037500.1	Uncharacterized conserved protein	107.47	5.48	1	14.53
Gomus.D09G054100.1	ATP-dependent Clp protease	25.52	9.31	1	14.51
Gomus.D04G171000.1	Thylakoid formation protein	33.79	8.41	1	14.48
Gomus.A13G269600.1	Large subunit ribosomal protein L10e	24.96	10.23	1	14.48
Gomus.A01G208200.1	Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	47.02	8.21	1	14.47
Gomus.A13G259000.2	Starch phosphorylase	95.30	6.52	2	14.46
Gomus.A04G118500.1	Pyridoxine biosynthesis protein	33.04	6.80	1	14.45
Gomus.D04G002700.1	Exocyst complex component 4	116.88	5.94	1	14.43
Gomus.A08G235100.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	37.61	6.86	1	14.42
Gomus.D11G329000.1	Uncharacterized protein	25.41	9.26	1	14.40
Gomus.A13G120700.1	Beta catenin-related armadillo repeat-containing	47.97	5.94	1	14.40
Gomus.D11G068000.1	20S proteasome subunit alpha 3	27.39	6.23	1	14.35
Gomus.A07G062000.1	Neoplastic transformation suppressor Pdcd4/MA-3, contains MA3 domain	78.90	5.17	3	14.34
Gomus.D08G065200.1	6-phosphogluconate dehydrogenase	53.37	6.48	1	14.30
Gomus.D09G279200.1	Calnexin	60.65	4.87	1	14.28
Gomus.A05G381200.1	2-oxoglutarate dehydrogenase E1 component	115.69	6.68	1	14.27
Gomus.A08G061900.1	6-phosphogluconate dehydrogenase	53.33	6.27	1	14.24
Gomus.A11G340600.1	Diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	10.00	6.07	3	14.24
Gomus.A03G001500.1	Putative serotonin transporter	60.25	8.82	1	14.22
Gomus.A05G289900.1	Large subunit ribosomal protein L3e	44.36	10.17	2	14.22
Gomus.A12G197500.1	F-type H+-transporting ATPase subunit gamma	35.60	8.98	2	14.21
Gomus.A07G087800.1	Hsp70-interacting protein Hip/Transient component of progesterone receptor complexes and an Hsp70-binding protein	46.70	5.91	2	14.21
Gomus.A01G088400.2	Microtubule-associated protein essential for anaphase spindle elongation	64.80	5.00	1	14.21
Gomus.A11G019000.4	Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	110.39	8.68	1	14.19
Gomus.D13G163700.1	Cell division protein FtsZ	43.24	7.34	2	14.18
Gomus.A13G009000.1	Protein of unknown function (DUF1118)	20.60	6.19	2	14.17
Gomus.A08G121700.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	68.41	8.27	1	14.16
Gomus.D12G032200.1	Uncharacterized protein	38.91	5.97	1	14.16
Gomus.A08G271700.1	Aspartyl aminopeptidase	51.18	6.80	1	14.16
Gomus.A07G097500.1	Heterogeneous nuclear ribonucleoprotein A1/A3	35.43	8.90	1	14.15
Gomus.D12G196400.1	Mitotic checkpoint protein MAD1	140.67	5.26	1	14.14
Gomus.D05G427800.1	Aconitase	66.61	6.20	1	14.14
Gomus.D13G148300.1	Thiosulfate/3-mercaptopyruvate sulfurtransferase	41.65	7.01	1	14.11
Gomus.D01G246400.1	Adenylosuccinate synthase	53.47	7.15	1	14.09
Gomus.D08G250500.1	Histone H2A	15.03	10.43	2	14.03
Gomus.A05G301000.3	Xylose isomerase	52.95	5.74	1	14.02
Gomus.A01G167300.1	Transporter, ABC superfamily (Breast cancer resistance protein)	78.30	8.78	2	14.02
Gomus.A13G122700.1	Prefoldin subunit 4	14.72	4.49	1	13.99
Gomus.A11G160000.1	Glucose-1-phosphate adenylyltransferase	56.60	6.47	3	13.96
Gomus.A01G193300.1	Inorganic pyrophosphatase/Nucleosome remodeling factor, subunit NURF38	31.82	8.28	1	13.96
Gomus.A01G057700.1	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis	46.40	7.83	2	13.95
Gomus.D05G421600.1	Apoptotic ATPase	84.11	8.22	1	13.93

Gomus.A05G357400.1	Large subunit ribosomal protein LP0	34.05	5.44	1	13.93
Gomus.A03G174500.1	Pre-mRNA-processing factor 6	115.32	8.18	1	13.92
Gomus.A06G060000.1	Uncharacterized protein	32.10	4.86	3	13.92
Gomus.D09G275600.3	Predicted haloacid-halidohydrolase and related hydrolases	30.87	7.31	2	13.92
Gomus.D06G053200.1	L-ascorbate peroxidase	46.10	7.56	3	13.91
Gomus.A13G167800.2	Enolase-phosphatase E-1	36.17	5.67	1	13.90
Gomus.A01G126600.1	Uncharacterized protein	16.67	4.54	1	13.89
Gomus.A07G191200.1	Large subunit ribosomal protein L13e	23.70	10.76	2	13.89
Gomus.A11G159300.1	Uncharacterized protein	18.80	9.29	1	13.88
Gomus.A04G076900.1	Photosystem I P700 chlorophyll a apoprotein A2	49.97	7.39	1	13.86
Gomus.A02G103700.1	Protein of unknown function (DUF2439)	43.34	9.38	1	13.85
Gomus.D02G221700.2	Hydroxymethylbilane synthase	30.94	5.33	1	13.85
Gomus.A05G274700.1	Transcription initiation factor IIF, small subunit (RAP30)	29.88	7.02	1	13.84
Gomus.A13G004100.1	gb def: Hypothetical protein	14.45	5.03	1	13.81
Gomus.D13G071200.1	Subgroup I aminotransferase related	36.18	6.64	1	13.79
Gomus.D06G150600.1	Uncharacterized protein	21.50	6.89	1	13.78
Gomus.A08G130800.1	V-type H+-transporting ATPase subunit E	27.15	7.01	1	13.76
Gomus.A12G021300.1	BRG-1 associated factor 60 (BAF60)	14.88	10.07	1	13.75
Gomus.A04G043900.1	Small subunit ribosomal protein S20	20.80	10.24	2	13.74
Gomus.A11G147900.1	Glutaredoxin and related proteins	19.15	8.60	1	13.74
Gomus.D11G189400.5	Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	41.49	8.43	1	13.72
Gomus.A09G032100.1	Glutaredoxin 3	11.30	7.24	1	13.69
Gomus.D10G123900.1	40S ribsomal protein S6	10.18	9.73	1	13.68
Gomus.D11G155700.2	Uncharacterized protein	26.02	9.66	1	13.65
Gomus.A11G332500.2	Apoptotic ATPase	100.06	8.03	1	13.65
Gomus.A11G126100.1	Large subunit ribosomal protein L22e	14.00	9.48	3	13.64
Gomus.D01G126800.1	Thioredoxin 1	13.26	5.20	1	13.63
Gomus.D07G185600.1	60S ribosomal protein L28	13.89	10.87	1	13.63
Gomus.D10G290100.1	Large subunit ribosomal protein LP0	34.08	5.08	1	13.63
Gomus.A12G201300.1	Sulfotransferase	38.30	6.30	1	13.62
Gomus.D10G227000.1	Cystatin family member	26.90	6.27	2	13.61
Gomus.D04G071000.1	2-oxoglutarate dehydrogenase E1 component	115.60	6.73	2	13.58
Gomus.D08G082600.1	Large subunit ribosomal protein L20	23.90	11.12	1	13.56
Gomus.A05G078700.1	Glutamine amidotransferase	27.40	5.86	1	13.52
Gomus.A03G001900.1	Uncharacterized protein	91.90	9.19	1	13.52
Gomus.A09G265600.1	Jumonji domain containing protein	182.40	8.85	1	13.51
Gomus.D05G410700.1	Uridine monophosphate synthetase	51.61	6.99	1	13.51
Gomus.D07G019500.1	Predicted membrane protein	23.40	9.42	2	13.50
Gomus.D06G164100.2	Predicted dehydrogenase	56.86	7.21	1	13.49
Gomus.D03G025600.2	Uncharacterized protein	26.38	7.12	1	13.48
Gomus.A13G157200.1	Cell division protein FtsZ	43.20	8.05	4	13.47
Gomus.A12G049100.1	Glycine cleavage system H protein	16.95	4.86	1	13.46
Gomus.D10G139800.1	Chitinase	29.34	8.21	2	13.45
Gomus.A11G006600.1	T-complex protein 1 subunit delta	64.30	8.03	1	13.44
Gomus.D02G089400.1	Alcohol dehydrogenase, class III	41.08	6.10	2	13.44
Gomus.A12G069600.2	Xaa-Pro aminopeptidase	71.22	6.11	1	13.43
Gomus.A08G216100.1	Eukaryotic translation initiation factor 2C	101.90	8.76	2	13.39
Gomus.A07G248400.1	Large subunit ribosomal protein L7/L12	19.90	5.41	2	13.39
Gomus.A01G183500.1	26S proteasome regulatory subunit N3	55.20	8.50	1	13.36
Gomus.D13G067200.1	PPR repeat	34.61	9.38	1	13.35
Gomus.A03G191600.1	Endosulfine	12.60	5.07	2	13.34
Gomus.A03G052100.1	Large subunit ribosomal protein L23Ae	17.10	10.29	3	13.34
Gomus.A05G368000.1	Mitochondrial 28S ribosomal protein S21	19.90	9.41	1	13.32
Gomus.A01G089800.1	Small subunit ribosomal protein S8e	24.90	10.55	1	13.32
Gomus.A04G080300.1	Alcohol dehydrogenase, class III	41.20	6.47	1	13.25
Gomus.A03G074400.1	Uncharacterized protein	45.20	9.22	2	13.25
Gomus.A13G140500.1	HSP20 family protein	20.70	5.73	1	13.24
Gomus.D09G206700.1	Importin subunit beta-1	95.66	4.75	1	13.23
Gomus.A08G256400.2	Aspartate kinase	91.01	6.96	1	13.21
Gomus.D06G210100.1	DnaJ homolog subfamily A member 2	46.50	6.48	2	13.20
Gomus.A08G006000.1	HSP20 family protein	17.60	6.09	2	13.19
Gomus.A11G171200.1	Glutathione S-transferase	22.39	5.31	1	13.15
Gomus.A13G175400.1	Glutathione S-transferase	25.50	7.34	2	13.14
Gomus.A05G367400.1	Plant specific mitochondrial import receptor subunit TOM20	23.00	5.12	2	13.13
Gomus.A02G034900.1	Predicted hydrolase related to dienelactone hydrolase	25.75	5.62	1	13.11
Gomus.D10G046600.2	Calcyclin binding protein	25.22	7.28	1	13.09
Gomus.D11G032100.2	Thioredoxin reductase (NADPH)	39.88	6.99	2	13.09
Gomus.D08G006200.1	HSP20 family protein	17.62	6.09	1	13.07
Gomus.D01G025800.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	37.90	8.84	1	13.07
Gomus.A09G266200.1	Nucleoside diphosphate kinase	27.40	9.61	2	13.05
Gomus.D01G227600.1	S-formylglutathione hydrolase	31.71	7.30	1	13.03
Gomus.A08G017800.1	Enoyl-[acyl-carrier protein] reductase I	41.50	9.04	1	13.02
Gomus.A09G051000.1	ATP-dependent Clp protease	25.50	9.28	2	13.01
Gomus.A10G158500.1	Lysyl-tRNA synthetase, class II	69.20	6.38	1	13.01
Gomus.D12G260100.1	Glutathione peroxidase	25.47	8.47	1	12.97
Gomus.D13G015300.1	UMP-CMP kinase	23.17	6.80	1	12.94
Gomus.D09G251800.1	Small subunit ribosomal protein S15e	17.21	10.43	2	12.92
Gomus.D11G306300.1	Aspartyl protease	44.87	8.32	1	12.92
Gomus.A07G245700.2	Uncharacterized protein	17.98	5.90	3	12.90
Gomus.D05G152600.1	Alanine transaminase	58.60	6.19	2	12.90
Gomus.A05G371300.1	Succinate dehydrogenase (ubiquinone) flavoprotein subunit	32.02	8.62	1	12.87
Gomus.A05G397400.1	Cell division protease FtsH	73.10	6.24	1	12.86
Gomus.D13G067300.1	Putative serine/threonine protein kinase	106.83	7.33	1	12.84
Gomus.A02G046800.1	Large subunit ribosomal protein L14e	15.42	10.15	1	12.84
Gomus.D06G161700.1	Ribosomal protein S7	14.01	9.72	2	12.83
Gomus.D12G143000.1	Iron-sulfur cluster scaffold protein NFU-related	24.01	6.06	2	12.83
Gomus.D07G163800.1	ATP-dependent RNA helicase DDX6/DHH1	57.10	8.40	1	12.82
Gomus.A13G253700.1	Large subunit ribosomal protein L7e	28.30	9.91	1	12.82
Gomus.D08G292400.1	Enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	78.43	9.14	1	12.81
Gomus.D09G083400.1	PAP_fibrillin	36.84	5.00	1	12.81
Gomus.A09G160100.1	Isocitrate dehydrogenase (NAD+)	40.80	6.98	2	12.80
Gomus.A06G087800.2	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	56.84	9.19	1	12.76
Gomus.A12G270100.1	Importin subunit beta-1	96.10	4.72	1	12.76
Gomus.D04G132100.1	Nucleolin	30.20	6.11	1	12.76
Gomus.D13G034000.1	Minichromosome maintenance protein 4 (cell division control protein 54)	92.87	6.55	1	12.75
Gomus.A01G120200.1	Dynactin subunit p25	29.70	6.55	1	12.75
Gomus.D07G173700.1	Succinyl-CoA synthetase beta subunit	45.20	5.91	4	12.75
Gomus.A12G138400.1	Uncharacterized protein	27.01	6.81	1	12.75
Gomus.D06G236000.1	Histone-binding protein RBBP4	51.04	6.32	1	12.74
Gomus.D10G096500.4	Cytochrome c1	30.20	5.33	2	12.74
Gomus.D05G197500.1	Thioredoxin	33.73	6.60	1	12.73
Gomus.A12G128500.1	Cupin	22.80	8.70	1	12.71
Gomus.A13G073400.1	Endosulfine	11.88	8.09	1	12.71
Gomus.A12G221200.1	Leucine-rich repeat-containing protein	43.97	5.73	1	12.70
Gomus.A10G033700.1	Magnesium chelatase subunit I	46.00	5.87	3	12.67
Gomus.A02G127400.1	Actin regulatory proteins (gelsolin/villin family)	103.89	5.50	1	12.67
Gomus.A10G057600.1	Nascent polypeptide-associated complex subunit beta	17.90	7.25	2	12.66
Gomus.D07G164400.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	33.45	5.52	1	12.66
Gomus.A13G250700.1	Nuclear cap-binding protein subunit 1	97.90	5.17	1	12.63
Gomus.A12G193900.2	Cleavage and polyadenylation specificity factor subunit 6/7	75.40	6.04	2	12.60
Gomus.A12G300300.1	Exocyst subunit - Sec10p	90.00	5.22	2	12.60
Gomus.A01G112600.1	Dehydrin	22.30	5.58	1	12.58

Gomus.D05G087900.1	Large subunit ribosomal protein L10Ae	24.55	9.86	1	12.58
Gomus.A10G220000.3	Pyruvate kinase	54.74	7.25	2	12.57
Gomus.D02G068400.1	Large subunit ribosomal protein L19e	24.08	11.44	2	12.56
Gomus.A12G209000.1	Transcriptional coactivator p100	108.56	6.49	1	12.56
Gomus.D12G020100.1	Uncharacterized	36.40	8.79	3	12.55
Gomus.D01G072100.2	Conserved WD40 repeat-containing protein	81.59	6.70	1	12.55
Gomus.A08G077900.1	Ran GTPase-activating protein 1	58.42	4.72	2	12.53
Gomus.D06G105000.1	Endonuclease/Exonuclease/phosphatase family	43.74	9.95	1	12.53
Gomus.A04G041700.1	Uncharacterized protein	30.84	10.02	1	12.48
Gomus.A02G191400.1	20S proteasome subunit alpha 4	27.10	7.43	2	12.48
Gomus.A07G107000.1	Small subunit ribosomal protein S15Ae	20.10	10.08	2	12.46
Gomus.D04G187500.1	D-3-phosphoglycerate dehydrogenase, D-isomer-specific 2-hydroxy acid dehydrogenase superfamily	63.50	8.78	3	12.45
Gomus.A09G093500.1	Uncharacterized protein	31.64	4.60	2	12.44
Gomus.D03G120700.1	Peptide-methionine (S)-S-oxide reductase	28.60	8.50	2	12.42
Gomus.A07G140600.1	Thioredoxin/protein disulfide isomerase	37.22	5.26	1	12.41
Gomus.D11G311400.1	Microtubule-binding protein (translationally controlled tumor protein)	19.08	4.67	1	12.41
Gomus.A05G269800.1	Cytochrome c	12.30	9.44	2	12.41
Gomus.D01G022800.1	Pyruvate dehydrogenase E1 component subunit beta	39.22	6.09	1	12.39
Gomus.D08G159300.1	Uncharacterized protein	17.60	9.39	1	12.37
Gomus.A04G050700.2	Uroporphyrinogen decarboxylase	45.41	7.80	1	12.37
Gomus.A07G101600.1	Large subunit ribosomal protein L32e	15.61	10.51	3	12.37
Gomus.D01G264200.1	Ran-binding protein RANBP1 and related RanBD domain proteins	24.86	4.93	1	12.34
Gomus.A07G234500.1	Histone H2A	14.70	10.32	2	12.30
Gomus.D03G188600.1	Large subunit ribosomal protein L19	27.05	9.64	1	12.29
Gomus.A12G285300.1	Phosphoglucomutase	69.30	7.72	1	12.29
Gomus.A11G184600.1	Histone 2A	10.85	10.73	1	12.28
Gomus.A05G067100.1	Vesicle coat complex COPI, beta subunit	105.60	5.73	4	12.26
Gomus.A11G277900.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	38.80	7.27	2	12.25
Gomus.D05G440900.2	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	40.54	7.71	1	12.25
Gomus.D05G273400.1	Ubiquitin-like protein, regulator of apoptosis	92.59	5.60	1	12.24
Gomus.A07G184600.1	Small subunit ribosomal protein S7	17.30	11.28	2	12.23
Gomus.A03G009100.1	Regulator of nonsense transcripts 1	137.82	6.76	1	12.21
Gomus.D08G092700.2	Large subunit ribosomal protein L18e	16.48	10.32	1	12.20
Gomus.D11G300300.2	Uncharacterized high-glucose-regulated protein	65.54	6.73	1	12.18
Gomus.D02G233400.1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	29.20	4.83	2	12.16
Gomus.A05G146900.1	HSP20 family protein	17.10	6.58	3	12.15
Gomus.A12G252100.1	Phosphoglycerate mutase	40.40	7.09	1	12.15
Gomus.A06G021800.1	Polyadenylate-binding protein (RRM superfamily)	67.95	7.77	1	12.13
Gomus.A03G222600.1	Uncharacterized protein	40.20	4.74	2	12.11
Gomus.D01G107500.1	Small subunit ribosomal protein S19e	15.90	10.35	1	12.09
Gomus.A04G078100.1	Large subunit ribosomal protein L6e	25.92	10.14	1	12.06
Gomus.A03G039800.1	Interferon, gamma-inducible protein 30	29.10	6.84	1	12.04
Gomus.A13G124700.4	Ser/Thr dehydratase, Trp synthase	24.15	9.25	1	12.04
Gomus.D05G405600.1	3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)	32.80	7.40	1	12.00
Gomus.D07G085700.1	Predicted N6-adenine methylase involved in transcription regulation	132.31	7.23	1	11.99
Gomus.A09G125900.1	Protein disulfide-isomerase A1	48.40	5.07	1	11.98
Gomus.D11G157400.1	FK506-binding protein 2	16.40	7.24	2	11.95
Gomus.D07G262900.1	Protein required for fusion of vesicles in vesicular transport, alpha-SNAP	32.60	5.22	2	11.94
Gomus.D11G397500.1	Mitochondrial F1F0-ATP synthase, subunit d/ATP7	16.85	4.89	3	11.94
Gomus.D07G095900.3	Uncharacterized protein	72.24	4.63	1	11.94
Gomus.A13G132500.2	Predicted haloacid-halidohydrolase and related hydrolases	107.09	6.15	1	11.91
Gomus.A12G042600.1	Ubiquitin fusion degradation protein 1	36.00	7.77	1	11.91
Gomus.A06G084100.1	20S proteasome subunit alpha 1	27.20	6.55	1	11.89
Gomus.A08G254400.1	ATP-dependent DNA helicase Q1	80.95	6.86	1	11.89
Gomus.A05G253100.1	Zinc finger CCCH type domain containing protein 3	235.92	8.72	1	11.89
Gomus.A12G015400.2	Endosulfine	13.00	7.24	2	11.86
Gomus.A05G343100.1	ATP synthase B/B' CF(0)	10.96	5.10	2	11.84
Gomus.A06G125100.2	Uncharacterized PHD Zn-finger protein	28.38	5.25	1	11.83
Gomus.A11G094300.6	Peroxisomal biogenesis protein (peroxin)	25.90	9.88	1	11.83
Gomus.A09G032100.2	Glutaredoxin and related proteins	10.51	7.97	1	11.83
Gomus.D08G158400.2	Chitinase	51.18	6.14	1	11.82
Gomus.D02G239000.2	Predicted dehydrogenase	55.94	6.81	1	11.82
Gomus.A05G346900.2	Trigger factor chaperone and peptidyl-prolyl cis/trans isomerase	23.40	9.23	1	11.81
Gomus.D02G239000.1	Predicted dehydrogenase	62.30	6.61	3	11.80
Gomus.A05G377600.1	Protein of unknown function (DUF3252)	25.20	7.94	1	11.79
Gomus.A03G040300.1	Ubiquitin-activating enzyme E1	128.80	5.94	1	11.79
Gomus.D04G182300.1	Uncharacterized protein	79.20	7.71	1	11.79
Gomus.D12G132600.1	Cytochrome b5	15.50	5.05	2	11.79
Gomus.D03G025600.5	Uncharacterized protein	27.30	7.55	2	11.77
Gomus.D05G428200.1	Aconitate hydratase 1	108.60	7.68	2	11.75
Gomus.A13G021600.1	Ras-related protein Rab-8A	23.62	7.81	1	11.75
Gomus.A01G010700.1	Uncharacterized protein	63.48	6.24	1	11.75
Gomus.D07G033400.4	YbaB/EbfC DNA-binding family	17.23	8.38	1	11.74
Gomus.A04G023000.1	Uncharacterized protein	19.10	5.40	2	11.74
Gomus.A04G062500.1	Alpha crystallins	15.93	7.25	1	11.73
Gomus.A03G198800.1	Protein of unknown function (DUF677)	43.03	6.07	1	11.73
Gomus.A07G186400.1	Indole-3-glycerol phosphate synthase	43.23	8.05	2	11.72
Gomus.A07G075100.2	Heterogeneous nuclear ribonucleoprotein G	23.00	9.11	1	11.71
Gomus.A01G185200.1	Geranylgeranyl diphosphate synthase, type II	37.30	5.71	1	11.69
Gomus.A07G059600.1	Argininosuccinate synthase	54.10	7.15	1	11.69
Gomus.A07G092900.1	Large subunit ribosomal protein L13e	23.69	10.86	1	11.68
Gomus.D06G121800.1	Chorismate mutase	31.30	6.55	3	11.67
Gomus.A04G148900.2	Uncharacterized protein	53.71	6.09	1	11.67
Gomus.D06G124600.1	Ubiquitin carboxyl-terminal hydrolase 36/42	78.06	6.16	1	11.66
Gomus.A12G031700.1	Predicted oxidoreductase	34.90	5.43	3	11.63
Gomus.D03G011700.1	Uncharacterized protein	17.28	9.22	1	11.62
Gomus.D04G213800.1	Probable lipid transfer	20.02	8.10	1	11.61
Gomus.A01G120100.1	20S proteasome subunit alpha 6	29.78	5.16	1	11.57
Gomus.A12G138100.2	Karyopherin (importin) alpha	44.31	5.05	1	11.57
Gomus.D09G205900.1	Nuclear distribution protein NUDC	33.01	5.17	2	11.57
Gomus.D07G053900.1	Superoxide dismutase, Fe-Mn family	35.47	4.94	1	11.55
Gomus.D09G186400.1	Glutaredoxin-related protein	32.49	6.37	2	11.53
Gomus.A12G238100.1	Calcium-binding protein CML	16.60	4.88	2	11.51
Gomus.D09G241800.1	Glucose-1-phosphate adenylyltransferase	58.60	9.03	1	11.51
Gomus.D09G233000.3	Phosphoenolpyruvate phosphomutase	50.07	7.09	1	11.51
Gomus.D13G250100.1	Uncharacterized protein	31.30	6.39	1	11.50
Gomus.A13G267800.1	Ran-binding protein RANBP1 and related RanBD domain proteins	24.08	5.08	1	11.47
Gomus.A11G089900.2	Small subunit ribosomal protein S13e	15.97	10.54	1	11.45
Gomus.D13G256400.1	Enoyl-[acyl-carrier protein] reductase I	43.10	9.25	2	11.45
Gomus.A11G281200.1	Electron transport oxidoreductase	22.43	7.01	1	11.43
Gomus.D06G037200.1	Uncharacterized protein	38.10	9.03	1	11.42
Gomus.D13G126400.1	Prefoldin subunit 4	14.73	4.49	1	11.40
Gomus.A12G193900.1	Cleavage and polyadenylation specificity factor subunit 6/7	75.38	6.04	1	11.39
Gomus.A09G043100.1	Uncharacterized protein	62.41	6.38	1	11.38
Gomus.A07G093900.1	Small ubiquitin-related modifier	10.86	5.10	1	11.37
Gomus.D12G144800.1	Uncharacterized protein	13.41	4.96	1	11.36
Gomus.A05G137700.1	Photosystem I subunit VI	15.20	9.82	2	11.35
Gomus.D11G312800.1	PUA domain protein	20.10	8.38	1	11.33
Gomus.A12G243500.1	Thaumatin family	26.40	7.14	2	11.33
Gomus.D05G302100.1	Uroporphyrinogen decarboxylase	44.80	7.91	1	11.33
Gomus.D04G153700.1	Uncharacterized protein	36.82	5.91	1	11.32
Gomus.A06G005300.1	Plant protein of unknown function (DUF869)	116.30	5.08	1	11.30

Gomus.A09G267300.1	Large subunit ribosomal protein L17e	20.10	10.26	1	11.24
Gomus.A05G402100.1	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	57.71	8.34	1	11.23
Gomus.A10G102200.1	Calcium-binding protein CML	19.30	5.08	2	11.22
Gomus.D01G168600.1	Glutamate decarboxylase	37.75	5.35	1	11.21
Gomus.A13G051700.1	Protein of unknown function (DUF677)	43.37	6.90	1	11.20
Gomus.A09G087000.1	Phospholipid:diacylglycerol acyltransferase	77.10	6.51	1	11.19
Gomus.A11G284100.1	Uncharacterized high-glucose-regulated protein	66.50	6.61	1	11.18
Gomus.A08G007200.1	Predicted K+/H+-antiporter	83.63	7.52	1	11.17
Gomus.D09G192000.1	26S proteasome regulatory subunit T3	47.10	5.85	1	11.15
Gomus.D08G163300.1	HGG motif-containing thioesterase	20.30	9.22	1	11.14
Gomus.D04G161600.1	Uncharacterized protein	12.21	8.85	1	11.13
Gomus.A01G246700.1	Ran-binding protein RANBP1 and related RanBD domain proteins	25.00	4.91	1	11.12
Gomus.A12G043300.3	Uncharacterized protein	38.90	5.77	2	11.12
Gomus.A05G194400.1	Multicopper oxidases	60.00	9.03	1	11.11
Gomus.D05G385300.1	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis	46.22	6.98	1	11.11
Gomus.A11G330300.1	Uncharacterized protein	17.21	9.70	1	11.10
Gomus.D11G127000.1	Large subunit ribosomal protein L19e	24.40	11.40	1	11.07
Gomus.A04G160300.1	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	39.60	5.53	4	11.06
Gomus.D11G122600.1	ATP-dependent Clp protease, protease subunit	33.00	7.94	1	11.04
Gomus.D03G104700.1	1-pyrroline-5-carboxylate dehydrogenase	61.40	7.61	3	11.03
Gomus.D04G065300.2	Small subunit ribosomal protein S17e	16.10	10.15	2	11.03
Gomus.A08G159400.1	Large subunit ribosomal protein L1	38.80	9.38	1	11.02
Gomus.D07G076400.1	Heterogeneous nuclear ribonucleoprotein G	22.18	9.11	1	11.00
Gomus.A05G284400.1	Cytochrome c oxidase, subunit VIb/COX12	20.34	4.35	1	11.00
Gomus.D05G185100.2	Glycosyltransferase	121.37	6.65	1	11.00
Gomus.D04G087200.1	Mitochondrial 28S ribosomal protein S21	19.97	9.66	2	10.99
Gomus.A03G199000.1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	52.10	5.62	1	10.99
Gomus.A08G056400.1	Photosystem I subunit IV	15.70	9.39	2	10.97
Gomus.A03G107800.1	Aldose 1-epimerase	36.60	7.25	1	10.96
Gomus.D07G015400.1	Uncharacterized protein	28.70	7.17	2	10.94
Gomus.A12G298500.1	Peroxin-14	57.90	5.94	1	10.93
Gomus.A10G190400.4	Uncharacterized protein	85.66	6.65	1	10.92
Gomus.A03G185600.1	Pyruvate kinase	54.90	7.52	2	10.91
Gomus.A04G087000.1	Signal recognition particle subunit SRP54	61.80	9.60	1	10.91
Gomus.A03G051800.1	Cupin	38.43	6.80	1	10.87
Gomus.D13G204900.1	Histone H1/5	22.30	10.95	1	10.86
Gomus.A11G215700.1	Large subunit ribosomal protein L30e	12.30	9.55	1	10.86
Gomus.D05G291000.1	Protein disulfide-isomerase A1	55.40	4.96	2	10.86
Gomus.D02G281200.1	Uncharacterized protein	29.10	5.01	3	10.86
Gomus.D05G276700.1	Transcription initiation factor IIF, small subunit (RAP30)	30.26	7.02	1	10.86
Gomus.A11G366100.1	40S ribosomal protein S23	15.92	10.37	1	10.85
Gomus.A12G141100.1	Large subunit ribosomal protein L22e	14.00	9.45	3	10.81
Gomus.A12G214100.1	HSP20 family protein	23.50	5.85	1	10.78
Gomus.D04G019900.1	Uncharacterized protein	28.60	5.44	1	10.78
Gomus.D10G056300.3	Plasma membrane H+-transporting ATPase	90.05	6.61	1	10.77
Gomus.A01G176200.1	20S proteasome subunit beta 5	29.10	6.23	3	10.76
Gomus.D13G272700.1	RRM motif-containing protein	25.26	10.17	2	10.75
Gomus.A11G359400.1	Small subunit ribosomal protein S14e	16.33	10.70	1	10.75
Gomus.A07G160600.1	Small subunit ribosomal protein S13e	17.11	10.39	1	10.74
Gomus.A10G117200.2	Uncharacterized protein	35.34	5.83	1	10.73
Gomus.D03G005500.2	Phospholipase D1	89.00	7.43	1	10.73
Gomus.A12G047500.1	Ras-related protein Rab-1A	22.40	5.30	2	10.70
Gomus.A03G006800.1	Mitochondrial carnitine-acylcarnitine carrier protein	30.62	9.47	2	10.69
Gomus.A01G016100.1	Prefoldin alpha subunit	17.01	7.18	1	10.68
Gomus.D01G097200.1	Cytochrome P450	26.55	6.32	1	10.66
Gomus.D08G295000.1	Aspartyl aminopeptidase	51.08	6.89	1	10.64
Gomus.A07G227200.1	Cytochrome b5	15.20	5.53	2	10.63
Gomus.A08G260800.1	Putative drug exporter of the RND superfamily	15.20	8.57	1	10.62
Gomus.D03G068200.1	Histone H2A	11.83	9.83	2	10.62
Gomus.D04G190700.1	Translocon-associated protein subunit alpha	27.77	5.26	1	10.62
Gomus.A05G160300.2	Apoptosis inhibitor 5-related	88.30	5.45	2	10.61
Gomus.A08G051400.1	HSP90 co-chaperone p23	21.00	4.58	2	10.60
Gomus.D01G149000.1	Copper chaperone	7.46	8.47	1	10.59
Gomus.A03G108600.1	Calcium-binding protein CML	18.00	4.64	2	10.59
Gomus.D11G385700.1	Small subunit ribosomal protein S14e	17.10	10.14	2	10.57
Gomus.A13G027700.1	Aspartate-semialdehyde dehydrogenase	40.70	7.80	2	10.56
Gomus.A10G154000.1	Fructokinase	35.20	5.16	3	10.56
Gomus.A05G438200.1	Hydroxyacylglutathione hydrolase	28.57	6.30	1	10.55
Gomus.A06G062400.1	Cytochrome-b5 reductase	35.70	8.81	1	10.54
Gomus.D01G254400.2	Ca2+-transporting ATPase	113.69	5.60	1	10.52
Gomus.D03G178800.1	ATP-dependent Clp protease	25.50	9.60	1	10.49
Gomus.D11G038900.1	Heterogeneous nuclear ribonucleoprotein A1/A3	28.10	4.96	2	10.49
Gomus.A05G367600.1	Copine	34.36	7.52	1	10.49
Gomus.D09G213600.1	Small subunit ribosomal protein S10e	19.54	9.58	1	10.48
Gomus.A12G280800.1	CAP160 repeat	60.30	5.31	1	10.47
Gomus.A08G008000.1	Phosphoglycerate mutase	55.80	6.43	1	10.45
Gomus.A03G053600.1	THO complex subunit 4	25.70	10.10	2	10.45
Gomus.D08G290000.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	59.22	9.28	1	10.44
Gomus.A05G255300.1	Methyltransferase	93.83	5.92	1	10.44
Gomus.A07G184000.1	Large subunit ribosomal protein L2	29.90	10.84	2	10.42
Gomus.A03G186400.1	Myotrophin and similar proteins	38.50	4.63	3	10.39
Gomus.A13G231700.1	Alba	14.70	5.34	2	10.38
Gomus.D13G279000.1	Heat shock 70kDa protein 1/8	71.31	5.26	1	10.38
Gomus.D09G263500.1	Zinc finger FYVE domain containing protein	40.37	8.91	1	10.37
Gomus.A01G234400.1	Small subunit ribosomal protein S23e	15.70	10.52	3	10.37
Gomus.D08G129900.1	Nascent polypeptide-associated complex subunit alpha	24.70	4.44	2	10.35
Gomus.D11G228900.1	Uncharacterized protein	42.63	8.73	1	10.34
Gomus.D12G277800.3	DNA mismatch repair MutS related proteins	80.55	8.69	1	10.34
Gomus.A11G198000.1	Glucose-6-phosphate 1-epimerase	34.50	6.43	1	10.33
Gomus.D13G143900.1	Phosphatidylinositol transfer protein SEC14 and related proteins	65.70	4.72	2	10.30
Gomus.A05G353600.1	Pyruvate dehydrogenase E1 component subunit alpha	43.20	7.49	1	10.30
Gomus.A13G095200.1	Uncharacterized protein	22.50	9.79	2	10.28
Gomus.A03G144200.2	Glyceraldehyde 3-phosphate dehydrogenase	27.80	9.45	1	10.28
Gomus.A07G085400.1	ATP-dependent Clp protease, protease subunit	33.71	9.01	1	10.28
Gomus.D05G102800.1	HSP20 family protein	17.70	7.42	1	10.25
Gomus.A01G040400.1	Heme-binding protein-related	25.60	4.91	1	10.24
Gomus.D12G262400.1	Phosphoglycerate mutase	39.24	7.83	2	10.24
Gomus.A01G211800.1	DnaJ homolog subfamily C member 9	32.13	7.36	1	10.23
Gomus.A13G173400.1	Large subunit ribosomal protein L13	28.00	10.05	2	10.22
Gomus.D13G145900.1	Proprotein convertase subtilisin/kexin	13.45	6.51	1	10.20
Gomus.A06G126200.1	Photosystem II protein	18.76	5.45	1	10.20
Gomus.D09G050700.1	MttA/Hcf106 family	28.50	8.10	1	10.19
Gomus.A13G061200.1	Alpha/beta hydrolase fold	25.79	6.00	1	10.17
Gomus.A12G230300.1	ATP-dependent Clp protease, protease subunit	33.50	8.78	2	10.16
Gomus.A11G101600.3	Uncharacterized protein	118.50	6.11	2	10.16
Gomus.A04G157100.1	Ubiquitin fusion degradation protein 1	35.65	6.43	1	10.14
Gomus.A08G133800.1	Sucrose synthase	92.11	6.37	1	10.14
Gomus.A05G259900.1	Large subunit ribosomal protein L3e	44.42	10.17	1	10.13
Gomus.A06G063200.1	GTP-binding nuclear protein Ran	25.10	6.93	2	10.13
Gomus.A05G236100.2	ZF-HD protein dimerisation region	27.80	7.56	1	10.13
Gomus.A12G142000.2	HSP90 co-chaperone p23	21.62	4.63	1	10.08
Gomus.A09G170100.1	Ras-related protein Rab-8A	23.80	7.83	2	10.05

Gomus.A13G209800.1	Splicing factor, arginine/serine-rich 7	21.00	11.15	1	10.04
Gomus.D04G129800.2	S-adenosylmethionine synthetase	37.43	8.68	1	10.04
Gomus.A08G191500.1	Uncharacterized protein	54.29	9.06	1	10.04
Gomus.A01G015300.1	Glutamyl-tRNA synthetase	62.40	6.90	1	10.01
Gomus.A02G089700.1	Serine/threonine protein kinase	106.94	8.18	1	10.00
Gomus.A10G068100.2	Large subunit ribosomal protein L28e	16.80	10.73	2	10.00
Gomus.D03G054500.3	Uncharacterized protein	22.56	9.74	1	10.00
Gomus.A09G225900.1	Fructokinase	35.00	5.45	3	9.99
Gomus.A07G249100.2	Mitogen-activated protein kinase kinase (MAP2K)	60.46	8.78	1	9.98
Gomus.D13G131600.2	Uncharacterized protein	23.72	7.09	1	9.96
Gomus.D01G243300.1	1,4-alpha-glucan branching enzyme	99.70	5.26	1	9.96
Gomus.D02G089300.1	Alcohol dehydrogenase, class III	41.09	6.39	1	9.95
Gomus.A08G271300.1	Profilin	12.87	5.74	1	9.94
Gomus.D03G080500.2	HIV Tat-specific factor 1	56.88	4.83	1	9.93
Gomus.A09G235200.1	Uncharacterized protein	18.58	5.64	1	9.90
Gomus.A13G015600.1	Biotin-requiring enzyme	30.70	8.59	2	9.90
Gomus.D07G056200.2	Sterol regulatory element-binding protein	31.58	8.78	1	9.90
Gomus.A11G040100.1	Heterogeneous nuclear ribonucleoprotein A1/A3	27.89	5.05	1	9.89
Gomus.A03G165300.1	2-amino-3-carboxylmuconate-6-semialdehyde decarboxylase	37.60	7.18	3	9.88
Gomus.A11G033700.1	Thioredoxin reductase (NADPH)	40.70	7.68	2	9.88
Gomus.A09G266200.2	Nucleoside-diphosphate kinase	25.96	8.85	1	9.88
Gomus.A12G263800.1	Mitochondrial import inner membrane translocase, subunit TIM13	9.37	5.36	1	9.87
Gomus.A07G141800.1	ATP-dependent Clp protease, protease subunit	32.98	7.91	1	9.87
Gomus.A05G251500.1	Molecular chaperone (DnaJ superfamily)	31.00	9.45	1	9.85
Gomus.D11G390500.1	Large subunit ribosomal protein L24e	18.49	10.71	1	9.85
Gomus.D11G126300.1	COBRA-like protein	71.70	5.34	1	9.83
Gomus.A06G108900.1	Aspartate aminotransferase	50.50	8.57	2	9.82
Gomus.A13G108000.1	Heat shock protein 90	34.04	5.00	1	9.82
Gomus.A11G047000.1	Large subunit ribosomal protein L15e	24.20	11.44	2	9.79
Gomus.A02G121700.1	Cyanobacterial and plastid NDH-1 subunit M	23.90	5.69	1	9.73
Gomus.D01G025700.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	47.50	8.66	2	9.72
Gomus.A09G218100.2	Malate dehydrogenase	33.87	6.24	1	9.71
Gomus.A11G151000.1	Cytochrome b5	14.90	5.02	2	9.70
Gomus.A05G340800.1	T-complex protein 1 subunit epsilon	59.10	5.48	2	9.69
Gomus.A07G078700.2	40S ribosomal protein S2/30S ribosomal protein S5	24.69	10.78	1	9.69
Gomus.A11G068600.1	Citrate synthase	56.18	8.16	1	9.68
Gomus.A05G437900.1	60s ribosomal protein L10	22.45	10.23	1	9.68
Gomus.A01G171100.2	T-complex protein 1 subunit epsilon	59.20	5.81	2	9.67
Gomus.D10G150300.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	37.60	6.62	3	9.66
Gomus.A07G036300.2	Chromodomain-helicase-DNA-binding protein 4	162.01	5.38	2	9.65
Gomus.D12G205500.1	mRNA cleavage factor I subunit/CPSF subunit	53.97	8.59	1	9.65
Gomus.A01G004900.1	Small subunit ribosomal protein S25e	12.00	10.59	2	9.63
Gomus.D06G137600.1	Acetyl-CoA carboxylase biotin carboxyl carrier protein	29.44	7.09	1	9.62
Gomus.D01G127300.1	Uncharacterized protein	30.63	8.85	1	9.61
Gomus.D09G118800.2	Strictosidine synthase-related	22.50	4.75	1	9.59
Gomus.D05G149000.1	HSP20 family protein	17.14	6.79	1	9.59
Gomus.D05G028700.1	Phosphoinositide-3-kinase, regulatory subunit 4, p150	173.71	7.46	1	9.57
Gomus.A04G142000.1	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit	27.40	7.15	2	9.56
Gomus.A01G078900.1	Thiamine biosynthetic enzyme	38.10	6.23	1	9.56
Gomus.D07G037500.1	Chromodomain-helicase-DNA-binding protein 4	165.34	5.39	2	9.56
Gomus.D07G054900.1	Uncharacterized conserved protein	20.42	9.52	2	9.55
Gomus.A13G136000.1	Far upstream element-binding protein	80.47	4.96	1	9.55
Gomus.D01G028800.2	Translation initiation factor eIF-2 gamma subunit	50.30	8.41	1	9.55
Gomus.A01G113000.2	Multicopper oxidases	51.13	9.79	1	9.53
Gomus.A13G175300.1	Glutathione S-transferase	20.19	8.10	1	9.53
Gomus.A05G171200.1	Dormancy/auxin associated protein	14.40	9.51	1	9.51
Gomus.A07G077100.1	Heterogeneous nuclear ribonucleoprotein A1/A3	28.05	4.77	2	9.47
Gomus.A08G094000.1	Glutaredoxin 3	14.42	7.24	1	9.46
Gomus.A11G084600.1	Ras-related protein Rab-1A	22.46	5.26	1	9.45
Gomus.A10G161300.1	Sep-tRNA:Cys-tRNA synthetase	54.81	4.72	1	9.45
Gomus.A07G133800.2	Peptidylprolyl isomerase	32.18	5.63	2	9.44
Gomus.D09G094500.1	Predicted dehydrogenase	32.79	8.50	3	9.44
Gomus.A11G153800.1	FK506-binding protein 2	16.40	6.55	2	9.44
Gomus.A07G036300.1	Chromodomain-helicase-DNA-binding protein 4	165.10	5.39	2	9.42
Gomus.A05G192100.1	Catalase	40.17	6.95	1	9.41
Gomus.D03G053000.1	Cinnamyl-alcohol dehydrogenase	39.06	6.25	1	9.37
Gomus.D13G095600.2	Uncharacterized protein	10.80	8.50	2	9.37
Gomus.D01G013900.1	Clathrin assembly protein AP180 and related proteins, contain ENTH domain	65.39	5.06	1	9.37
Gomus.A13G159400.1	Putative translation initiation inhibitor UK114/IBM1	19.50	8.82	3	9.35
Gomus.A11G042200.1	CCCH-type Zn-finger protein	52.80	5.24	1	9.35
Gomus.A03G087000.1	F-type H+-transporting ATPase subunit gamma	35.50	8.87	3	9.34
Gomus.A09G267200.1	Adenylate kinase	26.80	7.80	2	9.32
Gomus.A08G157600.1	Protein transport protein SEC31	119.50	5.30	2	9.29
Gomus.A04G159900.1	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	39.35	5.59	1	9.27
Gomus.A12G278700.1	Prolyl-tRNA synthetase	61.78	7.36	1	9.26
Gomus.D12G258700.1	Thaumatin family	26.53	7.64	1	9.25
Gomus.D03G080500.1	HIV Tat-specific factor 1	57.70	4.82	1	9.20
Gomus.A09G137800.1	PAP_fibrillin	33.30	7.12	1	9.20
Gomus.D13G077600.1	UV excision repair protein RAD23	40.60	4.78	2	9.20
Gomus.A08G124000.1	Nuclear pore complex protein Nup98-Nup96	103.20	8.28	1	9.19
Gomus.A05G331400.1	Porin/voltage-dependent anion-selective channel protein	29.62	8.63	1	9.18
Gomus.A11G138100.2	MPBQ/MSBQ methyltransferase	32.83	8.35	1	9.18
Gomus.D02G011700.1	FBD	48.55	6.73	2	9.18
Gomus.A04G136400.1	Thylakoid formation protein	33.72	8.41	1	9.18
Gomus.D05G423400.4	Apoptotic ATPase	157.43	5.74	1	9.17
Gomus.D08G004800.1	Triosephosphate isomerase (TIM)	18.22	5.87	1	9.16
Gomus.A07G059100.5	Ulp1 peptidase	19.40	9.31	1	9.14
Gomus.A11G030400.2	Serine/threonine protein kinase of the CDC7 subfamily involved in DNA synthesis, repair and recombination	77.57	9.32	1	9.14
Gomus.D05G214800.1	Serpin B	42.72	7.27	1	9.14
Gomus.D12G280300.1	6-phosphogluconolactonase	35.19	8.57	1	9.14
Gomus.A03G027500.1	Replication factor C subunit 2/4	36.82	7.33	1	9.13
Gomus.D12G215400.1	Adenylate kinase	25.09	8.40	1	9.13
Gomus.A03G006900.1	Acetylornithine deacetylase	48.00	5.40	2	9.11
Gomus.A09G223500.1	Acetylglucosaminyltransferase EXT1/exostosin 1	61.11	9.01	1	9.10
Gomus.D13G066100.1	U3 small nucleolar RNA-associated protein 19	67.88	7.87	1	9.10
Gomus.D12G293300.1	Putative steroid membrane receptor Hpr6.6/25-Dx	23.89	4.53	1	9.08
Gomus.A04G157100.2	Ubiquitin fusion degradation protein 1	35.60	6.43	1	9.08
Gomus.D09G217100.1	Calmodulin and related proteins (EF-Hand superfamily)	16.22	5.02	1	9.08
Gomus.A09G059900.1	Preprotein translocase subunit YidC	56.36	8.94	1	9.06
Gomus.A12G133600.1	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15/PRP43	82.60	7.33	2	9.05
Gomus.A07G029800.1	Methyltransferase	29.86	5.69	1	9.05
Gomus.D03G110500.1	F-type H+-transporting ATPase subunit gamma	35.60	8.87	1	9.03
Gomus.A10G230000.1	Ypt/Rab GTPase activating protein	96.50	5.00	1	9.03
Gomus.A03G125500.1	Splicing factor 3A subunit 1	90.11	5.05	1	9.03
Gomus.A12G046300.3	Plant transposase (Ptta/En/Spm family)	107.92	9.17	1	9.02
Gomus.D07G151000.1	Translation initiation factor 5A-related	6.76	5.36	1	9.02
Gomus.A01G208400.1	Alpha-N-arabinofuranosidase	74.65	5.26	1	9.00
Gomus.D13G136500.1	ADP-ribosylation factor 1	20.68	8.46	2	8.99
Gomus.A08G269200.1	Enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	78.40	9.23	2	8.98
Gomus.D03G017000.1	Protein of unknown function (DUF677)	25.88	9.29	1	8.98
Gomus.D11G394000.2	50S ribosomal protein L15	29.22	10.70	1	8.98
Gomus.A05G206200.1	ZF-HD protein dimerisation region	32.71	8.53	1	8.95

Gomus.A10G225200.1	Apoptotic ATPase	89.14	6.68	1	8.95
Gomus.A11G363600.1	Calmodulin and related proteins (EF-Hand superfamily)	16.18	5.14	1	8.94
Gomus.A09G038700.1	Prohibitin	30.80	8.78	2	8.92
Gomus.A05G102300.1	Thaumatin family	26.60	7.97	1	8.92
Gomus.A06G174900.1	Predicted K+/H+-antiporter	90.31	8.43	1	8.91
Gomus.A11G249400.1	Glutathione S-transferase	25.30	5.95	2	8.90
Gomus.D08G147800.1	Heat shock factor binding protein	9.80	4.36	2	8.89
Gomus.D03G054300.1	Uncharacterized protein	13.50	6.80	1	8.88
Gomus.D04G066000.1	Sucrase/ferredoxin-like	44.40	6.79	2	8.84
Gomus.A12G134700.1	ATP-dependent Clp protease, proteolytic subunit	34.30	8.32	1	8.83
Gomus.A11G190000.1	Uncharacterized protein	37.28	4.61	1	8.82
Gomus.A12G027700.1	Uncharacterized protein	50.10	7.55	1	8.82
Gomus.D05G017200.1	Uncharacterized protein	34.90	5.05	1	8.79
Gomus.A11G067800.1	20S proteasome subunit alpha 3	27.40	7.09	1	8.78
Gomus.A06G096800.1	Thioredoxin-like protein	22.65	5.29	1	8.77
Gomus.A10G031600.1	Actin filament-coating protein tropomyosin	120.70	6.76	2	8.76
Gomus.D04G145300.1	Aldo/keto reductase family proteins	35.80	6.29	2	8.76
Gomus.A02G194200.1	Phospholipase D1	96.80	7.15	1	8.76
Gomus.D12G064900.1	Cellular nucleic acid-binding protein	25.47	7.09	1	8.74
Gomus.D13G012400.1	GTPase, IMAP family member-related	137.10	4.70	3	8.73
Gomus.D03G122900.1	Serine/threonine protein kinase	76.75	8.13	1	8.73
Gomus.D09G071400.1	Asparagine synthetase	27.10	6.79	1	8.72
Gomus.A08G060100.1	Aminocyclopropanecarboxylate oxidase	35.90	5.41	3	8.71
Gomus.A03G141600.1	Plant specific mitochondrial import receptor subunit TOM20	21.90	5.41	2	8.69
Gomus.A13G221800.1	Predicted alkaloid synthase/Surface mucin hemomucin	39.40	5.39	1	8.69
Gomus.A01G204100.1	Photosystem II	28.40	7.87	2	8.68
Gomus.A06G155600.1	Small subunit ribosomal protein SAe	34.10	5.16	2	8.68
Gomus.A01G249800.1	Small subunit ribosomal protein S4e	29.50	10.26	3	8.67
Gomus.A06G038800.1	Small subunit ribosomal protein S6e	28.30	10.71	2	8.67
Gomus.A04G174000.1	Large subunit ribosomal protein L27Ae	16.30	10.56	1	8.66
Gomus.A13G141400.1	Proprotein convertase subtilisin/kexin	13.60	6.51	1	8.66
Gomus.A12G249000.1	Photosynthetic reaction centre protein	32.84	6.86	1	8.66
Gomus.D04G175200.2	Serine/threonine specific protein phosphatase involved in cell cycle control, PP2A-related	30.46	5.17	1	8.65
Gomus.D03G155400.1	ATP-binding cassette, sub-family F, member 2	66.80	6.68	1	8.64
Gomus.A12G027800.1	Ferredoxin	14.80	4.70	1	8.63
Gomus.D05G291100.4	Proteasome subunit alpha/beta	15.22	9.54	1	8.62
Gomus.D12G185800.1	Histone H1/H5	45.01	10.61	1	8.62
Gomus.A02G101600.1	Uncharacterized protein	17.70	8.69	1	8.62
Gomus.D12G028400.1	Uncharacterized protein	50.05	7.85	1	8.61
Gomus.D12G253000.1	ATP-dependent Clp protease, protease subunit	31.00	9.33	2	8.61
Gomus.A09G184200.1	1-deoxy-D-xylulose-5-phosphate reductoisomerase	51.20	6.21	2	8.57
Gomus.A10G056100.1	Histone H3	8.46	9.82	1	8.56
Gomus.D04G039900.1	Uncharacterized conserved protein, contains PCI domain	46.21	5.24	1	8.56
Gomus.A11G047000.2	60s ribosomal protein L15	22.08	11.63	1	8.56
Gomus.A06G001400.1	Thioredoxin	26.90	8.66	2	8.54
Gomus.D11G183700.2	Poly(A)-specific exoribonuclease PARN	77.32	9.66	1	8.54
Gomus.A02G041000.1	MPBQ/MSBQ methyltransferase	39.00	9.26	1	8.53
Gomus.A03G185400.1	Uncharacterized protein	38.00	6.04	1	8.53
Gomus.D13G166400.1	Putative translation initiation inhibitor UK114/IBM1	19.50	8.56	3	8.51
Gomus.A10G171200.1	U2 small nuclear ribonucleoprotein A'	32.10	5.06	2	8.51
Gomus.D06G209800.1	Glycosyltransferase	42.95	6.04	2	8.51
Gomus.D04G186100.1	ATP-dependent Clp protease, protease subunit	42.42	8.75	1	8.50
Gomus.D04G086500.1	Plant specific mitochondrial import receptor subunit TOM20	23.09	5.26	1	8.50
Gomus.D07G268700.1	Leucine rich repeat proteins, some proteins contain F-box	64.25	7.91	1	8.49
Gomus.D10G256600.1	26S proteasome regulatory complex, subunit PSMD10	60.77	8.91	1	8.48
Gomus.D05G062500.1	Aspartate aminotransferase	51.30	8.56	3	8.48
Gomus.D13G000700.1	Zinc-binding protein of the histidine triad (HIT) family	16.90	6.79	1	8.48
Gomus.A04G011300.1	Small subunit ribosomal protein S8e	23.97	10.43	1	8.47
Gomus.A05G056700.1	Serine/threonine protein kinase	99.24	6.47	1	8.47
Gomus.A10G073600.1	Ferredoxin	21.40	8.09	1	8.47
Gomus.D12G135100.1	Large subunit ribosomal protein LP1	11.43	4.09	1	8.46
Gomus.D07G046900.1	Small subunit ribosomal protein S20e	13.67	9.67	2	8.46
Gomus.A08G027700.1	Uncharacterized protein	25.50	9.41	2	8.44
Gomus.A09G075000.1	Transcriptional adapter 2-alpha	62.15	6.55	1	8.44
Gomus.D02G166100.1	Nuclear pore complex protein Nup155	163.30	5.85	2	8.43
Gomus.D05G095800.1	Thylakoid soluble phosphoprotein TSP9	10.40	9.66	2	8.41
Gomus.A01G250500.1	Phenylpyruvate tautomerase	12.14	8.10	1	8.41
Gomus.A04G161500.1	Ubiquilin	58.70	4.83	2	8.39
Gomus.A05G238500.1	Cytochrome c oxidase subunit Vib	19.32	4.45	1	8.39
Gomus.D01G085100.1	Uncharacterized protein	19.01	5.68	2	8.38
Gomus.D03G008300.1	20S proteasome subunit alpha 4	27.20	7.43	2	8.38
Gomus.D05G092800.1	Large subunit ribosomal protein L9	21.87	9.72	1	8.37
Gomus.A05G172200.1	Small subunit ribosomal protein S5	34.30	8.48	1	8.37
Gomus.A07G072900.1	Xyloglucan fucosyltransferase	66.90	6.24	1	8.37
Gomus.D01G224100.1	Transcription factor HEX, contains HOX and HALZ domains	32.31	8.82	1	8.36
Gomus.A01G207500.1	KH domain containing RNA binding protein	31.00	9.22	1	8.33
Gomus.A13G260100.1	Short chain dehydrogenase	16.09	6.14	2	8.33
Gomus.A07G069800.1	Guanine nucleotide-binding protein subunit beta-2-like 1 protein	36.00	7.44	1	8.30
Gomus.D11G104800.1	Late embryogenesis abundant protein	16.40	5.02	2	8.30
Gomus.A04G090300.2	mRNA cleavage and polyadenylation factor I/II complex, subunit Pcf11	108.77	6.79	1	8.29
Gomus.A01G203500.1	Aminoacylase	48.10	5.52	1	8.27
Gomus.A10G053600.1	H+-transporting ATPase	104.90	5.83	2	8.27
Gomus.A02G170200.1	Large subunit ribosomal protein L26e	16.70	10.90	1	8.27
Gomus.A08G227200.1	Translation initiation factor eIF-3 subunit 10	115.20	9.47	2	8.26
Gomus.A09G147000.4	Enolase	31.03	5.35	1	8.23
Gomus.D08G226300.1	Chalcone isomerase	32.31	9.10	1	8.23
Gomus.A04G000500.1	PPR repeat	95.46	7.64	1	8.22
Gomus.A09G033900.1	Heterogeneous nuclear ribonucleoprotein A1/A3	38.60	7.66	1	8.20
Gomus.D05G150900.1	Proprotein convertase subtilisin/kexin	81.30	6.83	1	8.19
Gomus.D02G099500.1	Uncharacterized protein	170.69	5.02	1	8.18
Gomus.A09G098800.1	Cis-prenyltransferase, dehydrodolichyl diphosphate synthase	35.10	5.95	2	8.18
Gomus.A07G179200.2	GDP-mannose pyrophosphorylase/mannose-1-phosphate guanylyltransferase	50.21	7.50	1	8.16
Gomus.D02G146000.1	Aldose 1-epimerase	36.58	7.53	1	8.16
Gomus.D12G263600.1	Monodehydroascorbate reductase (NADH)	57.50	8.63	1	8.16
Gomus.D08G182900.1	ATP-dependent Clp protease, protease subunit	31.04	6.24	1	8.14
Gomus.A09G198400.1	Large subunit ribosomal protein LP1	11.30	4.28	1	8.13
Gomus.A05G424300.1	Regulator of ribonuclease activity A	17.77	5.88	1	8.12
Gomus.A09G071900.1	Dihydrolipoamide dehydrogenase	60.10	8.28	2	8.11
Gomus.A13G263100.1	Ras-related protein Rab-8A	23.60	7.81	1	8.10
Gomus.D02G218100.1	Universal stress protein family	31.70	5.80	1	8.10
Gomus.A07G236500.1	Small subunit ribosomal protein S15e	7.78	11.00	1	8.10
Gomus.A08G132200.1	OTU (ovarian tumor)-like cysteine protease	36.10	6.13	1	8.09
Gomus.A08G235600.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	37.30	6.74	2	8.09
Gomus.A05G086200.1	Ferredoxin	16.10	5.15	1	8.07
Gomus.A03G031700.1	AP-1 complex subunit beta-1	100.00	5.12	3	8.06
Gomus.A10G117200.1	Uncharacterized protein	35.50	5.83	2	8.06
Gomus.A04G113300.1	Universal stress protein family	16.10	6.32	1	8.06
Gomus.A05G092800.1	Light-harvesting complex I chlorophyll a/b binding protein 1	26.80	6.68	3	8.04
Gomus.D05G005700.1	Small nuclear ribonucleoprotein F	9.80	4.54	1	8.04
Gomus.A05G308400.1	Uncharacterized protein	12.24	9.41	1	8.03
Gomus.D08G274200.1	Isopentenyl-diphosphate delta-isomerase	34.20	6.54	2	8.02
Gomus.A10G224500.1	Ras-related protein Rab-5C	21.90	7.14	1	8.02

Gomus.A06G073100.1	Predicted dehydrogenase	35.60	8.66	1	8.01
Gomus.D12G029300.1	Vesicle coat complex COPI, gamma subunit	98.14	5.24	1	8.01
Gomus.D12G153100.2	Myosin class V heavy chain	107.82	7.06	1	7.99
Gomus.A03G106700.1	Dihydroxyacetone kinase	61.74	5.41	1	7.99
Gomus.A13G114300.1	Histone H2B	14.79	10.05	1	7.98
Gomus.D07G155200.1	Cytochrome b5	15.50	4.82	1	7.97
Gomus.D02G014600.1	Tam3-transposase (Ac family)	91.00	6.14	1	7.96
Gomus.D11G096200.1	Peroxisomal biogenesis protein (peroxin)	25.90	9.82	1	7.95
Gomus.A11G307700.1	(+)-delta-cadinene synthase.	65.05	5.80	1	7.94
Gomus.A12G254100.1	Reticulon	28.40	8.81	1	7.94
Gomus.D08G210300.2	Uncharacterized	24.09	6.05	1	7.92
Gomus.D05G338600.1	Nuclear transport factor 2	13.40	6.11	1	7.91
Gomus.A06G080700.1	Ser/Thr dehydratase, Trp synthase	53.41	8.00	1	7.91
Gomus.A13G149600.2	Nuclear AAA ATPase (VCP subfamily)	88.12	6.68	1	7.90
Gomus.A02G001800.1	Uncharacterized protein	36.62	9.31	1	7.90
Gomus.A07G133600.1	Cytochrome P450, family 75, subfamily A (flavonoid 3',5'-hydroxylase)	57.30	9.06	1	7.89
Gomus.D10G160500.1	Alkyl hydroperoxide reductase/peroxiredoxin	21.30	8.35	3	7.88
Gomus.A05G217100.1	Weak chloroplast movement under blue light	101.40	5.48	1	7.88
Gomus.A08G037000.1	Predicted RNA-binding protein	27.94	5.19	1	7.87
Gomus.A02G086000.1	Enoyl-CoA hydratase	28.90	9.17	1	7.86
Gomus.D10G199300.2	Photosystem II Pbs27	22.20	9.09	1	7.86
Gomus.A09G205600.1	Translation initiation factor eIF-2 alpha subunit	38.50	5.27	2	7.86
Gomus.D12G240700.1	Ferredoxin	21.16	7.09	1	7.86
Gomus.D08G146100.1	KIP1-like protein	26.42	8.21	1	7.84
Gomus.A04G153000.1	Small subunit ribosomal protein S16e	16.60	10.24	1	7.84
Gomus.A05G158700.1	Large subunit ribosomal protein L18Ae	21.40	10.42	1	7.83
Gomus.A12G067400.1	Inorganic pyrophosphatase	24.17	6.15	1	7.83
Gomus.D05G385700.1	Uncharacterized protein	45.90	9.41	1	7.82
Gomus.A05G057700.1	ATP-dependent RNA helicase UAP56/SUB2	48.46	5.64	1	7.81
Gomus.D09G006500.1	AMP-activated protein kinase, gamma regulatory subunit	57.20	7.43	3	7.80
Gomus.D08G063500.1	Coproporphyrinogen III oxidase	44.20	6.95	2	7.80
Gomus.A05G296700.1	Large subunit ribosomal protein L10e	25.00	10.32	1	7.80
Gomus.D10G185800.1	Uncharacterized protein	35.60	5.66	2	7.80
Gomus.A05G268300.1	Serine/threonine protein kinase	107.85	7.15	1	7.79
Gomus.D13G025100.1	Leukotriene-A4 hydrolase	70.10	6.07	1	7.77
Gomus.A07G025400.1	profilin	12.79	4.75	1	7.77
Gomus.D08G024400.1	Cell membrane glycoprotein	35.44	4.40	1	7.75
Gomus.A13G059700.2	Nucleotide excision repair factor NEF2, RAD23 component	38.85	4.67	1	7.75
Gomus.A09G093100.1	Ubiquinol-cytochrome c reductase cytochrome c1 subunit	34.16	6.99	1	7.74
Gomus.D13G259200.1	Nuclear cap-binding protein subunit 1	98.00	5.20	1	7.73
Gomus.A11G145900.1	MYB-CC type transfactor, LHEQLE motif	52.60	5.88	1	7.72
Gomus.A10G131500.1	Asparagine synthetase	27.10	6.21	1	7.71
Gomus.D10G045600.1	Outer membrane protein, OmpA-related	13.15	6.89	1	7.70
Gomus.A05G044700.2	UDP-sulfoquinovose synthase	53.50	8.54	1	7.69
Gomus.A04G080300.2	Alcohol dehydrogenase, class III	37.76	6.46	1	7.69
Gomus.A05G190700.1	Uncharacterized protein	19.68	9.25	1	7.67
Gomus.D13G010700.1	Protein of unknown function (DUF1118)	20.53	6.19	2	7.66
Gomus.D08G294900.1	Mitochondrial processing peptidase	54.30	6.32	2	7.65
Gomus.A12G085800.2	Peptidylprolyl isomerase	23.10	9.38	2	7.65
Gomus.A05G126200.1	Uncharacterized protein	47.10	6.30	1	7.65
Gomus.A12G225400.1	Ferredoxin	21.10	6.84	1	7.64
Gomus.A13G163300.1	Photosystem II oxygen-evolving enhancer protein 3	25.20	9.36	1	7.64
Gomus.A06G035700.1	Glucose-6-phosphate isomerase	67.40	5.48	1	7.62
Gomus.D09G145300.1	PAP_fibrillin	33.27	7.12	1	7.62
Gomus.A08G112400.2	Uncharacterized protein	86.51	4.59	1	7.61
Gomus.A10G064700.1	Predicted dehydrogenase	37.90	8.91	2	7.61
Gomus.D01G244000.1	Fructose-bisphosphate aldolase, class I	38.53	6.99	1	7.60
Gomus.A08G282000.1	Late embryogenesis abundant protein	24.78	4.79	1	7.57
Gomus.D08G158100.3	Uncharacterized protein	11.95	7.50	1	7.57
Gomus.D06G250100.9	LisH motif-containing protein	22.62	4.65	1	7.56
Gomus.D03G042500.1	Predicted haloacid-halidohydrolase and related hydrolases	35.80	5.95	1	7.56
Gomus.A05G194000.1	Dehydrin	23.77	5.05	2	7.54
Gomus.A07G178100.1	Large subunit ribosomal protein L5e	34.30	9.47	1	7.53
Gomus.A13G211900.1	Transcription factor MEIS1 and related HOX domain proteins	48.60	6.42	1	7.52
Gomus.A03G078400.1	26S proteasome regulatory subunit N7	44.60	5.68	1	7.51
Gomus.A04G151100.1	ATP-dependent Clp protease, protease subunit	42.40	8.75	2	7.51
Gomus.D05G080500.1	Glutamine amidotransferase	27.35	5.86	2	7.51
Gomus.A05G307100.1	Fe-S cluster assembly ATP-binding protein	35.30	6.37	1	7.47
Gomus.D07G085600.1	Putative transcriptional regulator DJ-1	41.84	5.73	1	7.47
Gomus.A03G222700.1	5'-methylthioadenosine nucleosidase	28.20	5.08	2	7.47
Gomus.A07G062000.2	Neoplastic transformation suppressor Pdcd4/MA-3, contains MA3 domain	72.58	5.22	1	7.46
Gomus.D05G103500.1	Thaumatin family	26.57	7.97	1	7.46
Gomus.A13G263100.2	GTP-binding protein SEC4, small G protein superfamily, and related Ras family GTP-binding proteins	21.37	8.24	1	7.44
Gomus.D13G105900.1	Heterogeneous nuclear ribonucleoprotein G	22.47	8.44	1	7.44
Gomus.D05G102000.1	Methyl-CpG binding protein, MBD	23.70	5.52	1	7.43
Gomus.D01G012000.1	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	62.62	8.00	1	7.42
Gomus.A12G098000.1	Uncharacterized protein	33.60	4.93	1	7.42
Gomus.A13G128400.1	PsbP	29.90	8.48	1	7.41
Gomus.A10G148800.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	37.60	6.99	3	7.39
Gomus.A05G092100.1	Large subunit ribosomal protein L9	21.90	9.72	2	7.37
Gomus.D01G179400.1	PIN; auxin efflux carrier family	70.80	8.25	1	7.34
Gomus.D12G148000.1	Uncharacterized protein	26.90	7.03	1	7.32
Gomus.D03G070500.2	Nuclear pore complex component NPAP60L/NUP50	46.90	4.75	2	7.31
Gomus.D12G138300.1	Cupin	22.80	8.70	1	7.29
Gomus.D11G114700.1	Uncharacterized protein	19.17	8.73	1	7.29
Gomus.A13G196100.1	Histone H1/5	22.30	10.95	2	7.27
Gomus.A08G220900.1	Ran-binding protein RANBP1 and related RanBD domain proteins	25.03	4.92	1	7.27
Gomus.A10G131500.2	Asparagine synthetase	24.32	5.88	1	7.25
Gomus.A03G030000.1	Aquaporin PIP	30.80	8.40	1	7.22
Gomus.A07G072800.1	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	15.10	9.42	1	7.21
Gomus.D03G147800.1	HSP20 family protein	18.39	6.00	1	7.17
Gomus.A11G101600.1	Uncharacterized protein	118.51	6.11	1	7.17
Gomus.D02G172600.1	Ubiquitin-like proteins	13.00	9.11	1	7.17
Gomus.A12G299700.1	Anthranilate phosphoribosyltransferase	43.57	7.83	1	7.17
Gomus.A02G113500.1	Long-chain acyl-CoA synthetase	73.65	6.89	1	7.16
Gomus.D03G190900.1	Regulator of nonsense transcripts 1	138.20	6.81	1	7.16
Gomus.A05G429400.1	Transcription elongation factor SPT6	161.52	6.77	1	7.16
Gomus.A12G155100.2	Uncharacterized protein	52.88	8.40	1	7.15
Gomus.A05G103000.1	Small subunit ribosomal protein S15Ae	8.22	10.15	1	7.15
Gomus.A10G195300.1	Large subunit ribosomal protein L10e	19.68	10.43	1	7.13
Gomus.A04G077900.2	Actin, alpha cardiac muscle	31.74	5.44	1	7.13
Gomus.A04G160200.1	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	29.77	5.15	1	7.11
Gomus.A05G339900.1	3-oxoacyl-[acyl-carrier protein] reductase	34.30	9.03	1	7.08
Gomus.A05G394600.1	Polyribonucleotide 5'-hydroxyl-kinase	48.40	6.71	1	7.08
Gomus.D01G206300.1	Niemann-Pick C1 protein	119.90	5.17	1	7.07
Gomus.D12G308800.1	Glutamate decarboxylase	56.33	6.39	1	7.06
Gomus.A09G224600.2	Isocitrate lyase	50.05	7.09	1	7.06
Gomus.A08G215600.1	C2H2 Zn-finger protein	83.80	8.31	1	7.04
Gomus.D02G090000.1	PsbP	29.80	6.70	1	7.04
Gomus.D11G381200.1	NADH dehydrogenase I subunit 1	40.30	5.25	1	7.02
Gomus.A05G280900.1	Transcription initiation factor TFIID subunit 4	100.50	9.28	1	6.96
Gomus.A06G086300.1	Sucrose synthase	91.60	6.44	1	6.95

Gomus.A05G056200.1	YbaB/EbfC DNA-binding family	21.30	8.66	1	6.95
Gomus.D12G304500.1	MYB proto-oncogene protein, plant	122.61	8.18	1	6.95
Gomus.A01G003700.1	Aldehyde reductase	34.90	7.46	2	6.93
Gomus.D07G001000.2	Aspartyl-tRNA synthetase	59.32	6.37	1	6.92
Gomus.A08G039300.1	20S proteasome subunit beta 6	24.60	7.24	1	6.87
Gomus.A03G238000.1	Cytochrome c	12.20	9.45	2	6.86
Gomus.A08G031100.1	Phytepsin	55.98	5.44	1	6.86
Gomus.A12G180100.1	Prohibitins and stomatins of the PID superfamily	31.40	5.43	2	6.85
Gomus.A03G162800.1	Large subunit ribosomal protein L15	28.70	10.98	2	6.83
Gomus.D02G016700.1	Thiamine pyrophosphate-requiring enzyme	63.65	5.95	1	6.82
Gomus.A05G103100.1	Ras-related protein Rab-8A	24.00	8.22	1	6.78
Gomus.D01G134300.1	Tic22-like family	30.31	9.44	1	6.75
Gomus.A08G220200.1	Uncharacterized nodulin-like protein	62.75	9.11	1	6.73
Gomus.A01G058900.1	Heterogeneous nuclear ribonucleoprotein A1/A3	44.50	7.56	2	6.73
Gomus.A01G246000.1	26S proteasome regulatory subunit N8	35.10	6.48	1	6.72
Gomus.A12G176600.1	26S proteasome regulatory subunit N6	47.00	6.29	2	6.69
Gomus.A05G339000.1	Nuclear transport factor 2	13.39	6.11	1	6.68
Gomus.A07G001500.1	Aspartyl-tRNA synthetase	60.80	6.90	2	6.64
Gomus.D07G109700.1	FAE1/Type III polyketide synthase-like protein	52.79	8.66	1	6.63
Gomus.A09G073400.1	Beta-glucosidase, lactase phlorizinhydrolase, and related proteins	73.20	6.47	1	6.63
Gomus.A10G253300.2	UDP-glucuronosyl and UDP-glucosyl transferase	52.28	6.23	1	6.62
Gomus.D13G157500.1	Cleavage site for pathogenic type III effector avirulence factor Avr	8.25	7.99	1	6.61
Gomus.D04G192000.1	Coatomer protein complex, subunit alpha (xenin)	137.10	7.05	1	6.61
Gomus.A10G116600.1	WD repeat-containing protein 23	52.59	7.12	1	6.60
Gomus.A05G356100.1	NADH-cytochrome b-5 reductase	36.10	8.18	2	6.60
Gomus.A01G054500.1	Putative transcription factor	15.70	9.91	1	6.59
Gomus.D12G195700.1	Uncharacterized protein	109.40	6.10	2	6.58
Gomus.D09G088100.2	Uncharacterized	55.79	5.80	1	6.57
Gomus.A01G219200.1	Ubiquitin-conjugating enzyme E2 variant	16.59	6.68	1	6.56
Gomus.D08G124000.1	Tripeptidyl peptidase II	154.00	7.09	1	6.56
Gomus.A06G125100.1	Uncharacterized PHD Zn-finger protein	29.20	5.26	1	6.56
Gomus.A04G043400.1	Serine/threonine kinase 24	75.80	6.96	1	6.55
Gomus.A04G147200.1	Uncharacterized protein	79.40	6.65	1	6.55
Gomus.A11G052400.1	Cell cycle-regulated histone H1-binding protein	51.21	4.56	1	6.53
Gomus.A05G137500.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	34.20	6.35	1	6.53
Gomus.A01G105800.3	DNA-binding proteins Bright/BRCAA1/RBP1 and related proteins containing BRIGHT domain	47.10	5.19	2	6.52
Gomus.D11G005700.1	T-complex protein 1 subunit delta	57.55	7.71	1	6.52
Gomus.A11G003200.1	Amidases	64.50	8.16	1	6.51
Gomus.D06G043500.1	Protein of unknown function (DUF4057)	31.10	6.90	2	6.51
Gomus.D05G311100.1	Ubiquitin--protein ligase.	9.89	5.19	1	6.51
Gomus.D04G211200.1	Uncharacterized protein	26.54	9.76	1	6.49
Gomus.A02G030900.1	Chalcone synthase	42.50	6.38	2	6.49
Gomus.D11G230800.2	Branched-chain amino acid aminotransferase	46.25	8.00	1	6.48
Gomus.D06G002100.1	SCF ubiquitin ligase, Skp1 component	15.95	4.82	1	6.47
Gomus.A10G142400.1	Uncharacterized protein	14.70	8.13	2	6.46
Gomus.D02G114500.1	NmrA-like family	81.30	9.50	1	6.44
Gomus.D02G185900.1	Plant specific eukaryotic initiation factor 4B	57.00	9.22	1	6.44
Gomus.A13G015600.2	Biotin-requiring enzyme	26.97	8.51	2	6.42
Gomus.A08G204300.1	Pre-mRNA-splicing factor 18	46.70	8.48	1	6.42
Gomus.A10G182000.1	Enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	79.30	8.81	1	6.41
Gomus.A13G054200.1	Striated muscle activator of rho-dependent signaling-related	10.00	5.17	1	6.41
Gomus.A08G240200.2	Uncharacterized protein	62.48	7.01	1	6.41
Gomus.A13G220200.1	Uncharacterized protein	44.82	5.33	1	6.38
Gomus.A09G074300.1	Nuclear protein, contains WD40 repeats	118.80	5.58	1	6.36
Gomus.D12G051100.1	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	144.90	5.62	1	6.35
Gomus.A06G080200.1	Glyoxylase I family protein	21.33	8.10	1	6.34
Gomus.A05G431000.1	Copper chaperone	10.56	5.01	1	6.33
Gomus.D11G363000.1	Uncharacterized protein	17.20	9.70	1	6.31
Gomus.D12G213000.1	Uncharacterized protein	32.30	8.82	2	6.26
Gomus.D10G013700.1	Senescence regulator	12.65	4.83	1	6.26
Gomus.D02G224800.1	Uncharacterized protein	38.50	6.04	1	6.23
Gomus.D05G334000.1	Photosynthetic reaction centre protein	19.65	5.05	1	6.22
Gomus.A06G061100.2	Protein of unknown function (DUF3119)	21.73	9.66	1	6.22
Gomus.A05G194500.1	T-complex protein 1 subunit beta	57.10	6.06	1	6.21
Gomus.A06G071800.1	Nuclear protein SKIP-related	34.54	8.59	1	6.20
Gomus.A07G043700.1	Translation initiation factor IF-3	30.10	9.66	1	6.19
Gomus.D06G167500.1	Chlorophyll A/B binding protein	26.88	5.10	1	6.18
Gomus.D12G152100.1	HSP90 co-chaperone p23	21.90	4.63	2	6.18
Gomus.A08G252100.1	Predicted translation factor, contains W2 domain	47.20	5.55	1	6.16
Gomus.D04G077200.1	Vesicle coat protein clathrin, light chain	30.10	5.58	1	6.16
Gomus.A05G387500.1	Small subunit ribosomal protein S17e	16.07	10.15	1	6.16
Gomus.A13G154300.1	CCAAT-binding factor, subunit A (HAP3)	18.60	6.55	1	6.15
Gomus.A10G042000.1	programmed cell death protein 5	14.80	6.89	1	6.15
Gomus.A10G039200.1	Large subunit ribosomal protein L11e	20.80	9.92	1	6.14
Gomus.A02G142900.1	Uncharacterized protein	19.50	9.48	1	6.14
Gomus.A05G282000.1	Uncharacterized protein	12.20	9.55	1	6.14
Gomus.A12G209900.1	Polyadenylate-binding protein 2	26.00	4.94	1	6.13
Gomus.A01G053900.1	Uncharacterized protein	26.70	5.59	1	6.13
Gomus.A08G087400.1	Universal stress protein family	17.25	7.33	1	6.13
Gomus.D09G222900.2	PAP_fibrillin	28.73	4.54	1	6.12
Gomus.D06G065100.1	Protein of unknown function (DUF3119)	23.38	9.70	1	6.11
Gomus.D13G137900.1	Thioredoxin 1	20.50	9.31	2	6.10
Gomus.A01G099200.1	Translation initiation factor IF-2	106.10	6.25	2	6.09
Gomus.D13G175600.1	Enolase-phosphatase E-1	45.50	6.25	1	6.08
Gomus.A06G136800.1	Polyphenol oxidase	67.10	6.80	2	6.08
Gomus.D03G111200.1	Uncharacterized protein	14.67	9.50	1	6.08
Gomus.A01G084600.1	ATP synthase gamma chain	28.49	8.95	1	6.08
Gomus.A07G029700.1	Methyltransferase	29.80	5.69	1	6.06
Gomus.A01G229700.1	Aquaporin PIP	25.50	6.35	1	6.04
Gomus.A13G191100.1	Group II pyridoxal-5-phosphate decarboxylase	37.45	7.33	1	6.04
Gomus.D04G038000.1	Charged multivesicular body protein 6	24.60	4.86	1	6.02
Gomus.A05G264900.1	Spindle pole body protein	57.20	5.06	1	6.00
Gomus.A06G222000.1	Small subunit ribosomal protein S5	32.48	9.38	1	5.99
Gomus.A07G229000.1	Glutaredoxin 3	19.24	9.26	1	5.99
Gomus.D11G242200.1	Heat shock factor binding protein 1	4.51	4.44	1	5.99
Gomus.D10G245800.1	Chorismate synthase	48.90	8.47	1	5.98
Gomus.D08G284400.1	Small nuclear ribonucleoprotein E	10.30	9.99	1	5.98
Gomus.A09G042000.1	Large subunit ribosomal protein L27	20.80	10.23	1	5.97
Gomus.D11G321400.1	Small subunit ribosomal protein S10	20.70	9.22	1	5.95
Gomus.A01G186400.1	Chitinase	34.86	6.49	1	5.95
Gomus.D05G173500.2	Dormancy/auxin associated protein	13.09	9.85	1	5.94
Gomus.A06G223000.1	DNA-directed RNA polymerase II subunit RPB2	134.80	7.71	1	5.93
Gomus.A05G080100.1	Nuclear inhibitor of protein phosphatase-1	23.90	6.81	1	5.93
Gomus.A06G086300.2	Sucrose synthase	90.15	6.24	1	5.93
Gomus.D01G195200.1	Cold shock domain containing proteins	16.70	7.24	1	5.92
Gomus.A08G126100.1	Prohibitins and stomatins of the PID superfamily	44.90	9.01	1	5.92
Gomus.A02G021200.1	Protein transport protein SEC23	85.20	6.27	2	5.92
Gomus.D05G440900.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	42.70	8.06	1	5.92
Gomus.A04G002900.1	Stress-induced protein UVI31+	37.52	6.89	1	5.92
Gomus.A11G162300.1	CCAAT-binding factor, subunit A (HAP3)	22.40	6.89	2	5.91
Gomus.A03G109500.1	Large subunit ribosomal protein L13Ae	23.70	10.42	1	5.91
Gomus.A04G109900.1	Hsp70-interacting protein	40.90	5.35	2	5.90

Gomus.A05G267100.1	Polyadenylate-binding protein	26.95	9.38	1	5.89
Gomus.A04G130600.1	FKBP-type peptidyl-prolyl cis-trans isomerase	27.00	8.82	1	5.89
Gomus.D04G185900.1	Ribosomal protein L2	13.59	11.05	1	5.89
Gomus.D03G034100.4	PPR repeat	33.11	7.49	1	5.88
Gomus.A05G041800.1	Small subunit ribosomal protein S3e	26.90	9.44	1	5.88
Gomus.A04G148900.1	Uncharacterized protein	53.90	6.09	1	5.88
Gomus.D01G216900.1	60S ribosomal protein L3 and related proteins	45.40	10.18	1	5.87
Gomus.A09G268500.1	Large subunit ribosomal protein L7Ae	29.30	10.27	1	5.87
Gomus.D02G159800.3	Splicing factor 3A subunit 1	90.40	5.08	1	5.87
Gomus.A05G424300.2	Regulator of ribonuclease activity A	17.80	5.88	1	5.86
Gomus.A13G239600.1	Ubiquinol-cytochrome c reductase subunit 7	14.50	9.45	1	5.86
Gomus.A13G227900.1	Hexokinase	54.02	6.29	1	5.86
Gomus.D07G091000.2	MYB family transcription factor	24.99	6.62	1	5.85
Gomus.D10G156000.1	Glycine hydroxymethyltransferase	52.00	7.69	2	5.84
Gomus.A02G189200.1	Large subunit ribosomal protein L8e	28.10	10.90	2	5.84
Gomus.A02G100000.1	OPC-8:0 CoA ligase 1	59.70	8.54	1	5.84
Gomus.A12G010600.1	Glutathione transferase	13.79	5.97	1	5.84
Gomus.A04G033700.1	Protochlorophyllide reductase	43.20	9.10	2	5.83
Gomus.D03G156100.1	Glyoxalase	20.73	5.27	1	5.82
Gomus.A06G222900.1	Vesicle-fusing ATPase	89.30	6.98	1	5.82
Gomus.A05G087800.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	44.00	8.03	2	5.82
Gomus.A04G024900.1	Apoptotic ATPase	99.34	6.96	1	5.82
Gomus.A11G230000.1	Branched-chain amino acid aminotransferase	46.40	7.66	2	5.81
Gomus.A09G117100.1	Chaperonin GroES	10.70	8.40	1	5.81
Gomus.A09G094100.1	Predicted hydrolase/acyltransferase (alpha/beta hydrolase superfamily)	41.10	8.02	2	5.81
Gomus.D13G131600.1	PsbP	29.50	8.19	2	5.79
Gomus.D02G002500.1	Uncharacterized protein	36.50	9.16	1	5.79
Gomus.A11G246200.1	26S proteasome regulatory complex, subunit PSMD10	82.18	7.39	1	5.79
Gomus.D10G096000.1	D-ribulose-5-phosphate 3-epimerase	22.75	5.59	1	5.78
Gomus.A08G257200.1	Leucine-rich repeat (LRR) protein associated with apoptosis in muscle tissue	53.80	8.88	1	5.78
Gomus.A04G041900.1	Serine/threonine protein phosphatase	31.40	6.62	1	5.78
Gomus.A03G033700.1	Small subunit ribosomal protein S10e	19.90	9.67	1	5.78
Gomus.A05G378900.1	Tropine dehydrogenase	29.60	7.65	1	5.78
Gomus.D05G392800.1	PPR repeat	35.55	6.15	1	5.77
Gomus.A01G052700.2	Uncharacterized conserved protein	56.91	5.74	1	5.77
Gomus.A11G264400.1	General transcription factor 2-related zinc finger protein	47.25	6.67	1	5.77
Gomus.A08G044700.1	RAP55	67.30	8.40	1	5.75
Gomus.A07G085100.1	Uncharacterized protein	15.20	8.47	1	5.75
Gomus.A08G079500.1	Small nuclear ribonucleoprotein D1	12.60	11.03	1	5.74
Gomus.D06G096500.1	Alpha-aminoadipic semialdehyde synthase	115.57	6.90	1	5.74
Gomus.A06G180700.1	Folylpolyglutamate synthase	63.70	6.44	1	5.73
Gomus.A01G208400.2	Alpha-N-arabinofuranosidase	74.60	5.26	1	5.72
Gomus.D11G386100.1	Cell division protein FtsZ	52.80	7.50	1	5.72
Gomus.A12G176200.2	Translation initiation factor 5A (eIF-5A)	16.56	5.72	1	5.71
Gomus.A01G208800.1	Uncharacterized protein	16.10	10.81	1	5.70
Gomus.D02G278700.1	Ras-related protein Rab-1A	22.33	6.21	1	5.69
Gomus.D12G051100.10	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	143.70	5.68	1	5.69
Gomus.A05G064100.1	Iron-sulfur domain containing protein	60.60	8.43	1	5.68
Gomus.A13G183500.1	BolA (bacterial stress-induced morphogen)-related protein	20.39	9.72	1	5.67
Gomus.A10G079800.2	3-isopropylmalate dehydrogenase	43.50	6.60	1	5.67
Gomus.A08G104500.1	Uncharacterized protein	9.56	10.13	1	5.66
Gomus.A02G064200.1	Bucentaur related	32.20	8.63	1	5.66
Gomus.A05G363600.1	Alpha-mannosidase	115.80	5.85	2	5.65
Gomus.A11G118900.1	Protein of unknown function (DUF952)	13.60	5.19	1	5.64
Gomus.A06G109000.1	Androgen induced inhibitor of proliferation (AS3) / PDS5-related	104.70	6.34	1	5.63
Gomus.A03G188600.1	Homoserine kinase	37.70	7.75	1	5.63
Gomus.A11G066200.1	Transcriptional coactivator	12.20	6.00	1	5.63
Gomus.D04G058500.1	Cytochrome b	13.00	10.11	1	5.62
Gomus.A05G048700.2	Malic enzyme-related	54.16	7.62	1	5.62
Gomus.A04G028000.1	Trp repressor binding protein	21.62	6.54	1	5.62
Gomus.D11G354300.1	Apoptotic ATPase	128.70	7.71	1	5.62
Gomus.D07G063300.1	Neoplastic transformation suppressor Pdcd4/MA-3, contains MA3 domain	79.00	5.17	1	5.61
Gomus.A02G128500.1	Transcription elongation factor TAT-SF1	36.44	5.34	1	5.60
Gomus.A05G150000.1	Peptidase inhibitor I9	81.56	8.66	1	5.60
Gomus.A09G030300.1	Oxidative-stress responsive protein 1	76.70	6.77	1	5.60
Gomus.D04G192700.2	40S ribosomal protein S25	10.62	10.49	1	5.60
Gomus.D12G023200.1	Cinnamyl-alcohol dehydrogenase	38.68	5.67	1	5.59
Gomus.A08G234400.1	Cysteine synthase A	33.90	5.58	1	5.58
Gomus.A03G038900.1	[acyl-carrier-protein] S-malonyltransferase	40.40	8.05	2	5.57
Gomus.A11G009200.1	Iron-binding zinc finger CDGSH type	12.20	9.67	1	5.56
Gomus.A05G148600.1	K+-dependent Na+:Ca2+ antiporter	149.20	6.55	2	5.56
Gomus.A03G229700.1	Predicted dehydrogenase	44.20	8.10	2	5.56
Gomus.A05G163600.1	Ras-related protein Rab-11A	24.10	5.69	2	5.54
Gomus.A09G027900.1	Ferredoxin thioredoxin reductase catalytic beta chain	16.40	7.61	1	5.53
Gomus.A05G039600.1	Pectinesterase	62.10	6.98	1	5.53
Gomus.D09G109000.2	NPH3 family	69.51	6.68	1	5.53
Gomus.A11G336000.1	Leucine-rich repeat-containing protein	21.09	8.50	1	5.52
Gomus.A05G430900.1	DNA gyrase subunit A	105.30	7.23	2	5.52
Gomus.A08G271600.1	Mitochondrial processing peptidase	54.40	6.64	2	5.49
Gomus.D09G220700.2	Tetraspanin	31.00	5.05	2	5.49
Gomus.D04G176400.2	SWIM zinc finger	57.84	6.73	1	5.49
Gomus.A12G245800.1	Small subunit ribosomal protein S11	14.80	12.18	1	5.48
Gomus.D11G301000.1	20S proteasome subunit alpha 2	11.20	9.79	1	5.47
Gomus.D06G237200.1	Anion exchange protein	75.30	6.98	1	5.47
Gomus.D13G183800.1	Glutathione S-transferase	25.50	7.28	1	5.47
Gomus.D04G183900.1	Uncharacterized protein	53.90	6.09	1	5.47
Gomus.A12G037500.2	Amine oxidase	57.53	5.44	1	5.47
Gomus.A03G167500.1	Uncharacterized protein	28.70	6.00	1	5.46
Gomus.D05G235800.3	Sentrin-specific cysteine protease (Ulp1 family)	101.93	4.51	1	5.45
Gomus.D13G156600.1	Apoptosis inhibitor 5-related	79.10	6.54	1	5.45
Gomus.A09G220500.1	Methylenetetrahydrofolate reductase (NADPH)	66.70	6.25	1	5.45
Gomus.A03G137800.1	Serine carboxypeptidases (lysosomal cathepsin A)	39.68	7.96	1	5.45
Gomus.A01G242300.1	DEAD/DEAH box helicase	32.10	7.72	1	5.44
Gomus.D04G056100.1	Aldose 1-epimerase	39.51	9.25	1	5.44
Gomus.D03G101400.5	Nuclear pore complex protein Nup98-Nup96	104.40	8.95	1	5.44
Gomus.A01G251500.4	Protein of unknown function (DUF1685)	20.90	4.72	1	5.44
Gomus.D11G051600.1	Uncharacterized protein	17.80	7.64	1	5.44
Gomus.A11G072200.1	V-type H+-transporting ATPase subunit C	42.70	5.43	1	5.44
Gomus.D05G275900.2	5'-3' exoribonuclease 2	125.87	7.05	1	5.44
Gomus.A01G091700.1	Predicted membrane protein, contains two CBS domains	73.61	4.96	1	5.44
Gomus.D01G221600.1	PsbP	28.33	7.33	1	5.43
Gomus.D12G049800.1	Glycine cleavage system H protein	16.90	4.86	1	5.43
Gomus.A11G164700.1	Uncharacterized protein	17.90	4.11	2	5.43
Gomus.A02G152200.2	Uncharacterized protein	35.80	8.79	1	5.41
Gomus.A10G217400.1	Copper chaperone	7.41	8.88	1	5.41
Gomus.A11G102800.1	Late embryogenesis abundant protein	16.40	5.02	2	5.40
Gomus.A04G061200.1	Uncharacterized protein	17.10	6.95	2	5.40
Gomus.A13G125500.1	MYB-CC type transfactor, LHEQLE motif	41.28	8.05	1	5.40
Gomus.A07G139400.1	Fumarate hydratase, class II	53.70	7.55	1	5.39
Gomus.A11G122000.1	DnaJ homolog subfamily B member 11	38.70	6.70	2	5.38
Gomus.D09G064900.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	36.62	7.28	1	5.37
Gomus.A07G051500.1	Polyadenylate-binding protein 2	26.17	5.03	1	5.36

Gomus.D03G053300.1	Uncharacterized protein	17.40	4.53	1	5.35
Gomus.A05G291200.1	Dimeric dihydrodiol dehydrogenase	39.60	6.73	2	5.34
Gomus.A05G145700.1	Glycylpeptide N-tetradecanoyltransferase	49.59	7.06	1	5.34
Gomus.A13G216500.1	Minichromosome maintenance protein 5 (cell division control protein 46)	81.00	7.50	2	5.33
Gomus.A02G072400.1	Peroxidase	40.40	7.31	2	5.33
Gomus.D12G036700.1	E3 ubiquitin protein ligase	143.00	5.72	1	5.32
Gomus.A02G003300.1	Predicted membrane protein	35.30	7.06	1	5.30
Gomus.D10G046600.1	Calcyclin binding protein	25.20	7.14	2	5.29
Gomus.A09G086800.1	Cupin	27.80	8.65	1	5.29
Gomus.D08G134700.1	Plant specific mitochondrial import receptor subunit TOM20	56.40	4.97	1	5.29
Gomus.D13G164200.2	Microtubule-associated protein essential for anaphase spindle elongation	63.88	5.16	1	5.28
Gomus.A09G185000.2	Retinaldehyde binding protein-related	24.36	8.59	1	5.28
Gomus.D08G094300.1	Heat shock factor binding protein 1	10.13	4.81	1	5.28
Gomus.D01G060000.1	Uncharacterized protein	43.27	9.52	1	5.28
Gomus.D05G074400.1	Predicted member of the intramitochondrial sorting protein family	21.30	8.75	1	5.27
Gomus.D05G082400.2	Molybdopterin biosynthesis protein	66.45	6.49	1	5.27
Gomus.A01G008400.1	Putative cyclase	29.30	6.23	1	5.26
Gomus.D04G145400.1	Uncharacterized protein	93.70	5.48	1	5.26
Gomus.D04G100800.1	WRC	39.05	9.33	1	5.26
Gomus.D07G146900.1	Uncharacterized protein	14.05	4.86	1	5.26
Gomus.A02G160000.2	Molecular chaperone DnaJ	48.00	9.28	2	5.25
Gomus.D02G225200.1	Lipoyl synthase	17.48	8.25	1	5.25
Gomus.D01G266500.1	Uncharacterized protein	35.65	4.72	1	5.25
Gomus.A09G238700.1	UPF0041 brain protein 44-related	20.90	9.76	1	5.24
Gomus.D07G076000.1	Light-harvesting complex I chlorophyll a/b binding protein 4	27.84	7.44	1	5.24
Gomus.D10G045100.1	Urease accessory protein	30.60	6.86	1	5.23
Gomus.A03G024800.1	3,5-epimerase/4-reductase	33.70	5.99	1	5.23
Gomus.A05G109600.2	Auxin response factor	77.32	8.78	1	5.22
Gomus.A07G133400.1	Cytochrome P450	39.67	7.42	1	5.20
Gomus.A06G144800.1	Ras-related protein Rab-11A	24.10	5.69	2	5.20
Gomus.A11G334300.3	Uncharacterized protein	35.90	9.51	1	5.20
Gomus.A01G152600.1	AP-1 complex subunit gamma-1	96.00	6.65	1	5.18
Gomus.A01G025700.1	Glyoxalase	15.90	6.54	1	5.18
Gomus.A11G300300.1	20S proteasome subunit beta 7	27.70	7.47	2	5.17
Gomus.A01G195600.1	Aspartyl-tRNA synthetase	74.70	7.59	1	5.17
Gomus.A09G196600.1	Transcription factor Pcc1	10.73	4.41	1	5.17
Gomus.A09G073400.3	Beta-glucosidase, lactase phlorizinhydrolase, and related proteins	68.69	6.35	1	5.16
Gomus.A08G256800.1	Dynamin GTPase	99.30	9.14	1	5.16
Gomus.A03G038100.1	U2 small nuclear ribonucleoprotein B"	26.40	9.32	2	5.16
Gomus.D03G033700.1	Lysosomal Pro-X carboxypeptidase	57.80	5.78	1	5.15
Gomus.D04G116500.1	Signal recognition particle subunit SRP54	62.00	9.61	2	5.15
Gomus.D01G157300.1	Large subunit ribosomal protein L6e	26.30	10.15	1	5.14
Gomus.A12G195700.1	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	121.41	5.87	1	5.12
Gomus.D06G023000.1	Proprotein convertase subtilisin/kexin	82.60	6.18	2	5.12
Gomus.D03G128600.2	Glutamate-1-semialdehyde 2,1-aminomutase	43.72	5.86	1	5.12
Gomus.A11G175700.1	Protein of unknown function (DUF2854)	30.00	9.06	1	5.11
Gomus.A11G344300.1	Translation initiation factor eIF-2 beta subunit	29.70	7.27	2	5.11
Gomus.A10G050500.1	Uncharacterized protein	40.30	7.97	1	5.11
Gomus.A03G155900.1	Spermidine synthase	37.90	5.03	1	5.09
Gomus.D11G016100.2	Uncharacterized protein	36.13	8.81	1	5.08
Gomus.A06G197400.1	Acetyl-CoA synthetase	83.36	7.23	1	5.07
Gomus.A08G023700.1	Cell membrane glycoprotein	35.50	4.40	1	5.07
Gomus.A12G124200.1	Essential for mitotic growth 1	32.50	9.14	1	5.07
Gomus.A09G263300.2	Cdc2-related protein kinase	74.23	9.47	1	5.07
Gomus.A11G005800.1	Small subunit ribosomal protein S7e	22.00	9.70	1	5.06
Gomus.A02G188800.1	V-type H+-transporting ATPase 16kDa proteolipid subunit	16.60	8.46	1	5.06
Gomus.D02G114000.2	Predicted nucleic acid-binding protein ASMTL	19.79	5.21	1	5.06
Gomus.A11G139800.1	Glutathione reductase (NADPH)	61.10	7.84	2	5.05
Gomus.A11G258600.1	CREG1 protein	36.00	7.01	1	5.04
Gomus.A06G017000.1	Dipeptidyl aminopeptidase	80.40	6.58	1	5.04
Gomus.A11G284100.2	Uncharacterized high-glucose-regulated protein	65.43	6.61	1	5.03
Gomus.A12G297400.1	Eukaryotic translation initiation factor 2C	117.00	9.36	1	5.02
Gomus.A07G032400.2	YbaB/EbfC DNA-binding family	21.20	8.51	1	5.02
Gomus.A11G116100.1	60S ribosomal protein 15.5kD/SNU13, NHP2/L7A family (includes ribonuclease P subunit p38), involved in splicing	18.57	9.26	1	5.01
Gomus.A12G291500.1	Uncharacterized protein	29.30	9.76	1	5.00
Gomus.D05G392400.1	Serine/threonine kinase 24	78.00	7.52	1	4.99
Gomus.A06G195900.1	Small subunit ribosomal protein S26e	14.80	10.77	2	4.99
Gomus.A08G038700.1	Plant protein of unknown function (DUF641)	53.23	6.37	1	4.99
Gomus.D03G144900.1	THO complex subunit 4	25.68	10.10	1	4.96
Gomus.A11G054700.1	Cathepsin B	39.10	6.52	1	4.96
Gomus.A04G187200.1	Large subunit ribosomal protein L34e	13.70	11.59	1	4.95
Gomus.A05G152700.1	Photosystem I subunit III	24.50	9.41	2	4.95
Gomus.A02G156800.1	Uncharacterized protein	13.50	6.80	1	4.95
Gomus.A12G125400.2	D-arabinono-1, 4-lactone oxidase	64.72	8.19	1	4.95
Gomus.A07G090300.1	Uncharacterized protein	15.10	8.19	1	4.93
Gomus.D11G147700.1	Oligosaccharyltransferase complex subunit delta (ribophorin II)	75.70	6.49	1	4.92
Gomus.D13G186000.1	DNA mismatch repair MutS related proteins	18.16	8.82	1	4.92
Gomus.A03G123900.3	RNA-binding translational regulator IRP (aconitase superfamily)	81.85	6.77	1	4.91
Gomus.A05G387000.1	Sucrase/ferredoxin-like	43.98	6.79	1	4.91
Gomus.A12G047400.1	Ras-related protein Rab-11A	23.90	7.24	2	4.91
Gomus.A11G076400.1	Uncharacterized protein	32.80	6.43	1	4.90
Gomus.D05G127600.1	Uncharacterized protein	42.78	5.87	1	4.90
Gomus.D12G207300.1	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	121.33	5.82	1	4.89
Gomus.A13G085300.1	Photosystem II oxygen-evolving enhancer protein 3	22.70	9.10	1	4.89
Gomus.D13G263500.1	Protein transport protein SEC61 subunit beta	10.90	11.72	1	4.89
Gomus.A10G003700.1	Reductases with broad range of substrate specificities	25.90	8.87	1	4.88
Gomus.D10G051700.1	Vesicle-associated membrane protein 72	25.00	8.56	1	4.88
Gomus.D10G246100.1	Interleukin-1 receptor-associated kinase 4	42.02	8.46	1	4.86
Gomus.D11G051500.1	Cell cycle-regulated histone H1-binding protein	51.20	4.55	1	4.86
Gomus.A09G098600.1	Peptidylprolyl isomerase	22.30	9.50	1	4.86
Gomus.D05G053800.1	Uncharacterized	83.97	6.00	1	4.86
Gomus.D04G157100.1	Importin subunit beta-1	96.26	4.70	1	4.84
Gomus.A13G197700.1	Small subunit ribosomal protein S24e	16.50	10.65	2	4.84
Gomus.D11G004900.1	Small subunit ribosomal protein S7e	22.01	9.74	1	4.83
Gomus.A05G203800.1	26S proteasome regulatory subunit T4	44.50	8.18	2	4.83
Gomus.D11G200400.1	Hydrolytic enzymes of the alpha/beta hydrolase fold	55.30	7.46	1	4.83
Gomus.A05G054500.1	Glycerophosphoryl diester phosphodiesterase	83.95	5.67	1	4.83
Gomus.A13G011900.1	Diphosphomevalonate decarboxylase	45.90	6.65	1	4.82
Gomus.D11G085100.1	Serine/threonine protein kinase	49.27	9.39	1	4.82
Gomus.A08G252000.1	Isopentenyl-diphosphate delta-isomerase	34.30	6.54	2	4.80
Gomus.A01G243900.1	Large subunit ribosomal protein L35Ae	12.90	10.40	1	4.80
Gomus.A12G251900.1	V-type H+-transporting ATPase subunit E	26.15	6.89	1	4.80
Gomus.D06G082400.1	Large subunit ribosomal protein L31e	14.01	9.86	1	4.78
Gomus.A13G107100.1	Sulfotransferase	42.70	6.39	1	4.77
Gomus.A08G251800.1	Histidyl-tRNA synthetase	81.70	6.77	2	4.76
Gomus.A08G104200.1	Tam3-transposase (Ac family)	76.40	6.19	1	4.76
Gomus.A05G245400.1	PPR repeat	69.02	7.91	1	4.76
Gomus.D04G184900.1	DYW family of nucleic acid deaminases	76.23	6.49	1	4.75
Gomus.D07G064700.1	30S ribosomal protein S18	8.20	11.72	1	4.75
Gomus.A07G078000.1	UDPglucose 6-dehydrogenase	52.80	7.59	2	4.74
Gomus.A13G147900.1	Isocitrate dehydrogenase	47.09	7.72	1	4.73

Gomus.A09G269900.1	Peptide methionine sulfoxide reductase	22.91	6.67	1	4.72
Gomus.A03G233600.1	Seryl-tRNA synthetase	51.10	6.74	1	4.70
Gomus.D12G245700.1	Methylglutaconyl-CoA hydratase	33.60	8.00	1	4.67
Gomus.A06G081000.1	Uncharacterized protein	123.69	5.34	1	4.67
Gomus.A10G243800.2	DNA topoisomerase II	164.22	7.27	1	4.66
Gomus.A12G284400.1	Sorbitol dehydrogenase	36.21	6.38	1	4.64
Gomus.D09G113600.1	116 kDa U5 small nuclear ribonucleoprotein component	110.40	5.20	2	4.63
Gomus.A01G159000.1	Tetratricopeptide repeat	36.90	5.08	1	4.62
Gomus.A07G034400.2	Vesicle-associated membrane protein 7	25.10	9.55	1	4.62
Gomus.A12G058200.1	Probable lipid transfer	10.40	8.41	1	4.61
Gomus.A05G208400.1	Uncharacterized protein	23.70	9.26	1	4.60
Gomus.A06G179200.1	Aquaporin PIP	30.80	8.62	1	4.59
Gomus.A07G092100.1	Large subunit ribosomal protein L27e	15.60	10.37	1	4.57
Gomus.D05G252900.1	Protein disulfide-isomerase A1	55.40	5.24	1	4.56
Gomus.A01G095800.1	Cleavage site for pathogenic type III effector avirulence factor Avr	8.40	7.94	1	4.54
Gomus.A05G350500.1	NADH dehydrogenase I subunit I	19.60	7.85	2	4.54
Gomus.A07G216500.1	Uncharacterized protein	13.10	9.17	1	4.54
Gomus.A05G294500.1	Large subunit ribosomal protein L21	25.30	9.17	1	4.51
Gomus.A09G117200.1	Uncharacterized protein	13.10	6.68	1	4.51
Gomus.A11G192400.2	Protease S28 PRO-X carboxypeptidase-related	35.30	6.43	1	4.49
Gomus.D12G174600.1	Histone H1/H5	19.60	11.05	1	4.46
Gomus.A05G181800.1	FeS cluster assembly protein SUF	61.70	5.94	1	4.42
Gomus.D07G160000.1	Uncharacterized protein	27.47	8.98	1	4.42
Gomus.D10G234100.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	32.10	7.03	1	4.41
Gomus.A13G110600.1	Large subunit ribosomal protein L6	24.90	9.96	2	4.41
Gomus.A01G198300.1	Uncharacterized conserved protein	53.50	6.55	1	4.38
Gomus.D04G198300.11	Arginine and glutamate-rich protein 1	28.45	9.80	1	4.37
Gomus.D10G234500.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	25.56	7.09	1	4.31
Gomus.D05G297500.1	Large subunit ribosomal protein L21	25.34	9.04	1	4.30
Gomus.A03G034900.1	Pyruvate kinase	55.00	6.74	2	4.28
Gomus.D05G195800.1	Dehydrin	23.67	5.19	1	4.27
Gomus.D13G030800.1	Serine/threonine protein kinase	101.50	6.16	1	4.26
Gomus.A12G107400.1	Translation initiation factor eIF-4F	205.00	6.93	1	4.25
Gomus.A08G204100.1	Chalcone isomerase	32.30	9.10	1	4.24
Gomus.A09G069200.1	Translation initiation factor eIF-2 gamma subunit	50.70	8.56	1	4.22
Gomus.A06G076300.1	Large subunit ribosomal protein L28e	16.77	11.17	1	4.22
Gomus.A02G147900.1	Uncharacterized protein	33.60	5.52	1	4.21
Gomus.A06G093400.2	DEAD/DEAH box helicase	32.95	5.81	1	4.18
Gomus.A12G063200.1	Cellular nucleic acid-binding protein	25.50	7.28	1	4.18
Gomus.D13G154900.3	DNA damage-inducible protein 1	44.90	5.08	1	4.16
Gomus.A05G299300.2	Uroporphyrinogen decarboxylase	29.72	6.89	1	4.16
Gomus.A03G076400.1	Peptide-methionine (S)-S-oxide reductase	28.54	8.51	1	4.14
Gomus.D02G120500.1	Uncharacterized protein	17.64	7.99	1	4.14
Gomus.A03G023700.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	35.39	6.44	1	4.12
Gomus.A01G125000.1	Tic22-like family	30.40	9.51	1	4.12
Gomus.A01G024000.1	Pyruvate dehydrogenase E1 component subunit beta	39.18	5.64	1	4.10
Gomus.A09G023800.1	Thioredoxin 1	14.80	5.30	1	4.07
Gomus.A01G008700.1	Acetylxylan esterase	29.41	6.62	1	4.07
Gomus.A06G126500.1	Cobalamin synthesis protein	50.00	6.68	1	4.06
Gomus.A09G016000.1	Glycosyltransferase	64.41	6.02	1	4.04
Gomus.A13G239200.1	IMP dehydrogenase	52.20	6.62	1	4.04
Gomus.D13G223900.1	Minichromosome maintenance protein 5 (cell division control protein 46)	81.10	7.49	2	4.03
Gomus.D11G018200.1	Nuceloporin	114.30	8.51	1	4.03
Gomus.D02G267900.1	Signal recognition particle 43 kDa protein	45.90	4.74	1	4.03
Gomus.A04G013900.1	Sulfotransferase	37.70	6.68	1	4.02
Gomus.A03G084700.1	Translation initiation factor eIF-5A	17.50	5.99	1	4.02
Gomus.A03G086200.1	C2H2-type zinc finger	47.93	7.68	1	3.98
Gomus.D10G123400.1	Cyanobacterial and plant NDH-1 subunit O	24.71	9.86	1	3.97
Gomus.A08G041400.1	Uncharacterized conserved protein	29.30	9.33	1	3.96
Gomus.A03G023600.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	36.30	6.05	1	3.96
Gomus.D01G009300.1	Acetylxylan esterase	30.20	6.73	1	3.95
Gomus.D13G179600.1	Ubiquitin-conjugating enzyme E2 N	17.70	8.10	1	3.94
Gomus.D03G192600.1	Acetylornithine deacetylase	48.00	5.40	1	3.93
Gomus.A03G199100.1	Predicted dehydrogenase	62.30	7.87	1	3.90
Gomus.A06G061100.1	Protein of unknown function (DUF3119)	23.30	9.73	1	3.90
Gomus.D05G296400.1	TCP family transcription factor	44.69	7.43	1	3.89
Gomus.A04G177400.1	Probable lipid transfer	20.20	8.29	1	3.89
Gomus.D06G200000.1	Light-harvesting complex II chlorophyll a/b binding protein 4	30.80	6.00	1	3.88
Gomus.A08G262200.1	Small nuclear ribonucleoprotein E	10.28	9.99	1	3.87
Gomus.D08G242800.1	Ran-binding protein RANBP1 and related RanBD domain proteins	30.30	5.22	1	3.87
Gomus.A07G008700.1	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	65.11	6.81	1	3.87
Gomus.D07G027200.1	Polyketide cyclase / dehydrase and lipid transport	18.80	5.35	1	3.85
Gomus.A01G162500.1	Ubiquitin-conjugating enzyme E2 variant	17.80	4.77	1	3.85
Gomus.A10G105600.1	Adenylyl-sulfate reductase (glutathione)	62.24	8.66	1	3.82
Gomus.A07G086600.1	NADH dehydrogenase I subunit 7	42.70	5.25	1	3.79
Gomus.D05G117300.3	Mitochondrial inheritance and actin cytoskeleton organization protein	89.00	5.94	1	3.78
Gomus.D11G263000.1	BRG-1 associated factor 60 (BAF60)	16.50	10.51	1	3.78
Gomus.A03G061500.1	Glutathione S-transferase	25.68	5.91	1	3.76
Gomus.A05G441900.1	Leucine rich repeat	64.98	8.47	1	3.75
Gomus.A11G036200.1	Uncharacterized protein	43.64	6.34	1	3.75
Gomus.A05G267200.1	Pyruvate dehydrogenase E2 component	48.40	7.47	1	3.75
Gomus.A11G133800.1	Small nuclear ribonucleoprotein D1	12.63	11.37	1	3.73
Gomus.A12G281400.1	Putative steroid membrane receptor Hpr6.6/25-Dx	23.70	4.58	1	3.73
Gomus.A07G051500.2	Polyadenylate-binding protein 2	26.20	5.03	1	3.72
Gomus.A02G128400.1	HIV Tat-specific factor 1	57.90	4.78	1	3.71
Gomus.D05G013900.1	Uncharacterized protein	28.61	5.21	1	3.70
Gomus.D02G017000.1	O-sialoglycoprotein endopeptidase	38.70	5.82	1	3.68
Gomus.A10G227100.2	Phosphoglucomutase/phosphomannomutase	56.32	6.73	1	3.68
Gomus.A05G431500.1	Uncharacterized protein	24.05	4.91	1	3.67
Gomus.D07G082500.3	Hypothetical heat domain-containing	160.46	5.17	1	3.67
Gomus.D01G111200.1	AT-rich interactive domain-containing protein (arid domain-containing protein)	24.39	4.65	1	3.64
Gomus.A07G080400.1	Uncharacterized conserved protein	183.60	5.12	1	3.62
Gomus.D13G089100.1	DEAD/DEAH box helicase	20.94	8.18	1	3.62
Gomus.D01G219400.1	Acetyl-CoA carboxylase / biotin carboxylase	252.40	6.57	1	3.61
Gomus.D05G310000.1	Fe-S cluster assembly ATP-binding protein	35.50	6.55	1	3.61
Gomus.A07G254700.1	Ribulose-phosphate 3-epimerase	24.40	5.60	1	3.61
Gomus.A12G064800.1	Protein of unknown function (DUF3353)	31.90	10.05	1	3.60
Gomus.A05G013800.1	Uncharacterized protein	28.60	5.33	1	3.60
Gomus.D04G043800.1	Tam3-transposase (Ac family)	75.99	6.20	1	3.59
Gomus.A03G082700.1	Template-activating factor I	30.70	4.21	1	3.58
Gomus.A01G246800.1	Metallopeptidase family M24	43.00	7.46	1	3.57
Gomus.A12G185100.1	Mitotic checkpoint protein MAD1	143.60	5.25	1	3.57
Gomus.A09G108900.1	Serine/threonine specific protein phosphatase PP1, catalytic subunit	108.00	6.13	1	3.57
Gomus.A05G206200.2	ZF-HD protein dimerisation region	32.70	8.53	1	3.56
Gomus.D02G057600.1	Uncharacterized protein	27.62	9.22	1	3.54
Gomus.D07G260100.1	Uncharacterized protein	798.10	4.32	1	3.53
Gomus.D09G035400.2	RNA-binding protein Musashi/mRNA cleavage and polyadenylation factor I complex, subunit HRP1	36.60	9.01	1	3.50
Gomus.A11G095400.2	Fused signal recognition particle receptor	42.20	8.09	1	3.50
Gomus.A01G056900.1	Phosphoenolpyruvate carboxylase	110.70	5.76	1	3.50
Gomus.A05G352400.1	Uncharacterized protein	49.70	5.39	1	3.50
Gomus.D02G201900.1	Uncharacterized protein	35.96	5.15	1	3.50
Gomus.A11G095400.1	Fused signal recognition particle receptor	42.17	8.09	1	3.49

Gomus.A01G186500.1	Chitinase	34.70	7.05	1	3.49
Gomus.D05G256600.1	Cytosolic sorting protein GGA2/TOM1	55.40	5.19	1	3.48
Gomus.A12G141600.1	NADH dehydrogenase (ubiquinone) Fe-S protein 5	9.88	8.37	1	3.48
Gomus.A02G047800.1	Uncharacterized protein	27.60	9.22	1	3.47
Gomus.D05G353700.1	Uncharacterized protein	49.42	5.53	1	3.46
Gomus.D05G252200.1	Porphobilinogen synthase	47.09	6.99	1	3.46
Gomus.A13G239700.1	Uncharacterized protein	54.10	6.38	1	3.45
Gomus.A06G194000.1	Beta-galactosidase	126.00	6.09	1	3.44
Gomus.A10G074900.1	Maleylacetoacetate isomerase	24.60	5.47	1	3.43
Gomus.A09G185000.3	Phosphatidylinositol transfer protein PDR16 and related proteins	30.40	7.69	1	3.42
Gomus.A01G047800.1	Aspartyl/lysyl-tRNA synthetase	16.75	8.34	1	3.41
Gomus.A12G046000.1	Phosphoribosylamine--glycine ligase	55.90	5.38	1	3.41
Gomus.D12G209100.1	F-type H+-transporting ATPase subunit gamma	35.56	8.85	1	3.41
Gomus.A11G274600.1	Chlorophyll A/B binding protein	20.25	9.42	1	3.40
Gomus.D08G247100.1	Lon-like ATP-dependent protease	106.00	5.95	1	3.40
Gomus.D10G086800.1	Signal peptidase, endoplasmic reticulum-type	20.00	7.56	1	3.40
Gomus.D10G273600.1	Uncharacterized protein	16.28	8.53	1	3.39
Gomus.D11G072700.1	V-type H+-transporting ATPase subunit C	42.60	5.53	1	3.39
Gomus.A12G290000.1	Poly(A)-specific exoribonuclease PARN	96.64	5.95	1	3.39
Gomus.A08G281000.1	ATP-dependent RNA helicase UAP56/SUB2	48.40	5.64	1	3.38
Gomus.A05G233800.3	Sentrin-specific protease 7	109.50	4.56	1	3.37
Gomus.D12G196700.1	Protein of unknown function, DUF617	29.40	9.09	1	3.37
Gomus.D12G047100.2	Phosphoribosylamine--glycine ligase	40.97	5.06	1	3.37
Gomus.A06G124000.1	PPR repeat	63.36	8.41	1	3.37
Gomus.D03G080100.2	Uncharacterized protein	23.16	5.40	1	3.36
Gomus.A07G157800.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	33.54	5.52	1	3.36
Gomus.D13G099400.1	Molecular chaperone (HSP90 family)	84.31	5.00	1	3.36
Gomus.A04G116400.1	DEAD/DEAH box helicase	27.68	6.79	1	3.36
Gomus.A07G228400.1	Zinc finger FYVE domain containing protein	40.50	8.88	1	3.35
Gomus.A11G017100.1	Uncharacterized protein	38.00	8.84	1	3.34
Gomus.A03G182000.1	Photosynthesis system II assembly factor YCF48	45.50	8.09	1	3.33
Gomus.A02G081800.1	20S proteasome subunit beta 3	22.88	5.47	1	3.32
Gomus.D07G129700.3	Ubiquitin carboxyl-terminal hydrolase 7	130.90	6.00	1	3.31
Gomus.A02G128900.1	Uncharacterized protein	31.30	7.49	1	3.31
Gomus.A03G087100.1	Heterogeneous nuclear ribonucleoprotein A1/A3	27.20	4.74	1	3.30
Gomus.A13G166800.1	Thioredoxin 1	19.35	9.52	1	3.30
Gomus.A09G253400.1	Acyl carrier protein/NADH-ubiquinone oxidoreductase, NDUFAB1/SDAP subunit	14.59	5.11	1	3.30
Gomus.A07G037800.1	Protein phosphatase 1B (formerly 2C)	39.70	5.15	1	3.29
Gomus.A09G184200.2	1-deoxy-D-xylulose 5-phosphate reductoisomerase	47.72	6.80	1	3.29
Gomus.A09G072700.1	Universal stress protein family	17.74	7.37	1	3.28
Gomus.A08G228100.1	60s ribosomal protein L18	16.58	11.25	1	3.28
Gomus.A03G029700.1	GMP synthase (glutamine-hydrolysing)	59.20	6.40	1	3.26
Gomus.D05G162800.1	Apoptosis inhibitor 5-related	92.60	5.92	1	3.25
Gomus.D13G027300.1	Uncharacterized protein	29.34	9.00	1	3.24
Gomus.D06G224600.1	Acetyl-CoA synthetase	83.80	7.27	1	3.24
Gomus.A11G293200.1	Small subunit ribosomal protein S21e	9.30	7.28	1	3.24
Gomus.D05G047300.1	Mitochondrial ATP synthase g subunit	14.54	9.16	1	3.23
Gomus.A05G137800.1	Small subunit ribosomal protein S17	16.90	10.10	1	3.23
Gomus.A04G032700.1	Uridine monophosphate synthetase	51.60	6.99	1	3.23
Gomus.A13G171600.1	Chlorophyll A/B binding protein	11.96	8.44	1	3.22
Gomus.A03G174400.1	Predicted transporter (major facilitator superfamily)	56.80	6.62	1	3.22
Gomus.D10G031600.1	Uncharacterized protein	31.50	8.85	1	3.22
Gomus.A05G030500.1	Large subunit ribosomal protein L31e	14.03	9.86	1	3.22
Gomus.D12G070300.2	Succinate dehydrogenase, flavoprotein subunit	62.59	7.27	1	3.21
Gomus.D11G004100.1	G1 to S phase transition protein	57.20	5.35	1	3.21
Gomus.A10G112900.1	Ras-related protein Rab-2A	23.20	7.40	1	3.20
Gomus.A09G108400.1	Uncharacterized conserved protein	15.20	6.93	1	3.20
Gomus.A02G153400.2	GTPase Rab1/YPT1, small G protein superfamily, and related GTP-binding proteins	21.74	8.98	1	3.20
Gomus.D02G073800.1	Huntingtin interacting protein HYPK	11.47	5.02	1	3.19
Gomus.A05G054300.1	Outer membrane lipoprotein Blc	21.40	5.91	1	3.19
Gomus.D09G059100.1	Kinesin (KAR3 subfamily)	60.57	7.78	1	3.18
Gomus.A09G186300.1	Dihydropyrimidine dehydrogenase (NADP+)	46.00	7.65	1	3.18
Gomus.D04G108200.1	Glycosyltransferase	48.80	6.27	1	3.18
Gomus.D10G241100.1	MEF2B protein	23.26	4.72	1	3.17
Gomus.D09G102400.1	Predicted hydrolase/acyltransferase (alpha/beta hydrolase superfamily)	32.58	7.47	1	3.16
Gomus.A05G246900.1	Calmodulin and related proteins (EF-Hand superfamily)	17.00	3.88	1	3.16
Gomus.A11G188300.1	MYB proto-oncogene protein, plant	26.04	9.11	1	3.16
Gomus.A06G142300.1	Ketol-acid reductoisomerase	63.88	7.33	1	3.15
Gomus.A09G188300.1	T-complex protein 1 subunit delta	57.60	7.93	1	3.15
Gomus.A06G135000.2	Translation initiation factor eIF-3 subunit 7	65.70	5.43	1	3.15
Gomus.D01G002900.1	Predicted E3 ubiquitin ligase	24.51	7.43	1	3.15
Gomus.A04G142500.1	DNA-binding proteins Bright/BRCAA1/RBP1 and related proteins containing BRIGHT domain	54.80	5.16	1	3.14
Gomus.A08G234000.1	Nucleolar protein 58	60.40	8.97	1	3.14
Gomus.D02G168400.2	Cofactor required for Sp1 transcriptional activation, subunit 3	179.79	6.87	1	3.14
Gomus.A13G265900.1	Uncharacterized	58.50	8.10	1	3.13
Gomus.D05G338700.1	Small nuclear RNA activating protein complex - 50kD subunit (SNAP50)	54.19	6.24	1	3.13
Gomus.D12G047000.1	Uncharacterized protein	67.68	8.47	1	3.12
Gomus.A02G159700.9	Inositol-1,3,4-trisphosphate 5/6-kinase / inositol-tetrakisphosphate 1-kinase	34.50	6.43	1	3.11
Gomus.A05G250500.3	Porphobilinogen synthase	47.20	6.80	1	3.11
Gomus.A13G166800.4	Thioredoxin 1	19.40	9.52	1	3.11
Gomus.D13G127600.1	Protein of unknown function, DUF573	50.93	5.21	1	3.10
Gomus.A04G094100.1	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	39.80	6.24	1	3.09
Gomus.D05G023900.1	Predicted ATPase, nucleotide-binding	57.80	5.39	1	3.09
Gomus.A04G154900.1	UDP-glucose:glycoprotein glucosyltransferase	146.90	6.25	1	3.09
Gomus.A08G024700.1	Valyl-tRNA synthetase	125.80	7.02	1	3.09
Gomus.D09G217700.1	Multicopper oxidases	66.70	8.68	1	3.08
Gomus.A03G155300.1	RNA-binding protein 25	105.10	5.45	1	3.08
Gomus.A02G141100.1	Serine-threonine kinase receptor-associated protein	38.00	6.10	1	3.08
Gomus.A12G016500.1	Splicing factor 3B subunit 1	142.00	5.92	1	3.08
Gomus.D02G171200.1	Vitellogenic carboxypeptidase-like protein	50.50	8.88	1	3.06
Gomus.D09G253100.1	Uncharacterized protein	28.32	5.82	1	3.06
Gomus.A08G078000.1	UDP-glucose 4-epimerase/UDP-sulfoquinovose synthase	43.61	7.78	1	3.06
Gomus.A05G357700.1	Clathrin light chain	29.98	5.48	1	3.05
Gomus.D09G145600.1	Riboflavin synthase	35.00	7.61	1	3.05
Gomus.D01G090200.1	Phytepsin	55.90	5.34	1	3.04
Gomus.D03G150900.1	RNA-binding protein LARP/SRO9 and related La domain proteins	100.50	7.12	1	3.04
Gomus.A12G261000.1	Uncharacterized protein	34.60	5.15	1	3.04
Gomus.A12G291500.3	Uncharacterized protein	19.56	9.82	1	3.03
Gomus.D01G110000.1	Nucleoprotein TPR	233.10	4.98	1	3.02
Gomus.A06G072100.1	SNW domain-containing protein 1	68.50	8.92	1	3.02
Gomus.A12G028100.1	UDP-glucose:glycoprotein glucosyltransferase	185.30	6.30	1	3.02
Gomus.D06G079200.1	Predicted dehydrogenase	35.49	8.66	1	3.01
Gomus.D04G112000.1	Uncharacterized protein	7.19	11.36	1	3.01
Gomus.A09G003800.1	Aspartate aminotransferase, mitchondrial	47.20	8.31	1	3.01
Gomus.A01G093400.1	Uncharacterized protein	36.30	9.31	1	2.99
Gomus.A11G012000.1	Uncharacterized protein	14.37	4.98	1	2.98
Gomus.A06G146300.1	Actin filament-coating protein tropomyosin	120.40	6.61	1	2.98
Gomus.A02G159800.4	Pathogenesis-related protein Bet v I family	17.40	5.15	1	2.98
Gomus.A08G234500.1	Small subunit ribosomal protein S24e	15.60	10.62	1	2.98
Gomus.A07G188600.1	Chlorophyll A/B binding protein	16.94	5.00	1	2.98
Gomus.A05G069500.1	20S proteasome subunit beta 1	25.50	5.21	1	2.97
Gomus.A06G187600.1	5-hydroxyisourate hydrolase / 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	36.40	7.25	1	2.97

Gomus.D11G097700.1	HGG motif-containing thioesterase	20.00	8.79	1	2.97
Gomus.A13G194100.1	Pre-mRNA-splicing factor CDC5/CEF1	107.70	5.41	1	2.97
Gomus.A11G014900.1	Uncharacterized protein	24.20	6.55	1	2.96
Gomus.A08G146100.1	HGG motif-containing thioesterase	20.30	9.72	1	2.95
Gomus.A11G148100.1	Photosystem I subunit IV	15.00	9.79	1	2.95
Gomus.D02G004000.3	Predicted membrane protein	35.17	7.06	1	2.95
Gomus.A08G030300.1	Calmodulin binding protein-like	71.90	6.18	1	2.94
Gomus.A03G090300.1	Enolase	52.20	6.23	1	2.94
Gomus.D10G106800.1	Xaa-Pro aminopeptidase	73.70	5.81	1	2.94
Gomus.A11G236300.1	Molecular co-chaperone STI1	124.00	6.07	1	2.93
Gomus.D07G238200.1	Uncharacterized conserved protein, contains WD40 repeat	69.90	6.00	1	2.93
Gomus.D03G170000.1	Kinesin family member C2/C3	117.20	7.55	1	2.92
Gomus.D13G177100.1	Ribosomal protein S20	9.69	10.54	1	2.92
Gomus.A09G248300.1	Cyanate lyase	18.60	6.55	1	2.91
Gomus.A04G175300.1	Uncharacterized protein	26.90	9.67	1	2.91
Gomus.A12G268900.1	6-phosphogluconolactonase	38.40	8.72	1	2.90
Gomus.A12G017500.1	Fructose-1,6-bisphosphatase I	44.00	6.96	1	2.90
Gomus.D09G115600.1	Predicted membrane protein	20.50	9.42	1	2.89
Gomus.A09G256500.1	Uncharacterized protein	23.40	8.92	1	2.89
Gomus.A09G270300.1	Splicing factor 1	84.80	6.51	1	2.88
Gomus.A06G051300.1	Replication factor C subunit 2/4	37.80	5.36	1	2.87
Gomus.A07G136500.1	Sulfite reductase (ferredoxin)	78.20	8.97	1	2.87
Gomus.A08G018000.2	Uncharacterized conserved protein (YdiU family)	71.60	6.28	1	2.87
Gomus.A12G237700.1	Coiled-coil-helix-coiled-coil-helix domain containing 6	20.60	8.62	1	2.86
Gomus.A02G092400.1	Cytochrome b5	15.50	6.68	1	2.86
Gomus.A12G164400.1	Histone H1/H5	19.60	10.92	1	2.86
Gomus.D01G098000.1	Uncharacterized protein	36.29	8.91	1	2.85
Gomus.A08G113000.1	Cleavage and polyadenylation specificity factor subunit 5	22.90	9.11	1	2.85
Gomus.A03G159600.1	Pyruvate dehydrogenase E1 component subunit alpha	43.50	7.44	1	2.85
Gomus.A01G219400.1	Reductases with broad range of substrate specificities	28.90	6.64	1	2.85
Gomus.A08G170000.1	26S proteasome regulatory subunit N9	44.50	5.50	1	2.84
Gomus.A05G028900.1	Arginyl-tRNA synthetase	72.80	7.06	1	2.84
Gomus.A03G197900.1	ATP-dependent Clp protease, protease subunit	29.30	8.32	1	2.84
Gomus.A07G029600.1	Pyrroline-5-carboxylate reductase	28.60	8.79	1	2.84
Gomus.A06G031500.1	Proteasome subunit alpha/beta	12.28	8.34	1	2.83
Gomus.A01G223000.1	Glutathione S-transferase, N-terminal domain	38.00	8.60	1	2.83
Gomus.D13G278100.1	Ran-binding protein RANBP1 and related RanBD domain proteins	24.10	4.98	1	2.83
Gomus.A06G019700.1	Protein involved in vacuole import and degradation	71.00	6.27	1	2.82
Gomus.A08G057100.1	Large subunit ribosomal protein L13Ae	23.60	10.42	1	2.81
Gomus.A11G114300.1	PAP_fibrillin	34.10	8.40	1	2.81
Gomus.D05G005600.1	Predicted haloacid-halidohydrolase and related hydrolases	26.10	5.91	1	2.81
Gomus.D08G061900.1	Predicted lipase	46.80	6.74	1	2.81
Gomus.D01G185300.1	Prefoldin subunit 6, KE2 family	15.30	7.18	1	2.80
Gomus.A08G243000.1	WW domain binding protein WBP-2, contains GRAM domain	23.30	7.18	1	2.80
Gomus.A13G259200.1	Proliferating cell nuclear antigen	29.80	4.72	1	2.79
Gomus.A11G116500.1	Protoporphyrinogen oxidase	58.10	8.65	1	2.79
Gomus.D13G247900.1	Translation initiation factor eIF-4F	87.80	8.50	1	2.79
Gomus.A11G011100.1	Berberine and berberine like	57.70	8.09	1	2.78
Gomus.D02G230900.1	CD2 antigen cytoplasmic tail-binding protein 2	46.10	4.49	1	2.78
Gomus.A03G033400.1	Extracellular signal-regulated kinase 1/2	42.80	6.54	1	2.78
Gomus.A11G357800.1	Ubiquitin-conjugating enzyme E2 variant	16.60	6.93	1	2.78
Gomus.D07G072800.1	Uncharacterized protein	23.20	5.36	1	2.78
Gomus.D13G262400.1	Soluble epoxide hydrolase	37.60	6.37	1	2.77
Gomus.D04G191700.1	Ubiquitin fusion degradation protein 1	35.60	6.43	1	2.77
Gomus.A02G169600.1	ADP-ribosylation factor-like 8A	20.50	8.15	1	2.76
Gomus.A08G164900.1	Pectin acetylesterase and similar proteins	43.60	8.54	1	2.76
Gomus.A07G076800.1	Protein of unknown function (DUF1118)	20.90	9.51	1	2.76
Gomus.A08G040600.1	Uncharacterized protein	33.90	6.83	1	2.76
Gomus.A13G075300.1	Phosphate-induced protein 1 conserved region	42.40	9.60	1	2.75
Gomus.1Z003700.1	Red chlorophyll catabolite reductase	53.00	4.97	1	2.75
Gomus.A13G143800.1	Thiosulfate/3-mercaptopyruvate sulfurtransferase	41.80	7.15	1	2.75
Gomus.A11G302900.1	ATP-dependent RNA helicase	82.00	7.18	1	2.74
Gomus.D08G214800.1	Copper chaperone for superoxide dismutase	34.30	6.38	1	2.74
Gomus.A05G066200.1	Predicted oxidoreductase	30.50	9.73	1	2.74
Gomus.D12G270300.1	Uncharacterized protein	16.90	7.77	1	2.74
Gomus.A11G240000.4	RNA-binding protein 39	71.30	6.62	1	2.72
Gomus.A08G263700.1	Alba	14.80	5.14	1	2.71
Gomus.D02G255300.1	Alternative splicing factor SRp20/9G8 (RRM superfamily)	15.30	6.76	1	2.71
Gomus.D07G010100.1	CCCH-type Zn-finger protein	43.60	7.37	1	2.71
Gomus.D12G194800.1	Uncharacterized protein	37.40	5.41	1	2.71
Gomus.D03G021700.1	Ca2+-independent phospholipase A2	42.20	6.34	1	2.70
Gomus.D13G008500.1	Hismacro and SEC14 domain-containing proteins	28.70	8.68	1	2.70
Gomus.A06G158900.1	Oligosaccharyltransferase complex subunit gamma	38.90	8.51	1	2.69
Gomus.A01G142700.2	Small subunit ribosomal protein S28e	7.50	11.17	1	2.69
Gomus.A11G187800.1	3-dehydroquinate synthase	49.30	6.55	1	2.68
Gomus.A06G208500.1	Charged multivesicular body protein 1	22.70	7.20	1	2.68
Gomus.A01G031900.1	Huntingtin interacting protein HYPK	12.00	5.38	1	2.68
Gomus.A02G097100.1	Peptidylprolyl isomerase	24.40	6.21	1	2.68
Gomus.D05G071600.1	AIG2-like family	19.20	5.38	1	2.67
Gomus.A13G122900.1	Ca2+-binding protein, EF-Hand protein superfamily	36.70	4.72	1	2.67
Gomus.D09G244500.1	Ferredoxin	16.80	5.73	1	2.67
Gomus.A07G051600.1	Pterin carbinolamine dehydratase PCBD/dimerization cofactor of HNF1	23.50	8.44	1	2.67
Gomus.D08G124100.1	Uncharacterized protein	104.80	4.75	1	2.67
Gomus.A11G301900.1	ATP citrate (pro-S)-lyase	47.50	5.38	1	2.66
Gomus.A01G026800.1	Enoyl-CoA hydratase-related	26.10	8.88	1	2.66
Gomus.A07G021200.1	Omega-amidase	40.30	8.32	1	2.66
Gomus.A10G004900.1	Ribosomal RNA large subunit methyltransferase N	44.40	6.70	1	2.66
Gomus.D05G083400.1	Structural maintenance of chromosome 3 (chondroitin sulfate proteoglycan 6)	138.50	6.44	1	2.66
Gomus.A08G052100.1	Uncharacterized protein	36.60	5.78	1	2.66
Gomus.D08G022400.1	Predicted lipase	46.20	6.00	1	2.65
Gomus.A07G161000.1	Golgi SNAP receptor complex member 1	26.40	9.44	1	2.64
Gomus.A02G009500.1	Large subunit ribosomal protein L5e	34.10	9.47	1	2.64
Gomus.A03G141300.1	Rubber elongation factor protein (REF)	25.30	7.99	1	2.64
Gomus.A01G138600.1	Uncharacterized protein	47.20	5.00	1	2.64
Gomus.A09G218700.1	Cytochrome b5	14.90	5.29	1	2.63
Gomus.D04G182400.1	RAB proteins geranylgeranyltransferase component A (RAB escort protein)	52.80	5.73	1	2.63
Gomus.D09G174100.1	Uncharacterized protein	14.49	10.01	1	2.62
Gomus.A10G044700.1	Calcyclin binding protein	25.40	7.90	1	2.62
Gomus.A11G219700.1	Large subunit ribosomal protein L29	19.50	9.99	1	2.62
Gomus.A05G369700.2	N-methyltransferase	55.60	7.34	1	2.62
Gomus.A07G193200.1	Synaptic vesicle protein EHS-1 and related EH domain proteins	134.10	5.50	1	2.62
Gomus.A02G158100.1	Nuclear transport receptor CRM1/MSN5 (importin beta superfamily)	123.80	5.74	1	2.61
Gomus.A01G182300.2	Serine/threonine protein kinase	75.94	6.38	1	2.61
Gomus.A10G119000.1	Predicted hydrolase (HAD superfamily)	30.50	8.07	1	2.60
Gomus.A08G093000.1	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)	33.80	5.52	1	2.59
Gomus.D08G130500.1	Prohibitins and stomatins of the PID superfamily	44.90	9.01	1	2.59
Gomus.D12G313700.1	Uncharacterized protein	11.10	4.56	1	2.59
Gomus.A12G247700.1	Acetyl-CoA carboxylase carboxyl transferase subunit beta	65.40	5.05	1	2.58
Gomus.A09G113200.1	Tryptophanyl-tRNA synthetase	45.80	6.61	1	2.58
Gomus.D06G189300.1	Uncharacterized protein	14.70	3.89	1	2.58
Gomus.A13G070500.1	Aminoacylase	51.10	6.64	1	2.57
Gomus.D10G104500.1	Thioredoxin 1	13.50	5.53	1	2.57

Gomus.D07G230900.1	FK506-binding protein 2	16.80	8.98	1	2.56
Gomus.A08G127500.1	HSP20 family protein	26.10	8.05	1	2.56
Gomus.D02G025100.1	Aerolysin toxin	50.40	5.45	1	2.55
Gomus.A11G054100.1	Predicted lipase	55.30	8.70	1	2.55
Gomus.D07G093400.1	Uncharacterized protein	12.40	7.71	1	2.55
Gomus.D10G289400.1	Uncharacterized protein	21.99	8.57	1	2.54
Gomus.A08G231300.3	Nuclear transcription factor Y, gamma	28.90	6.27	1	2.54
Gomus.A05G350000.1	26S proteasome regulatory subunit N2	110.40	5.43	1	2.53
Gomus.D08G251800.1	Lipoxygenase	93.40	6.19	1	2.53
Gomus.A09G002600.1	Minichromosome maintenance protein 2	106.20	5.17	1	2.53
Gomus.A10G187700.1	Regulator of ATP-sensitive K+ channels Alpha-endosulfine/ARPP-19 and related cAMP-regulated phosphoproteins	10.90	8.92	1	2.53
Gomus.A07G020200.1	Uncharacterized protein	25.70	6.93	1	2.53
Gomus.A02G056700.1	Microtubule-binding protein (translationally controlled tumor protein)	19.00	4.63	1	2.52
Gomus.A11G174100.1	E3 ubiquitin ligase involved in syntaxin degradation	135.30	5.27	1	2.51
Gomus.A09G068500.1	Regulator of ribonuclease activity A	24.10	8.19	1	2.51
Gomus.A04G023300.1	Uncharacterized protein	15.30	5.74	1	2.51
Gomus.A09G115200.1	Isovaleryl-CoA dehydrogenase	44.66	7.50	1	2.51
Gomus.A01G230500.6	5'-AMP-activated protein kinase, beta subunit	57.50	5.05	1	2.50
Gomus.D13G143600.1	Carboxymethylenebutenolidase	33.70	7.09	1	2.50
Gomus.A02G099200.1	Extended synaptotagmin-related	61.30	6.98	1	2.50
Gomus.A12G253100.1	Monodehydroascorbate reductase (NADH)	53.30	8.02	1	2.50
Gomus.D07G252000.1	Porin/voltage-dependent anion-selective channel protein	29.30	8.76	1	2.50
Gomus.A09G085300.1	Predicted dehydrogenase	32.60	8.12	1	2.49
Gomus.A08G260900.1	Ribokinase	38.80	6.68	1	2.49
Gomus.D09G126800.1	RNA-binding protein RBM8/Tsunagi (RRM superfamily)	22.80	4.96	1	2.49
Gomus.A09G176100.1	Aquaporin PIP	30.80	9.13	1	2.48
Gomus.A09G173400.1	Glutathione S-transferase	25.90	6.00	1	2.48
Gomus.A03G073000.1	Peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	34.90	8.47	1	2.48
Gomus.A05G412100.1	Serine/threonine protein kinase	69.70	6.71	1	2.48
Gomus.A11G118500.1	Uncharacterized protein	15.42	5.02	1	2.47
Gomus.D07G062900.3	Zinc finger protein-related	31.19	8.78	1	2.47
Gomus.A10G225900.1	Arsenite-transporting ATPase	44.70	8.21	1	2.47
Gomus.A11G088100.1	Uncharacterized protein	37.89	9.26	1	2.46
Gomus.A13G147100.1	Metacaspase involved in regulation of apoptosis	46.50	5.21	1	2.46
Gomus.A03G054100.1	UDP-glucuronate decarboxylase	39.00	7.91	1	2.46
Gomus.A09G233900.1	Lipoxygenase	99.60	6.39	1	2.45
Gomus.A04G139400.1	Thioredoxin-like protein	20.10	7.85	1	2.45
Gomus.A12G028500.1	Vesicle coat complex COPI, gamma subunit	98.50	5.26	1	2.45
Gomus.A01G031600.1	DNA-directed RNA polymerase II subunit RPB9	19.90	7.75	1	2.44
Gomus.A05G078800.1	Galactan 1,3-beta-galactosidase.	92.50	7.66	1	2.44
Gomus.D04G219600.1	Myosin II heavy chain-like	71.60	8.48	1	2.44
Gomus.A06G132000.1	Serine/threonine protein kinase	92.20	8.37	1	2.44
Gomus.A12G079400.1	Asparagine synthase (glutamine-hydrolysing)	69.60	6.93	1	2.43
Gomus.A03G238600.1	DNA damage-binding protein 1	121.10	5.34	1	2.43
Gomus.A10G086500.1	Peptide alpha-N-acetyltransferase	101.80	6.83	1	2.43
Gomus.D08G286700.1	Uncharacterized protein	35.60	5.30	1	2.43
Gomus.A13G065400.1	ATP-dependent RNA helicase	46.20	6.37	1	2.42
Gomus.A03G181700.1	Alanyl-tRNA synthetase	111.10	6.67	1	2.41
Gomus.A12G248000.1	NADH dehydrogenase I subunit K	25.30	8.24	1	2.41
Gomus.A04G184900.1	UDP-glucuronosyl and UDP-glucosyl transferase	51.90	6.61	1	2.41
Gomus.A05G076600.1	20S proteasome subunit alpha 7	27.30	6.54	1	2.40
Gomus.A05G435200.1	Peroxidase	35.40	9.33	1	2.40
Gomus.D05G368900.1	Photosystem II 10kDa protein	14.30	9.55	1	2.40
Gomus.D11G133400.1	Calcofluor white hypersensitive protein precursor	58.60	9.57	1	2.39
Gomus.A13G016100.1	Clathrin heavy chain	193.00	5.47	1	2.39
Gomus.A11G340500.1	Diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	10.20	5.52	1	2.39
Gomus.A10G222600.1	Heterogeneous nuclear ribonucleoprotein G	31.20	9.38	1	2.38
Gomus.D02G146200.1	Predicted dehydrogenase	143.90	6.73	1	2.38
Gomus.D12G011100.1	Uncharacterized protein	32.90	10.07	1	2.37
Gomus.A12G044500.1	Molecular chaperone (DnaJ superfamily)	38.20	6.37	1	2.36
Gomus.A05G263000.1	HSP90 co-chaperone p23	20.50	4.58	1	2.35
Gomus.A07G240000.1	Structural maintenance of chromosome 1	140.30	7.66	1	2.35
Gomus.A11G301400.1	Glucose-6-phosphate 1-dehydrogenase	72.00	6.68	1	2.33
Gomus.A10G133700.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 13	16.10	9.33	1	2.32
Gomus.A10G088800.1	Pyridoxine biosynthesis protein	32.90	5.31	1	2.32
Gomus.A08G087400.2	Universal stress protein family	17.20	7.33	1	2.32
Gomus.A09G072800.1	Universal stress protein family	17.90	6.92	1	2.31
Gomus.D09G109200.1	AP-2 complex subunit alpha	114.20	6.37	1	2.29
Gomus.A08G256400.1	Bifunctional aspartokinase / homoserine dehydrogenase 1	99.70	7.71	1	2.29
Gomus.A05G205200.1	Large subunit ribosomal protein L31	15.00	9.74	1	2.28
Gomus.A10G150100.1	2-isopropylmalate synthase	67.80	6.24	1	2.27
Gomus.A02G180100.1	Cell cycle-regulated histone H1-binding protein	50.90	4.49	1	2.27
Gomus.A06G117300.1	DNA topoisomerase III alpha	126.10	9.33	1	2.27
Gomus.D11G392100.1	Transcription initiation factor TFIID subunit 8	41.30	6.93	1	2.26
Gomus.A05G239200.1	3-deoxy-7-phosphoheptulonate synthase	59.30	8.60	1	2.25
Gomus.D02G023700.1	Aerolysin toxin	54.90	5.96	1	2.25
Gomus.A07G220400.1	Ribonuclease T2	29.00	5.85	1	2.25
Gomus.D06G100200.1	Small heat-shock protein (HSP20) family	16.00	7.91	1	2.25
Gomus.A06G112400.2	Karyopherin (importin) beta 3	122.90	4.87	1	2.24
Gomus.A10G148500.1	Chloroplast alpha-glucan water dikinase	130.50	6.07	1	2.23
Gomus.A08G057300.1	Small ubiquitin-related modifier	11.30	4.97	1	2.23
Gomus.A11G130800.1	mKIAA1688 protein	50.99	4.56	1	2.23
Gomus.A02G153400.1	GTPase Rab1/YPT1, small G protein superfamily, and related GTP-binding proteins	23.50	7.85	1	2.21
Gomus.A06G075700.1	Charged multivesicular body protein 4	23.90	4.84	1	2.21
Gomus.A05G292100.1	Phosphatidylinositol transfer protein SEC14 and related proteins	66.00	4.87	1	2.19
Gomus.A11G101200.1	Glycosyl hydrolases family 28	52.71	7.02	1	2.18
Gomus.D05G344800.1	Chalcone synthase	43.50	6.73	1	2.17
Gomus.D12G035700.1	GTPase, IMAP family member-related	127.60	5.02	1	2.15
Gomus.A02G076600.1	Photosystem II	29.70	6.42	1	2.15
Gomus.D09G172000.1	RNA helicase	32.10	10.07	1	2.14
Gomus.D12G260200.3	Cysteinyl-tRNA synthetase	47.81	6.54	1	2.14
Gomus.A08G194300.1	Copper chaperone for superoxide dismutase	35.00	6.57	1	2.13
Gomus.A10G270300.1	CGI-12 protein-related	31.56	7.90	1	2.12
Gomus.A03G182700.1	Succinyl-CoA synthetase alpha subunit	36.10	8.75	1	2.12
Gomus.D06G159400.1	Uncharacterized Zn ribbon-containing protein	12.30	4.93	1	2.08
Gomus.A02G143900.1	V-type H+-transporting ATPase 54 kD subunit	51.50	7.99	1	2.08
Gomus.D10G043500.1	Apoptosis inhibitor 5-related	93.00	5.81	1	2.06
Gomus.A04G033900.1	Pathogenesis-related protein Bet v I family	19.10	5.67	1	2.06
Gomus.A02G131500.1	Beta-galactosidase	94.00	7.33	1	2.05
Gomus.D06G128900.1	Predicted membrane protein	43.20	8.73	1	2.03
Gomus.A01G008100.1	Leucine-rich repeat (LRR) protein associated with apoptosis in muscle tissue	54.70	7.46	1	2.02
Gomus.A09G209300.2	Acyl-CoA oxidase	74.50	7.20	1	2.00
Gomus.A01G107300.1	Uncharacterized protein	17.10	7.44	1	2.00
Gomus.D13G129800.2	Branched chain aminotransferase BCAT1, pyridoxal phosphate enzymes type IV superfamily	63.10	7.55	1	1.96
Gomus.A11G149000.1	Acetyl-CoA acyltransferase 1	47.50	8.16	1	1.95
Gomus.A02G057000.1	UDP-glucuronate decarboxylase	49.40	9.28	1	1.95
Gomus.D01G161000.1	Uncharacterized conserved protein	19.70	5.19	1	1.95
Gomus.A09G038400.1	Glucose-6-phosphate 1-dehydrogenase	58.90	7.47	1	1.93
Gomus.A13G248500.1	Actin-like protein 6A	48.20	5.21	1	1.92
Gomus.A05G034600.1	Threonine synthase	58.70	7.64	1	1.90
Gomus.D09G087800.1	Soluble epoxide hydrolase	35.40	5.25	1	1.89

Gomus.A05G402200.1	Acetyl-CoA carboxylase biotin carboxyl carrier protein	30.70	5.99	1	1.88
Gomus.A11G076700.1	Glutamine amidotransferase / cyclase	64.10	7.46	1	1.83
Gomus.D05G309000.1	Uncharacterized protein	25.90	8.38	1	1.82
Gomus.A05G315800.1	Uncharacterized protein	22.80	4.50	1	1.67
Gomus.A07G183600.1	50S/60S ribosomal protein L16	15.40	10.64	1	1.66
Gomus.A07G053700.2	Signal recognition particle subunit SRP68	69.10	9.00	1	1.64