Short title: pPGI-independent responses to microbial VCs

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Title: Arabidopsis responds to *Alternaria alternata* volatiles by triggering pPGI-independent mechanisms

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One sentence summary:

The cytokinin-mediated responses of plants to volatile compounds emitted by pathogenic microorganisms involve the activation of plastidic phosphoglucose isomerase-independent mechanisms.

FOOTNOTES

Authors´ contributions: AM S-L, A B, N DD, M B, FJ M, E B-F and J P-R designed the experiments and analysed the data; AM S-L, A B, M B, N DD, F JM, G A, A R-B, P G-G, K A, J L, JF H, O N, S C, MC M, R N and E B-F performed most of the experiments; L S, K D, O N and J P-R supervised the experiments; AM S-L, A B, FJ M and J P-R wrote the article with contributions from all the authors; J P-R conceived the project and research plans.

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ABSTRACT

Volatile compounds (VCs) emitted by phylogenetically diverse microorganisms (including plant pathogens and microbes that do not normally interact mutualistically with plants) promote photosynthesis, growth and the accumulation of high levels of starch in leaves through cytokinin (CK) regulated processes. In the Arabidopsis plants not exposed to VCs, plastidic phosphoglucose isomerase (pPGI) acts as an important determinant of photosynthesis and growth, likely as a consequence of its involvement in the synthesis of plastidic CKs in roots. Moreover, this enzyme plays an important role in connecting the Calvin Benson cycle with the starch biosynthetic pathway in leaves. To elucidate the mechanisms involved in the responses of plants to microbial VCs, and to investigate the extent of pPGI involvement, we characterized pPGI null *pgi1-2* Arabidopsis plants cultured in the presence or absence of VCs emitted by *Alternaria alternata*. We found that volatile emissions from this fungal phytopathogen promote growth, photosynthesis and the accumulation of plastidic CKs in *pgi1-2* leaves. Notably, the mesophyll cells of *pgi1-2* leaves accumulated exceptionally high levels of starch following VCs exposure. Proteomic analyses revealed that VCs promote global changes in the expression of proteins involved in photosynthesis, starch metabolism and growth that can account for the observed responses in *pgi1-2* plants. The overall data show that Arabidopsis plants can respond to VCs emitted by phytopathogenic microorganisms by triggering pPGI-independent mechanisms.

INTRODUCTION

It is well known that volatile compounds (VCs) emitted by beneficial rhizosphere bacteria and fungi can promote plant growth (Ryu et al., 2003; Hung et al., 2013; Kanchiswamy et al., 2015). We have recently shown that this action is not only restricted to beneficial microorganisms, but extends to pathogens and microbes that do not normally interact mutualistically with plants (Sánchez-López et al., 2016). When Arabidopsis plants were exposed to VCs emitted by the fungal phytopathogen *Alternaria alternata,* growth promotion was accompanied by enhanced intracellular levels of plastidic-type, 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway-derived cytokinins (CKs), augmented photosynthesis, and accumulation of exceptionally high levels of starch in leaves (Ezquer et al., 2010; Li et al., 2011; Sánchez-López et al., 2016). Furthermore, mutants with reduced CK content or sensitivity responded poorly to VCs (Sánchez-López et al., 2016). Because CKs are major determinants of growth, photosynthesis and starch accumulation in mature leaves (Riefler et al., 2006; Werner et al., 2008; Kieber and Schaller, 2014; Bahaji et al., 2015b), we postulated that plant´s response to VCs involve CK action (Sánchez-López et al., 2016). The transcriptome changes of plants exposed to VCs emitted by phylogenetically distant microbial species, such as *A. alternata* and the beneficial plant growth promoting rhizobacterium *Bacillus subtilis* GB03 were strikingly similar (Sánchez-López et al., 2016), indicating that plants react to microbial VCs through highly conserved regulatory mechanisms. We have proposed that VC-promoted plant growth and metabolic changes prepare the plant for hosting the microorganism, which, in the case of phytopathogenic microorganisms, ensures proper continuation into the pathogenic phase (Sánchez-López et al., 2016).

Phosphoglucose isomerase (PGI) catalyzes the reversible isomerization of glucose-6-phosphate (G6P) and fructose-6-phosphate (F6P). This enzyme is involved in glycolysis and in the regeneration of G6P molecules in the oxidative pentose phosphate pathway. In mesophyll chloroplasts of illuminated leaves, the plastidic isoform of PGI (pPGI) also plays a fundamental role in starch biosynthesis, connecting the Calvin-Benson cycle (CBC) with the starch biosynthetic pathway that encompasses plastidic phosphoglucomutase (pPGM), ADP-glucose pyrophosphorylase (AGP) and starch synthase (SS) (Bahaji et al., 2014b). Recent studies have shown that the leaves of pPGI null *pgi1-2* mutants accumulate low levels of plastidic CKs (Bahaji et al., 2015b). These plants display reduced photosynthetic capacity and slow growth phenotypes, and accumulate low levels of starch in the mesophyll cells of leaves (Bahaji et al., 2015b). However, this phenotype can be reverted to wild type (WT) by exogenous CK supplementation (Bahaji et al., 2015b). Thus, pPGI is an important determinant of photosynthesis, starch accumulation and growth most likely as a consequence of its involvement in the production of oxidative pentose phosphate pathway/glycolysis intermediates that are required to synthesize plastidic CKs in roots, assimilate nitrogen and/or maintain plastid redox homeostasis (Bahaji et al., 2015b).

A. alternata emits highly reactive VCs such as sesquiterpenes (Weikl et al., 2016). These compounds are known to function as infochemicals, playing crucial roles in plant-to-microbe interactions (Peñuelas et al., 2014; Ditengou et al., 2015). Although there has been a considerable increase in our knowledge regarding the importance of metabolic adjustments to changing environmental conditions during recent years, little is known about the adjustments that occur in plants following exposure to microbial VCs. Thus, to obtain insights into the mechanisms involved in the *A. alternata* VCs promoted growth, photosynthesis and accumulation of CKs and starch, and to investigate the extent to which pPGI is involved in these responses, in this work we characterized *pgi1-2* plants exposed to *A. alternata* VCs. Our findings show that Arabidopsis is capable of responding to microbial volatile emissions by triggering pPGI-independent mechanisms, and raise important questions regarding the basic mechanisms of starch biosynthesis in leaves exposed to VCs.

RESULTS AND DISCUSSION

A. alternata VCs promote growth and the accumulation of high levels of starch in mesophyll cells of *pgi1-2* plants

pgi1-2 plants were cultured in the absence or continuous presence of *A. alternata* VCs for one week. As shown in Fig. 1A, VCs promoted growth in *pgi1-2* plants to the same extent than in WT plants, providing evidence that *A. alternata* VCs exert stimulatory effect on growth through pPGI-independent mechanisms.

Time-course analyses of starch content during illumination showed that *pgi1-2* and WT leaves accumulate starch at rates of ca. 2 and 20 nmol of glucose transferred to starch min^{-1} g^{-1} fresh weight (FW), respectively (Fig. 1B). The rate of starch accumulation in WT leaves after 2 h of exposure to *A. alternata* VCs increased to ca. 330 nmol glucose transferred to starch min^{-1} x g^{-1} FW (Fig. 1B). Consequently, leaves of WT plants exposed to fungal VCs for 16 h accumulated ca. 15 fold more starch than non-treated leaves. Notably, the rate of starch accumulation in *pgi1-2* leaves after 2-4 h of VCs exposure increased to ca. 240 nmol glucose transferred to starch min^{-1} x g^{-1} FW (Fig. 1B). Consequently, leaves of VC-treated *pgi1-2* plants accumulated exceptionally high levels of starch after 16 h of VCs exposure (ca. 8- and 85-fold higher than those of non-exposed WT and *pgi1-2* leaves, respectively). The starch levels in leaves of VC-treated WT and *pgi1-2* plants remained high during the following seven days of treatment (results not shown).

The finding that leaves of *pgi1-2* plants treated with fungal VCs accumulate high levels of starch was an unexpected result. To confirm that what we had measured was indeed starch, we analyzed iodine-stained leaves of WT and *pgi1-2* plants that had been cultured in the absence or presence of *A. alternata* VCs for 16 h. Furthermore, we conducted light microscopy analyses of toluidine-stained leaves and transmission electron microscopic (TEM) analyses of leaf mesophyll cells of VC-treated WT and *pgi1-2* plants. As shown in Fig. 2, A, B, I and J, the iodine staining of leaves of VC-treated WT and *pgi1-2* plants was darker than that of non-treated leaves. The iodine staining was homogenously distributed throughout the leaf in both VC-treated WT and *pgi1-2* plants, indicating that starch over-accumulation mainly occurs in the mesophyll. Light microscopy analyses of sections of the stained leaves showed that, unlike WT leaves, *pgi1-2* mesophyll cells were poorly stained when plants were cultured in the absence of VCs (Fig. 2, C and K). In clear contrast, the mesophyll cells of VC-treated WT and *pgi1-2* leaves were heavily stained (Fig. 2, D and L). The light microscopy (Fig. 2, E, F, M and N) and TEM analyses (Fig. 2, G, H, O and P) of leaves showed that the mesophyll chloroplasts of VC-treated WT and *pgi1-2* plants possess starch granules far larger than those of chloroplasts of plants cultured in the absence of VCs. Thus, the data show that *A. alternata* VCs stimulate important CBC-pPGI-pPGM-AGP-SS-independent starch biosynthetic pathways to allow the mesophyll cells of leaves to accumulate exceptionally high levels of starch.

A. alternata VCs increase the photosynthetic activities of exposed *pgi1-2* plants

pPGI null mutants have a lower photosynthetic capacity than WT plants, which can partly explain the reduced growth and low starch content of these mutants (Bahaji et al., 2015b). We thus hypothesized that the growth promotion and accumulation of high levels of starch in *pgi1-2* plants exposed to *A. alternata* VCs could be the consequence, at least in part, of enhanced photosynthetic capacity. To test this hypothesis, we measured key parameters of the light and dark phases of photosynthesis in *pgi1-2* plants exposed to *A. alternata* VCs over three days. During the light phase, maximum quantum yields of PSII in the dark-adapted state (Φ_{Po}) and the PSII operating efficiency (Φ_{PSII}) were higher in leaves of the VC-treated *pgi1-2* plants than in controls (Table 1), implying an improvement in the energy transfer within PSII. Furthermore, non-photochemical quenching of chlorophyll fluorescence (Φ_{NPQ}) was reduced by exposure to VCs (Table 1). These results indicate that leaves of VC-treated *pgi1-2* plants used the light more efficiently, dissipated less excitation energy as heat, had a better electron transport downstream from PSII, reduced more $NADP^+$ and hence, had higher net rates of CO_2 assimilation (A_n) than controls. This inference was corroborated by the analyses of both photosynthetic pigments and NADPH levels, as well as A_n under varying intercellular CO_2 concentrations (*Ci*). As shown in Fig. 3A, the leaves of VC-treated *pgi1-2* plants had higher chlorophyll and carotenoid levels than in controls. Also, the NADPH content of VC-treated *pgi1-2* plants leaves (6.09 ± 0.12 nmol NADPH g^{-1} FW) was higher than that of non-treated leaves (4.87 ± 0.11 nmol NADPH g^{-1} FW). Moreover, *pgi1-2* plants exposed to VCs had higher A_n values than controls at all *Ci* levels (Fig. 3B), reaching values that were comparable to those of VC-treated WT plants (Sánchez-López et al., 2016). The maximum rate of carboxylation by Rubisco (V_{cmax}), as well as the maximum electron transport demand for RuBP regeneration (J_{max}) determined from the A_n/Ci curves were both significantly higher in leaves of VC-treated *pgi1-2* plants than in controls, as was triose-phosphate use (TPU) (Table 1). Furthermore, the photosynthetic electron transport rate (ETR) was higher in the VC-treated *pgi1-2* plants than in controls (Fig.

3C), reaching values that were comparable to those of VC-treated WT plants (Sánchez-López et al., 2016). Moreover, the levels of primary photosynthates were significantly up-regulated by *A. alternata* VCs. Thus, as shown in Fig. 4A, the levels of sucrose, glucose, fructose, maltose, phosphorylated forms of glucose and fructose (glucose-1-P (G1P), G6P, F6P and fructose-1,6-bisphosphate), and CBC intermediates, such as glyceraldehyde-3-phosphate (GAP) and 3-phosphoglycerate (3PGA), were higher in the leaves of VC-treated *pgi1-2* plants than in controls. Also, total free amino acid content was higher in leaves of VC-treated plants than in controls (Fig. 4B; Supplemental Fig. S1). The most prominent free amino acids were the stress-responsive alanine as well as the high-N containing glutamine and asparagine, which reflected enhanced nitrogen assimilation under VCs exposure.

These results strongly indicate that *A. alternata* VCs stimulate pPGI-independent mechanisms that increase the efficiency of plants' use of light energy in photosynthesis and enhance the formation of photosynthates.

A. alternata VCs promote the accumulation of active forms of plastidic CKs in *pgi1-2* leaves

Plastidic MEP pathway derived CKs are mainly synthesized in roots and transported to the aerial parts of the plant, where they regulate plant growth (Ko et al., 2014). We have recently provided evidence that pPGI is an important determinant of plastidic CK content in leaves, and this is most likely based on its involvement in the synthesis of GAP (Bahaji et al., 2015b), the substrate for the initial reaction of the plastidic MEP pathway (Pulido et al., 2012; Pokhilko et al., 2015). To investigate the possible involvement of pPGI in the VC-promoted increase of plastidic CKs in WT leaves (Sánchez-López et al., 2016), we measured the levels of different CKs in the leaves of *pgi1-2* plants that had been cultured in the absence or presence of VCs emitted by *A. alternata* for three days. As shown in Table 2, exposure to VCs caused a significant increase of the total content of MEP-derived CKs in *pgi1-2* leaves. The total content of MEP-derived CKs in VC-treated *pgi1-2* leaves (1193.24 ± 100.89 pmol g^{-1} dry weight (DW), Table 2) was lower than that of VC-treated WT leaves (1534.78 ± 23.61 pmol g^{-1} DW, cf. Table 2 in Sánchez-López et al., 2016). Moreover, the VC-promoted augmentation of total CK content in *pgi1-2* leaves (ca. 400 pmol g^{-1} DW, Table 2) was comparable to that which had been observed in WT leaves (cf. Table 2 in Sánchez-López et al., 2016), indicating that pPGI plays only a minor role in the VC-promoted accumulation of CKs in WT leaves. The most prominent CK forms were the biologically active isopentenyladenine (iP) and *trans*-zeatin (tZ), as well as their ribosides (iPR and tZR, respectively) and precursors (iPRMP and tZRMP, respectively). On the other hand, the levels of the less biologically active CKs dihydrozeatin (DZ) and *cis*-zeatin (cZ) were substantially reduced (Table 2; Supplemental Fig. S2).

As for the pPGI-independent mechanisms that may have contributed to the increase in MEP-derived CKs in the leaves of VC-treated *pgi1-2* plants, it should be noted that the GAP content in VC-treated *pgi1-2* leaves was 2-fold higher than that of non-treated leaves (Fig. 4A), likely as a consequence of enhanced photosynthesis. Therefore, the accumulation of high levels of MEP-derived CKs in the leaves of VC-treated *pgi1-2* plants may be partly due to the enhanced photosynthetic production of GAP and its subsequent conversion to MEP-derived CKs (Supplemental Fig. S2). Another mechanism that could explain the pPGI-independent enhancement of plastidic CKs in VC-treated leaves is the conversion of cytosolic GAP into isopentenyl diphosphate (IPP) and/or dimethylallyl diphosphate (DMAPP), and subsequent transport of these metabolites into the chloroplast, which could increase the DMAPP pool available for plastid-localized isopentenyltransferases (Supplemental Fig. S2). This mechanism of IPP and/or DMAPP exchange between the cytosol and plastids has been proposed as the MVA-derived contribution to plastidic biosynthesis of gibberellins (Helliwell et al., 2001).

Regarding the mechanism(s) that may be involved in the VC-promoted increase in the active and transport forms of MEP-derived CKs and their precursors in *pgi1-2* leaves, it should be noted that levels of the less biologically active CKs cZ, cZR and DZ, and levels of *N*- and *O*-glycosylated inactive forms DZOG, DZ7G, cZOG and cZ9G, were lower than in controls (Table 2; Supplemental Fig. S2). This indicates that the down-regulation of enzymes involved in the conversion of tZ into DZ, as well as in the degradation of active plastidic CKs, could play a role in the VC-promoted accumulation of active and transport forms of MEP-derived CKs and their precursors.

A. alternata **VCs promote changes in the proteome of** ***pgi1-2*** **leaves that account for the observed physiochemical responses**

The results presented above show that *A. alternata* VCs stimulate important pPGI independent mechanisms, resulting in the enhancement of photosynthesis, growth and starch over-accumulation in leaves. To obtain insights into these mechanisms we carried out high-throughput, isobaric labeling-based differential proteomic and phosphoproteomic analyses of leaves from *pgi1-2* plants cultured in the absence or in the presence of VCs emitted by *A. alternata* for three days. As shown in Supplemental Table S1, these analyses revealed that, in the presence of *A. alternata* VCs, 226 out of the 3805 proteins identified in this study (Supplemental Table S2) were up-regulated, and 60 proteins were down-regulated. By using the broad characterizations outlined by MapMan, the 286 proteins that were differentially regulated by *A. alternata* VCs were assembled into 29 functional groups (Fig. 5). These proteins were also classified into 8 groups according to their subcellular localizations, and the chloroplastic proteins were shown to be the most differentially regulated (Supplemental Table S3; Supplemental Fig. S3). Nearly 9% of the proteins of *pgi1-2* leaves differentially regulated by VCs are encoded by CK-responsive genes (Supplemental Table S1; Fig. 5), which reinforces the idea that CKs play an important role in the response of plants to *A. alternata* VCs (Sánchez-López et al., 2016). Moreover, 21% of the proteins that where differentially regulated by VCs are encoded by genes which expression was also differentially regulated by *A. alternata* VCs (Sánchez-López et al., 2016) (Supplemental Table S1), indicating that VC-promoted changes in the proteome of *pgi1-2* leaves are subject to both transcriptional and post-transcriptional regulation. The general trend indicates that VC-promoted responses are the consequence, at least partly, of changes in the expression of proteins from the following groups: photosynthesis, protection against photoinhibition and photooxidative damage, cell wall biosynthesis as well as amino acid and central carbohydrate metabolisms.

Photosynthesis

VCs promoted the expression of proteins that directly participate in the synthesis of chlorophyll (e.g. PORB, PORC, PCB2, CHLH, CRD1, CHLI1 and GUN4) (Supplemental Table S1; Fig. 5), which is consistent with the enhanced chlorophyll content observed in the leaves of VC-treated plants (Fig. 3A). Exposure to VCs also up-regulated the expression of enzymes involved in the conversion of SO_4^{2-} into SO_3^{2-} (e.g. the CK up-regulated APR2, APR3, APS1 and APS3) (Supplemental Table S1; Fig. 5), and the conversion of SO_3^{2-} into sulfoquinovosyldiacylglycerol (SQD1 and SQD2), a sulfolipid that acts as an integral component of the PSII protein complex and helps maintain the negatively-charged lipid-water interface required for the proper functioning of photosynthetic membranes (Frentzen, 2004). VCs treatment also increased the expression of the PSII reaction center proteins PSBT and PsbH (Supplemental Table S1; Fig. 5). Notably, phosphoproteomic analyses revealed that VC-promoted changes in the phosphorylation status of PsbH and LHCB4.1 (Supplemental Table S1). The phosphorylation of PSII proteins is required for adequate lateral mobility of membrane proteins, sustained photosynthetic activity, and to prevent oxidative damage of photosynthetic proteins (Fristedt et al., 2009). The presented data would thus indicate that VC-promoted enhancement of photosynthesis in *pgi1-2* plants is the result of enhanced enzymatic production of chlorophyll and sulfoquinovosyldiacylglycerol, along with the up-regulation of, and changes in the phosphorylation status, of PSII proteins (Fig. 6).

Protection against photoinhibition and photooxidative damage

The *A. alternata* VC-promoted increase of ETR (Fig. 3C) could create conditions under which reactive oxygen species (ROS) are produced. Therefore, it is conceivable that VCs would trigger mechanisms that prevent ROS production and/or photooxidative damage, allowing the plant to convert more light into chemical energy under VCs exposure. In line with this presumption, we found that VCs positively influence the expression of enzymatic ROS scavengers (e.g. MSBP2, APX1, CAT3 and AHB2), as well as proteins that prevent the formation of ROS (e.g. FER1 and FER3) (Supplemental Table S1; Fig. 5). Some of these proteins (e.g. AHB2) have been shown to be transcriptionally up-regulated by CKs, and to act as important determinants of growth (Hunt et al., 2001, 2002).

Consistent with the increased content of carotenoids observed in VC-treated *pgi1-2* leaves (Fig. 3A), VCs exerted a negative effect on the expression of NCED4 (Supplemental Table S1; Fig. 5), a protein that is involved in carotenoid degradation and transcriptionally down-regulated by CKs (Gonzalez-Jorge et al., 2013). An essential role of carotenoids in photosynthesis is the protection against photooxidative damage (Ruiz-Sola and Rodríguez-Concepción, 2012), and in this way, NCED4 down-regulation may contribute to enhanced photosynthetic capacity observed in VC-treated plants (Fig. 5; Table 1).

Cell wall biosynthesis

Since cell wall composition and extensibility are major determinants of growth, it is conceivable that the VC-promoted growth of *pgi1-2* plants partly involved changes in the expression of cell wall-related enzymes. The proteomic analysis provided evidence for this hypothesis, as it revealed that VCs exposure altered the expression of a number of enzymes that participate in cell wall composition and extensibility (e.g. RHM1, RHM2, UGT74C1, AXS2, NRS/ER, RGP2, UGD2, UGD3, XTH24, BXL1, XYL4, BGAL1 and BGAL4) (Supplemental Table S1; Fig. 5). Some of these enzymes (e.g. RHM1 and XTH24) are regulated by CKs.

Amino acid metabolism

VCs positively affected the expression of enzymes that are involved in the conversion of 3PGA from the CBC and plastidic glutamine into methionine (e.g. the chloroplastic PGDH2, ASP3, AKHSDH1, AKHSDH2, CGS1 and CBL) (Supplemental Table S1; Fig. 5), as well as the conversion of glutamate into alanine through the γ-aminobutyrate (GABA) shunt (e.g. GAD2), which would explain the accumulation of high levels of alanine, GABA, glutamate, aspartate, asparagine and methionine observed in VC-treated leaves (Fig. 4B and Fig. 6).

VCs also up-regulated the expression of enzymes involved in the conversion of methionine and cysteine into aliphatic glucosinolates, including those involved in chain elongation reactions (e.g. BCAT3, BCAT4, IPMI1, IPMI2, IMD1, MAM1), the construction of the glucosinolate core (e.g. APK1, CYP79F1, CYP83A1, GSTU20, SUR1, UGT74C1, SOT17, SOT18) and secondary modifications (e.g. FMOGS-OX3) (Supplemental Table S1; Fig. 5). Glucosinolates are sulfur-rich, amino acid-derived secondary metabolites that act as important determinants of plant growth, development and defense against pathogens (Tantikanjana et al., 2001; Sonderby et al., 2010; He et al., 2011; Imhof et al., 2014). Some of the differentially regulated enzymes involved in glucosinolate biosynthesis (e.g. IPMI1 and GSTU20) are up-regulated by CKs (Brenner and Schmülling, 2015). Others (e.g. CYP79F1) play important roles in modulating the intracellular levels of CKs (Tantikanjana et al., 2004). Thus, it is likely that the VC-promoted up-regulation of enzymes involved in glucosinolate biosynthesis contributed to the enhanced growth of *pgi1-2* plants.

Central carbohydrate metabolism

VCs positively affected the expression of granule bound SS (GBSS) (Supplemental Table S1; Fig. 5). Moreover, VCs up-regulated the expression of a number of starch breakdown enzymes (e.g. AMY3, ISA3, SEX4, PHS1 and GWD3) (Supplemental Table S1; Fig. 5), which is consistent with the occurrence of high levels of maltose observed in VC-treated leaves (Fig. 4). The up-regulation of starch breakdown enzymes may reflect a mechanism that aims to prevent excessive accumulation of starch, and points to the possible stimulation by VCs of starch degradation and the cycling of starch breakdown products during illumination. The resulting "futile" cycle (Fig. 6) may entail advantages such as buffering of metabolite levels, improved sensitivity in metabolic regulation, and the rapid channeling of metabolites to various pathways in response to the physiological and biochemical needs imposed by VC exposure. For example, G1P derived from starch breakdown could be utilized to produce sulfolipids, which as discussed above, could result in enhanced photosynthesis. Also, hexose-Ps derived from starch breakdown could supply carbon to the CBC, a phenomenon that occurs when plants are cultured under photorespiratory conditions (Weise et al., 2006). Furthermore, maltose derived from starch degradation could act as protectant of proteins, membranes and the photosynthetic electron transport chain (Kaplan and Guy, 2004). On the other hand, the maltose could be exported to the cytosol for conversion into the UDP-glucose necessary for the synthesis of sucrose and/or cell wall polysaccharides (Fig. 6). In support of the latter hypothesis, we found that VCs positively affect the expression of enzymes involved in the starch-to-sucrose conversion process (e.g. UGP1 and DPE2).

CONCLUSION AND ADDITIONAL REMARKS

In Arabidopsis plants not exposed to VCs, pPGI acts as an important determinant of photosynthesis, starch accumulation and growth partly as a consequence of its involvement in the production of plastidic CKs in roots (Bahaji et al., 2015b). In this work we have shown that the promotion of photosynthesis, growth and starch over-accumulation by VCs involves the stimulation of pPGI-independent mechanisms partly as a consequence of the photosynthesis-driven enhancement of plastidic CK production in leaves, which, in turn, further promotes photosynthesis (Fig. 6). This phenomenon is accompanied by the accumulation of stress-responsive amino acids such as alanine and GABA (Fig. 4B), which may represent a strategy for adaptation to the environmental conditions caused by exposure to VCs emitted by *A. alternata*. The finding that leaves of *pgi1-2* plants exposed to fungal VCs accumulate exceptionally high levels of starch (Fig. 1 and Fig. 2) when the rate of photosynthesis increases (Fig. 3) conflicts with the widely accepted view that the whole photosynthesis-driven starch biosynthetic process occurs solely in the chloroplast by means of the CBC-pPGI-pPGM-AGP-SS pathway. On the other hand, this finding is consistent with the idea that the starch deficiency in *pgi1-2* leaves not exposed to VCs is partly due to the reduced CO_2 fixation capacity of this mutant, rather than only a consequence of the lack of pPGI-mediated flow between the CBC and the pPGM-AGP-SS starch biosynthetic pathways (Bahaji et al., 2015b).

Taken together, the results presented here indicate that VC-promoted starch over-accumulation in the mesophyll cells of *pgi1-2* leaves is the consequence of factors such as enhanced photosynthesis (Fig. 3), the allosteric and redox activation of AGP by enhanced levels of photosynthetically produced 3PGA and NADPH (Li et al., 2011), up-regulation of GBSS expression (Supplemental Table S1; Fig. 5), and stimulation of incorporation into the chloroplast of cytosolic hexoses that, once there, are converted into starch (Fig. 6). Regarding the mechanism(s) of uptake of cytosolic hexoses linked to starch biosynthesis within mesophyll chloroplasts of *pgi1-2* leaves, it should be noted that Arabidopsis contains two functional plastidic G6P/Pi translocators (GPT1 and GPT2) that are capable of transporting hexose-Ps (Kammerer et al., 1998). Although the chloroplasts of mature WT leaves are not capable of transporting hexose-Ps (Quick et al., 1995; Kunz et al., 2010), most likely as a consequence of the marginally low expression of *GPT1* and *GPT2* (Kammerer et al., 1998), *GPT2* has been shown to be expressed in *pgi1-2* leaves (Kunz et al., 2010). Therefore, it is likely that starch biosynthesis occurring in the mesophyll cells of VC-treated *pgi1-2* leaves involves the GPT2-mediated transport of cytosolic G6P into the chloroplast (Fig. 6). Chloroplasts possess both a glucose transporter (pGlcT) (Weber et al., 2000) and hexokinase (Giese et al., 2005), which potentially enable the incorporation of cytosolic glucose and its subsequent conversion into G6P, facilitating the bypass of the pPGI step in *pgi1-2* leaves (Fig. 6). However, pGlcT has been shown to export the glucose arising from starch breakdown to the cytosol during the night rather than import cytosolic glucose to the chloroplast (Weber et al., 2000; Cho et al., 2011). Chloroplasts from mature leaves also possess a yet to be identified ADPG transport machinery (Pozueta-Romero et al., 1991). Taking into account that a sizable pool of ADPG linked to starch biosynthesis has a cytosolic localization in leaves (Baroja-Fernández et al., 2004; Bahaji et al., 2011, 2014a), it is likely that the starch biosynthesis observed in the mesophyll cells of VC-treated mature leaves partly involves the cytosolic production of ADPG, its subsequent transport into the chloroplast, and then, conversion into starch (Fig. 6). Needless to say, further research will be necessary to identify the cytosolic hexose molecules that enter the chloroplast in VC-treated leaves for their subsequent conversion into starch.

MATERIALS AND METHODS

Plant and microbial cultures, growth conditions and sampling

The experiments were carried out using *Arabidopsis thaliana* L. (Heynh) ecotype Wasilewskija (Ws-2, NASC N1601) and the *pgi1-2* T-DNA insertion mutant (Kunz et al., 2010). Plants were cultured in Petri dishes containing sucrose-free solid Murashige and Skoog (MS) (Duchefa Biochemie, Haarlem, The Netherlands, cat. No. M0222) medium in growth chambers with a 16 h light/8 h dark photoperiod (80 µmol photons sec^{-1} m^{-2}, 22ºC during the light period and 18ºC during the dark period). *A. alternata* was cultured in Petri dishes containing solid MS medium supplemented with 90 mM sucrose. Unless otherwise indicated, the effect of *A. alternata* VCs on plants was investigated by placing microbial cultures without lids and plant cultures (14 days after sowing) into sterile plastic boxes (IT200N Instrument Try 200 x 150 x 50 mm, AWGregory, Kent, UK), and sealed with a plastic film (for details, see Sánchez-López et al., 2016). Leaves were harvested for characterization at specified incubation periods. As a negative control, Petri dishes containing fully developed plants were cultured in sealed plastic boxes together with Petri dishes containing sterile microbial culture media. Harvested leaves were immediately freeze-clamped and ground to a fine powder in liquid nitrogen with a pestle and mortar.

Determination of gas exchange rates and photosynthetic parameters

The determination of gas exchange rates and calculation of photosynthetic parameters were conducted as described by Sánchez-López et al. (2016) using a LI-COR 6400 gas exchange portable photosynthesis system (LI-COR, Lincoln, NE, USA). Chlorophyll fluorescence emission parameters were determined using a PlantScreen^{TM} XYZ System (Photon Systems Instruments, Brno, Czech Republic). The phenotyping system was equipped with a FluorCam unit for pulse amplitude modulated measurement of chlorophyll fluorescence. After 20 min of dark adaptation the standardized measurement protocol was applied, as described in Humplík et al. (2015). The parameters Φ_{Po} (also referred to as F_v/F_m), Φ_{PSII} and Φ_{NPQ} were calculated from the measured parameters according to Lazár (2015).

Analytical procedures

Soluble sugars were measured as described by Bahaji et al. (2015a). GAP and 3PGA were measured as described by Vogt et al. (1998) and Lytovchenko et al. (2002), respectively. The amino acids contents were determined as described by Loiret et al. (2009). Recovery experiments were carried out by adding known amounts of metabolite standards to the frozen tissue slurry immediately after the addition of extraction solutions. The difference between the measurements from samples with and without added standards was used as an estimate of the percentage of recovery. All data were corrected for losses during extraction.

Chlorophyll and carotenoid contents were quantified according to Lichtenthaler (1987) and González-Jorge et al. (2013), respectively. Starch was measured with an amyloglucosydase–based test kit (Boehringer Mannheim, Germany). To determine the levels of CKs, aliquots of the frozen leaves (see above) from *pgi1-2* plants were lyophilized and CKs were quantified according to the method described in Novák et al. (2008).

Iodine staining and microscopic localization of starch granules

Experiments were conducted essentially as described in Ovecka et al. (2012). Leaves harvested at the end of the light period were fixed by immersion into 3.7% formaldehyde in phosphate buffer. Leaf pigments were then removed in 96% ethanol. Re-hydrated samples were stained in an iodine solution (KI 2% (w/v) and I_2 1% (w/v)) for 30 min, rinsed briefly in deionized water, and photographed. Samples for sectioning were immersed in cryoprotective medium OCT (Tissue-Tec, USA) and frozen at -50ºC. A Thermo Shandon AS620 Cryotome (Shandon, England) was used to obtain cryosections of 10 μm thick. After thawing, the sections were stained in iodine solution for 2 min at room temperature, mounted to microscope slides, and observed using an Olympus MVX10 stereomicroscope (Japan). Microphotographs were captured with a DP72 video camera (Olympus, Japan) and Cell D software (Olympus, Japan).

Light and transmission electron microscopy

Small pieces (2 mm^2) of leaves were immediately fixed by submersion in a 3% glutaraldehyde (v/v) solution buffered by 0.05 M sodium cacodylate buffer, pH 7.4 (3 h at 4ºC, under vacuum). After fixing, the specimens were washed in a cacodylate buffer (0.05 M sodium cacodylate, 1% sucrose), three times for 30 min each at 4ºC, and post-fixed overnight at 4ºC with a solution of 1% osmium tetroxide in the cacodylate buffer specified above. After two washes, 30 min each, at 4ºC in the same cacodylate buffer, the samples were dehydrated in an ethanol series and progressively embedded in LR White resin (London Resin Co., Reading, UK). Ultrathin (70-90 nm) sections for TEM were contrasted with 2% aqueous uranyl acetate and lead citrate. Observations were performed with a STEM LEO 910 electron microscope (Carl Zeiss, Oberkochen, Germany) equipped with a Gatan Bioscan 792 camera (Gatan, Pleasanton, CA, USA), at 80 kV. Semi-thin (1 μm) sections for light microscopy were stained with 1% (w/v) toluidine blue in aqueous 1% sodium borate prior to direct observation with a Zeiss Axiophot photomicroscope (Carl Zeiss, Oberkochen, Germany).

Proteomic analysis

Protein sample preparation: Samples were prepared by grinding 200 mg of leaf material were ground into a fine powder under liquid nitrogen using a pre-cooled mortar and pestle. The powder was then mixed with 400 μl of cold protein extraction buffer (150 mM Tris-HCl (pH 8.0), 6 M urea, 2% (w/v) SDS, 5% (v/v) glycerol, 5 mM Tris(2-carboxyethyl) phosphine, 2% protease inhibitor cocktail 3 (Sigma-Aldrich, St. Louis, MO, cat nº P0044) and 2% Protease Inhibitor Cocktail (Sigma-Aldrich, cat nº P9599)). After 5 min at 95ºC, the mixture was centrifuged at 14,000 x g for 10 min at 4ºC.

Enzymatic digestion and TMT-6 plex labeling: Proteins (80 μg) from the supernatant were precipitated by the methanol/chloroform method (Fic et al., 2010), after which they were denatured in 7 M Urea/2M Thiourea/100mM TEAB (pH 7.5) and reduced with 50 mM Tris (2-carboxyethyl) phosphine, (pH 8.0) for 60 min at 37°C. Cysteines were then alkylated with 200 mM methyl methanethiosulfonate (Pierce^{TM} MMTS, Thermo Fisher Scientific, Waltham, MA) for 10 min at room temperature. The urea/thiourea concentration was adjusted to 2 M in TEAB prior to the addition of sequencing grade-modified trypsin (Sigma-Aldrich) in an enzyme-to-protein ratio of 1:20, and samples were then incubated overnight at 37°C. The resulting tryptic peptides were subsequently labeled using the TMT-6 plex Isobaric Mass Tagging Kit (Thermo Fisher Scientific, Foster City, Rockford, IL, USA) according to the manufacturer's instructions. After labeling, the samples were pooled, dried and desalted using a SEP-PAK C18 Cartridge (Waters, Milford, MA). Finally, the cleaned tryptic peptides were evaporated to dryness and stored at -20°C until further analysis.

2D LC-MS/MS analysis of labeled peptide mixtures

The first dimension consisted of a separation by reversed-phase chromatography at basic pH with an Ultimate 3000 HPLC (Dionex, Sunnyvale, CA) during which 30 fractions were collected. They were later alternatively combined into 6 fractions, and finally off-line injected into the tandem mass spectrometry system. The fractions were then divided into two aliquots for subsequent differential proteomics and phosphoproteomics.

LC-MS/MS triple TOF analysis of non-phosphorylated proteins

Peptide fractions were subjected to LC-MS/MS analysis using a nano liquid chromatography system (Eksigent Technologies nanoLC Ultra 1D plus, AB SCIEX, Foster City, CA) coupled to a high-speed Triple TOF 5600 mass spectrometer (AB SCIEX, Foster City, CA) with a nanoelectrospray ion source. Samples were injected into a C18 PepMap trap column (5 µm, 100 µm I.D. x 2 cm, Thermo Fisher Scientific) at 2 µL/min, in 0.1% formic acid in water, and the trap column was switched on-line to a C18 nanoAcquity BEH analytical column (1.7 µm, 100 Å, 75 µm I.D. x15 cm, Waters). Equilibration was done in mobile phase A (0.1% formic acid in water), and peptide elution was achieved in a 120 min linear gradient from 5% - 40% B (0.1% formic acid in acetonitrile) at 250 nL/min. The mass spectrometer was operated in a data-dependent acquisition mode. The accumulation time for the TOF scans was set to 250 ms, and per cycle, up to 30 precursor ions were monitored per cycle.

LC-MS/MS Triple TOF Analysis of phosphorylated protein fraction

Part of each fraction (75%) from the first chromatographic dimension was subjected to phosphopeptide purification. The enrichment procedure concatenates two in-house packed microcolumns, the IMAC microcolumn and the Oligo R3 reversed-phase column, that provides selective purification and sample cleanup prior to LC-MS/MS analysis, and was performed according to Navajas et al. (2011). After phosphopeptide enrichment, all the IMAC-eluates from the 6 fractions were combined and subjected to LC-MS/MS Triple TOF, following a 220 min linear gradient and data-dependent acquisition mode, with the same parameters described above.

Proteomics data analysis

MS/MS spectra were exported to MGF format using Peak View v1.2.0.3 (Sciex, Redwood City, CA) and searched using Mascot Server 2.5.1, OMSSA 2.1.9, X!TANDEM 2013.02.01.1 and Myrimatch 2.2.140 against a composite target/decoy database built from the 31551 sequences in the *Arabidopsis thaliana* reference proteome from the Uniprot Knowledgebase, together with commonly occurring contaminants. Search engines were configured to match potential peptide candidates with mass error tolerance of 25 ppm and fragment ion tolerance of 0.02Da, allowing for up to two missed tryptic cleavage sites and a maximum isotope error (^{13}C) of 1, considering fixed MMTS modification of cysteine and variable oxidation of methionine, pyroglutamic acid from glutamine or glutamic acid at the peptide N-terminus, and acetylation of the protein N-terminus. Score distribution models were used to compute peptide-spectrum match p-values as described in Ramos-Fernández et al. (2008), and spectra recovered by a false discovery rate (FDR) ≤ 0.01 (peptide level) filter were selected for quantitative analysis. The ca. 4% of signals with the lowest quality were removed prior to further analysis. Differential regulation was measured using linear models (López-Serra et al. 2014), and statistical significance was measured using q-values (FDR). All analyses were conducted using software from Proteobotics (Madrid, Spain). The cut-off for differentially regulated proteins was established at a FDR ≤ 2.7% and log2 ratios (+VCs treatment vs. –VCs treatment) of either > 0.475 (for proteins whose expression is up-regulated by VCs) and < -0.475 (for proteins whose expression is down-regulated by VCs).

Statistical analysis

The data are presented as the means of four independent experiments, with 3-5 replicates for each experiment (means ± SE). The significance of differences between non-treated plants and plants that were treated with VCs from *A. alternata* was statistically evaluated with the Student´s t-test using the SPSS software. Differences were considered significant at a probability level of $P<0.05$. The between-treatment differences in the hormone content analyses were evaluated by the one-way univariate analysis of variance (ANOVA) for parametric data and the Kruskal Wallis H test for non-parametric data, using the open source R software 2.15.1 (http://cran.r-project.org/). Multiple comparisons after ANOVA were calculated using the post hoc Tukey's honestly significant difference test.

SUPPLEMENTAL MATERIALS

The following materials are available in the online version of this article.

Supplemental Figure S1: Free amino acid contents in the leaves of *pgi1-2* plants cultured in the absence or presence of *A. alternata* VCs for three days. Asterisks indicate significant differences between microbial VC-treated plants and controls (non-treated plants) according to the Student´s t-tests ($p<0.05$). The amino acids are grouped according to their biosynthetic families.

Supplemental Figure S2: VCs emitted by *A. alternata* promote the augmentation of the CK levels in the leaves of *pgi1-2* plants. The presented scheme illustrates pathways of CK biosynthesis within the plastidic MEP and cytosolic MVA pathways in leaves of VC-treated *pgi1-2* plants. Black arrows show the biosynthesis, interconversions and metabolic flow of CKs in an *Arabidopsis* cell (adapted from Spíchal, 2012). Multistep reactions are depicted with hollow arrows. The green arrows indicate a hypothetical exchange of a common precursor(s) between the MEP and MVA pathways (adapted from Kasahara et al., 2004). The CKs with enhanced levels following VC exposure (cf. Table 2) are highlighted in blue, while the CKs with decreased levels following VC exposure (cf. Table 2) are highlighted in red.

Supplemental Figure S3: Categorization of the differentially expressed proteins in the leaves of *pgi1-2* plants cultured in the presence of VCs emitted by *A. alternata* according to their subcellular localization. Data are obtained from Supplemental Table S1.

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FIGURE LEGENDS

Figure 1: *A. alternata* VCs promote growth and the accumulation of exceptionally high levels of starch in the mesophyll cells of *pgi1-2* plants. (A) Rosette FW, and (B) time-course of starch content in the leaves of WT and *pgi1-2* plants cultured in the absence or continuous presence of adjacent cultures of *A. alternata.* Values represent the means ± SE determined from four independent experiments using 12 plants in each experiment. The asterisks in "A" indicate significant differences between microbial VC-treated plants and controls (non-treated plants) according to the Student´s t-tests ($p<0.05$). The plants in "A" were exposed to VCs for one week.

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Light microscopy of the mesophyll cells of leaves of WT (E,F) and *pgi1-2* (M,N) plants cultured in the absence or continuous presence of VCs emitted by *A. alternata* for 14 h. Bar = 10 µm.

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Asterisks indicate significant differences between the leaves of VC-treated and control (non-treated) plants according to the Student´s t-tests (*p*<0.05).

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Figure 5: Functional categorization of the differentially expressed proteins in leaves of *pgi1-2* plants cultured in the presence of VCs emitted by *A. alternata*. The proteins that were both significantly down- and up-regulated following VC exposure were sorted according to the putative functional category assigned by MapMan software. The number of up- and down-regulated proteins in each categorical group is indicated by gray and black bars, respectively. Proteins discussed here are boxed. The proteins encoded by genes that are differentially expressed in the leaves of VC-treated plants are indicated in gray and CK-regulated proteins are indicated with asterisks.

Figure 6: Scheme illustrating the metabolic adjustment that occurs in leaves of *pgi1-2* plants in response to *A. alternata* VCs exposure. VC-promoted up-regulation of PSII reaction center proteins and enzymes involved in the synthesis of sulfolipid and photosynthetic pigments results in enhanced photosynthetic activity. The resulting augmentation of GAP fuels the production of MEP-derived compounds, such as photosynthetic pigments and plastidic CKs, which initiate a cascade of reactions that cause various responses, for example, the production of proteins involved in photoprotection, cell wall production and modification, and amino acid biosynthesis (Sánchez-López et al., 2016). Glutamine is metabolized to glutamate, aspartate, asparagine, methionine and aliphatic glucosinolates. Also, cytosolic glutamate is metabolized to alanine through the GABA shunt. According to this model, VC-promoted

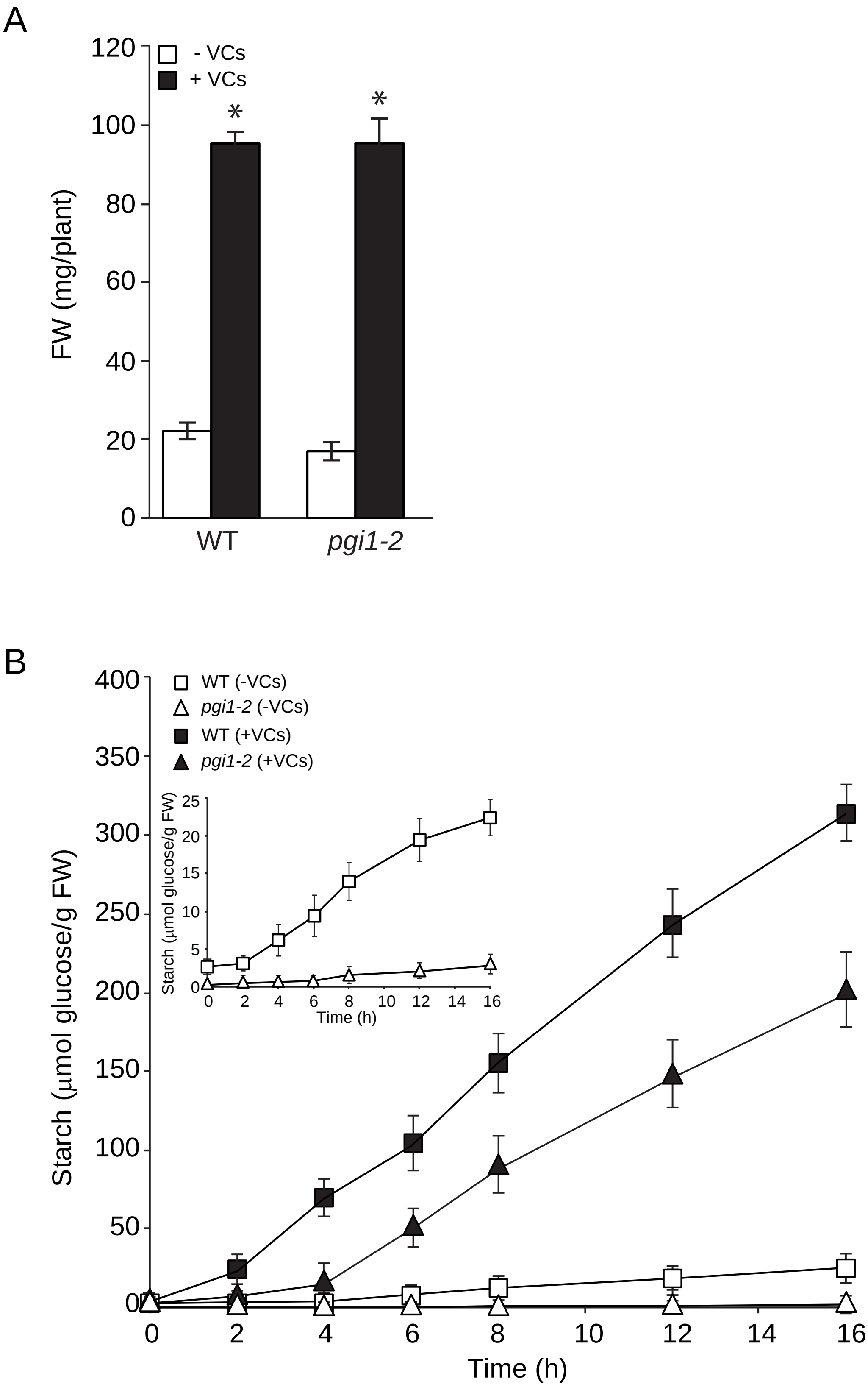
starch over-accumulation in *pgi1-2* leaves is the consequence of the stimulation of starch biosynthetic pathways that bypass pPGI through the transport of cytosolic hexoses (e.g. glucose and/or G6P) and/or ADPG into the chloroplast. The high levels of 3PGA and NADPH resulting from VC-enhanced photosynthesis activate AGP (Li et al., 2011), which in turn, facilitates the synthesis of starch. VCs also increase the expression of starch breakdown enzymes to prevent excessive accumulation of starch and establish a starch substrate cycle. Starch breakdown products can be exported to the cytosol for their subsequent conversion into UDP-glucose, which is necessary for the synthesis of sucrose and/or cell wall polysaccharides. The enzymes that are up-regulated by VCs are indicated with thick arrows. Multistep reactions are depicted with hollow arrows.

Table 1: Photosynthetic parameters of the leaves of *pgi1-2* plants cultured in the absence or presence of VCs emitted by *A. alternata* during three days. Values represent the mean ± SE of determinations from four independent experiments.

Treatment	Φ_{Po}	Φ_{PSII}	Φ_{NPQ}	J_{max} (µmol e^- m^{-2} s^{-1})	V_{cmax} (µmol CO_2 m^{-2} s^{-1})	TPU (µmol Pi m^{-2} s^{-1})
- VCs	0.69 ± 0.01	0.35 ± 0.01	0.89 ± 0.04	25.3 ± 0.33	15.5 ± 0.42	1.08 ± 0.06
+ VCs	0.82 ± 0.01	0.48 ± 0.01	0.35 ± 0.03	59.0 ± 0.46	25.3 ± 0.26	2.89 ± 0.09

Table 2. The CK contents (pmol g^{-1} DW) in leaves of *pgi1-2* plants that were, at 18 days after sowing, cultured in solid MS medium in the absence or presence of VCs emitted by *A. alternata* for three days. CK precursors, transport forms, active forms and glycosylated inactive forms are separated in two groups based on their origin from either the MEP or MVA pathway. Total sums and corresponding percentage are shown for individual forms. Symbols indicate significant differences according to ANOVA. *< 0.05; **<0.01; ***<0.001.

	MEP pathway (plastid) derived CKs			**MVA pathway (cytosol) derived CKs**		
		pgi1-2 -VCs	*pgi1-2* +VCs		*pgi1-2* -VCs	*pgi1-2* +VCs
Precursors	iPRMP	171.05 ± 21.87	392.91 ± 20.91***			
	tZRMP	129.90 ± 18.80	266,38 ± 53.22**	cZRMP	116.38 ± 13.30	141.51 ± 3.49*
	DZRMP	2.51 ± 0.30	1.23 ± 0.11**			
	∑ (%)	303.46 ± 28.77	660.53 ± 52.33**		116.38 ± 13.30	141.51 ± 3.49*
Transport forms	iPR	12.58 ± 2.07	18.74 ± 2.03*			
	tZR	10.56 ± 0.93	23.32 ± 2.40**	cZR	11.03 ± 0.61	5.46 ± 0.29***
	DZR	0.56 ± 0.03	0.17 ± 0.02***			
	∑ (%)	23.71 ± 0.84	42.23 ± 1.44***		11.03 ± 0.61	5.46 ± 0.29***
Active forms	iP	3.66 ± 0.20	5.92 ± 0.25***			
	tZ	6.49 ± 0.27	9.16 ± 1.55*	cZ	2.98 ± 0.09	1.73 ± 0.16***
	DZ	0.36 ± 0.02	0.02± 0.01***			
	∑ (%)	10.51 ± 0.25	15.10 ± 1.27*		2.98 ± 0.09	1.73 ± 0.16***
Glycosylated (inactive) forms	iP7G	86.25 ± 4.53	80.78 ± 8.79			
	tZ7G	112.54 ± 1.04	109.09 ± 7.70			
	DZ7G	33.35 ± 0.89	20.12 ± 2.77**			
	iP9G	14.83 ± 0.83	14.76 ± 0.95	cZ9G	4.22 ± 0.35	2.68 ± 0.63*
	tZ9G	133.17 ± 15.21	176.02 ± 45.30			
	DZ9G	2.01 ± 0.51	1.17 ± 0.37			
	tZOG	40.87 ± 0.92	38.76 ± 1.59	cZOG	17.18 ± 0.62	10.16 ± 0.92***
	DZOG	6.37 ± 1.49	3.89 ± 0.80			
	tZROG	27.45 ± 4.40	27.12 ± 8.35	cZROG	47.71 ± 12.60	40.01 ± 7.19
	DZROG	5.50 ± 1.19	3.67 ± 0.62			
	∑ (%)	462.55 ± 9.76	475.38 ± 47.36		69.11 ± 9.57	52.84 ± 5.36
TOTAL	∑ (%)	800.24 ± 24.59	1193.24 ± 100.89*		199.50 ± 14.15	201.53 ± 8.02



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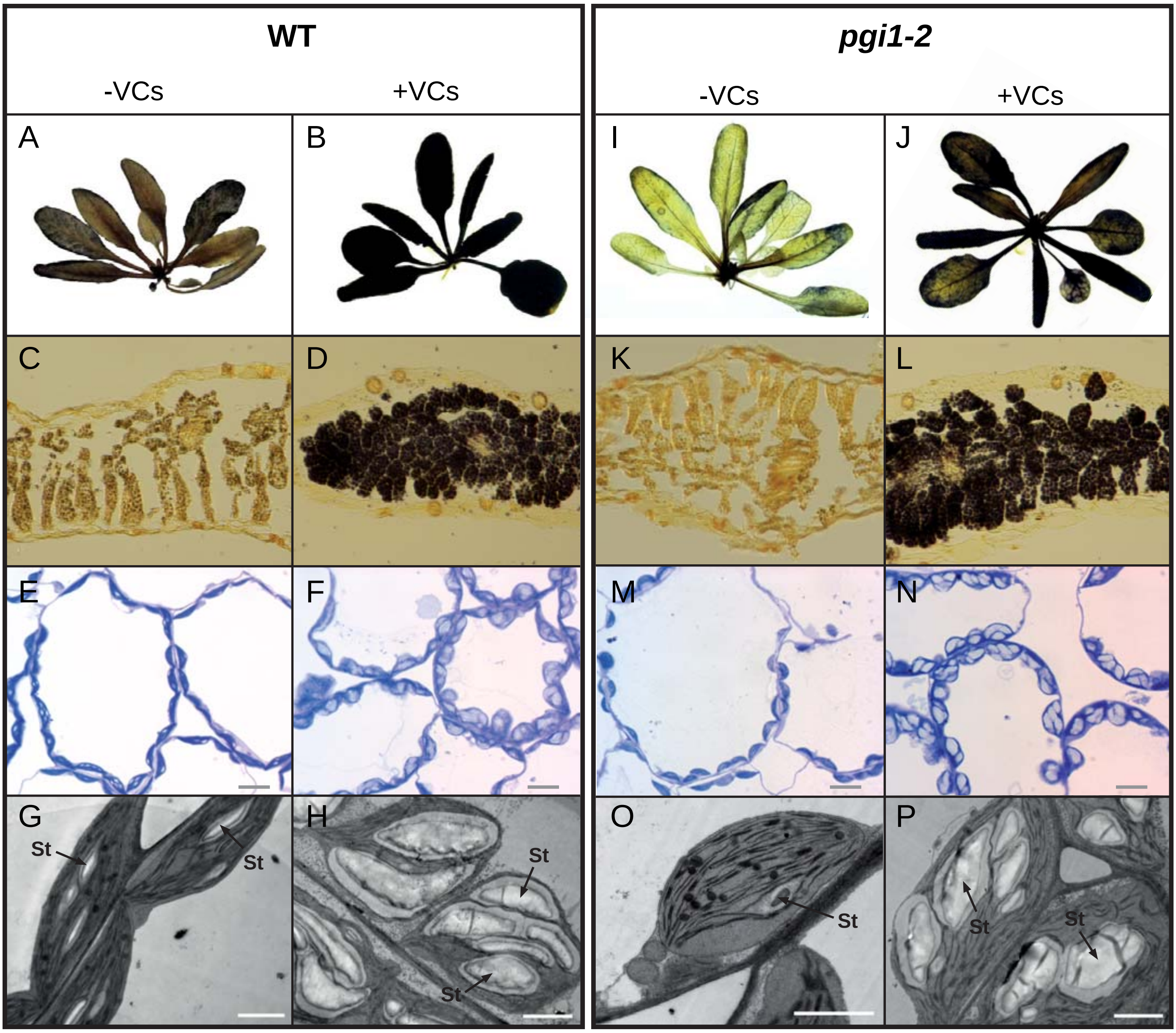

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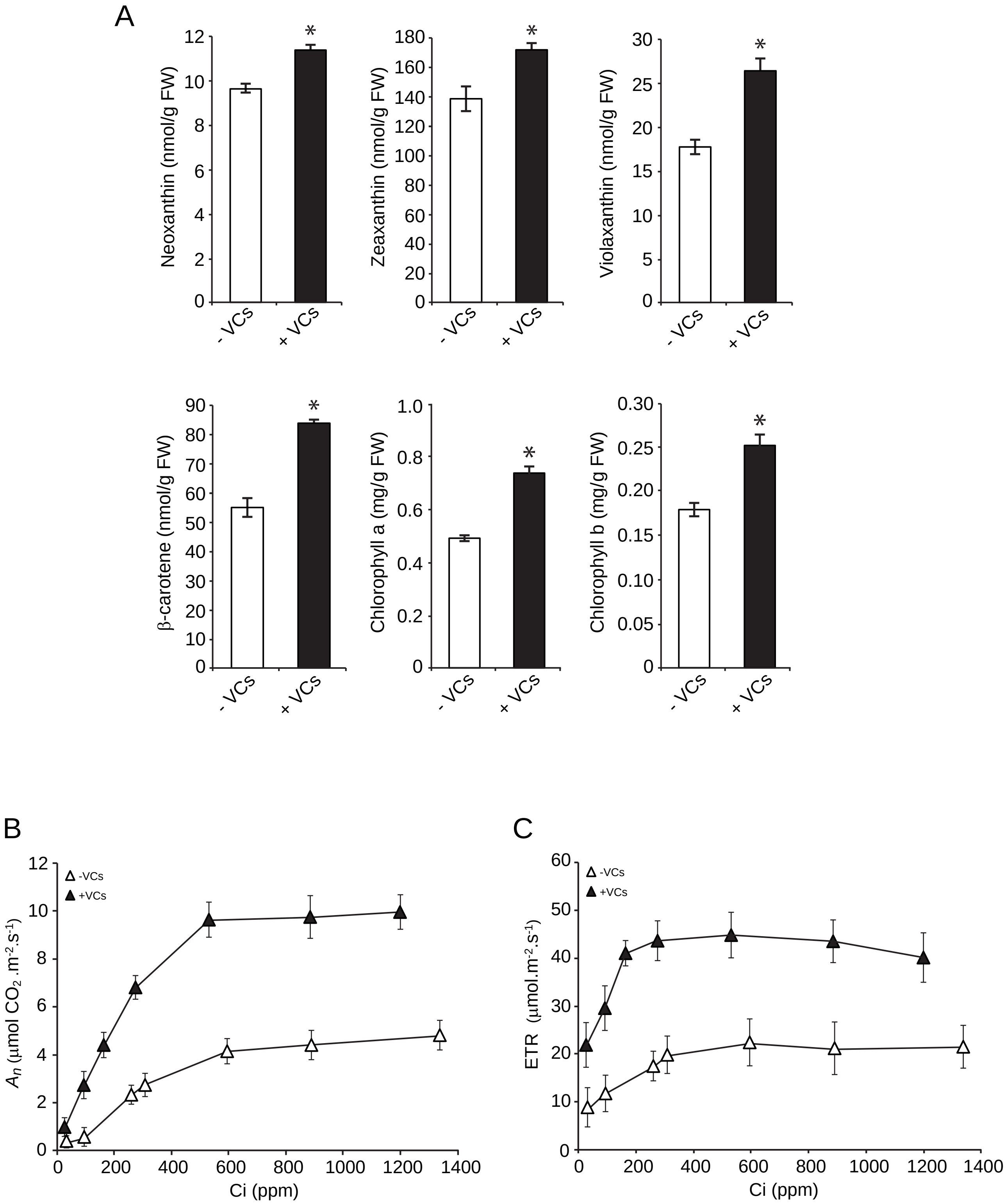

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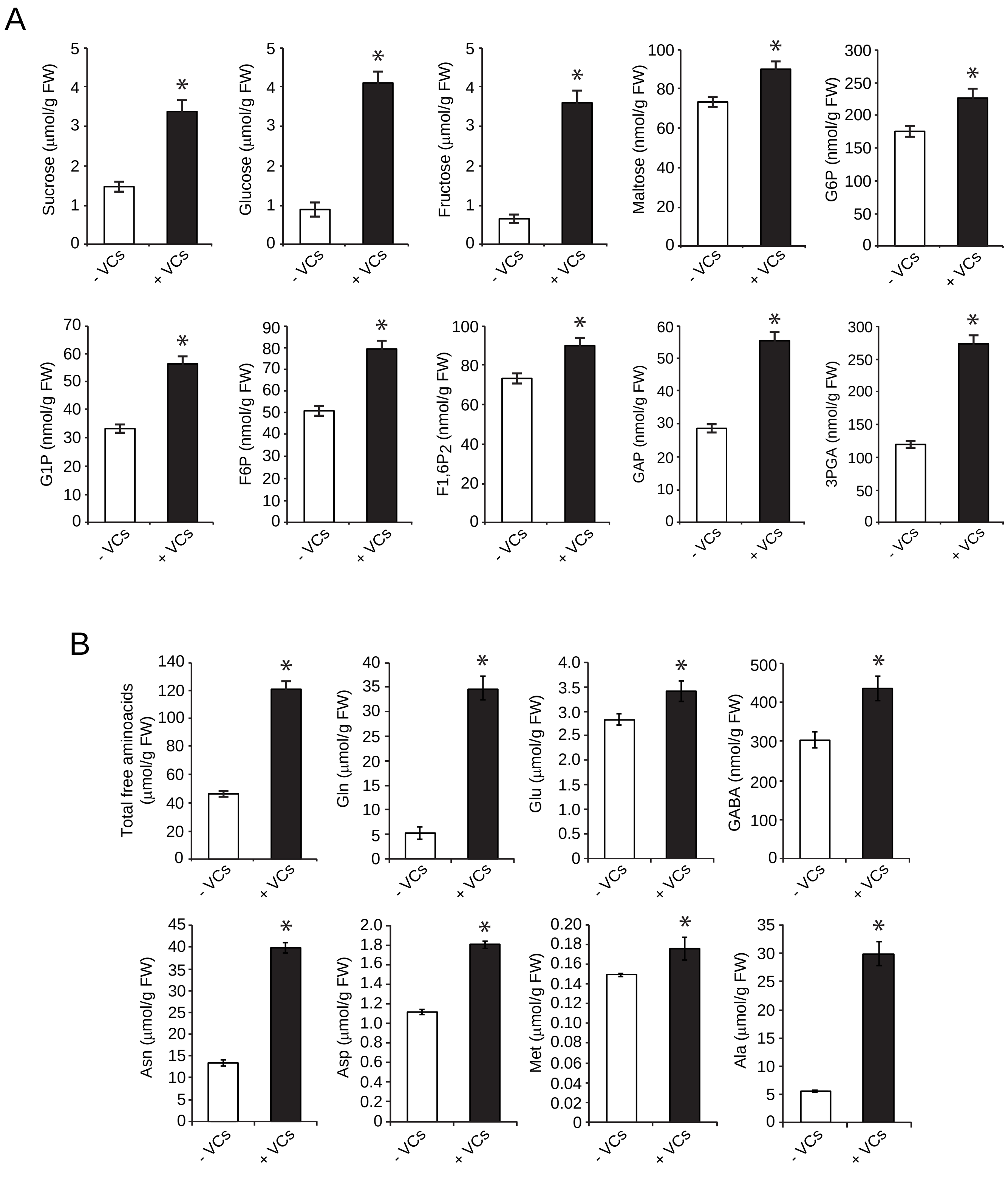

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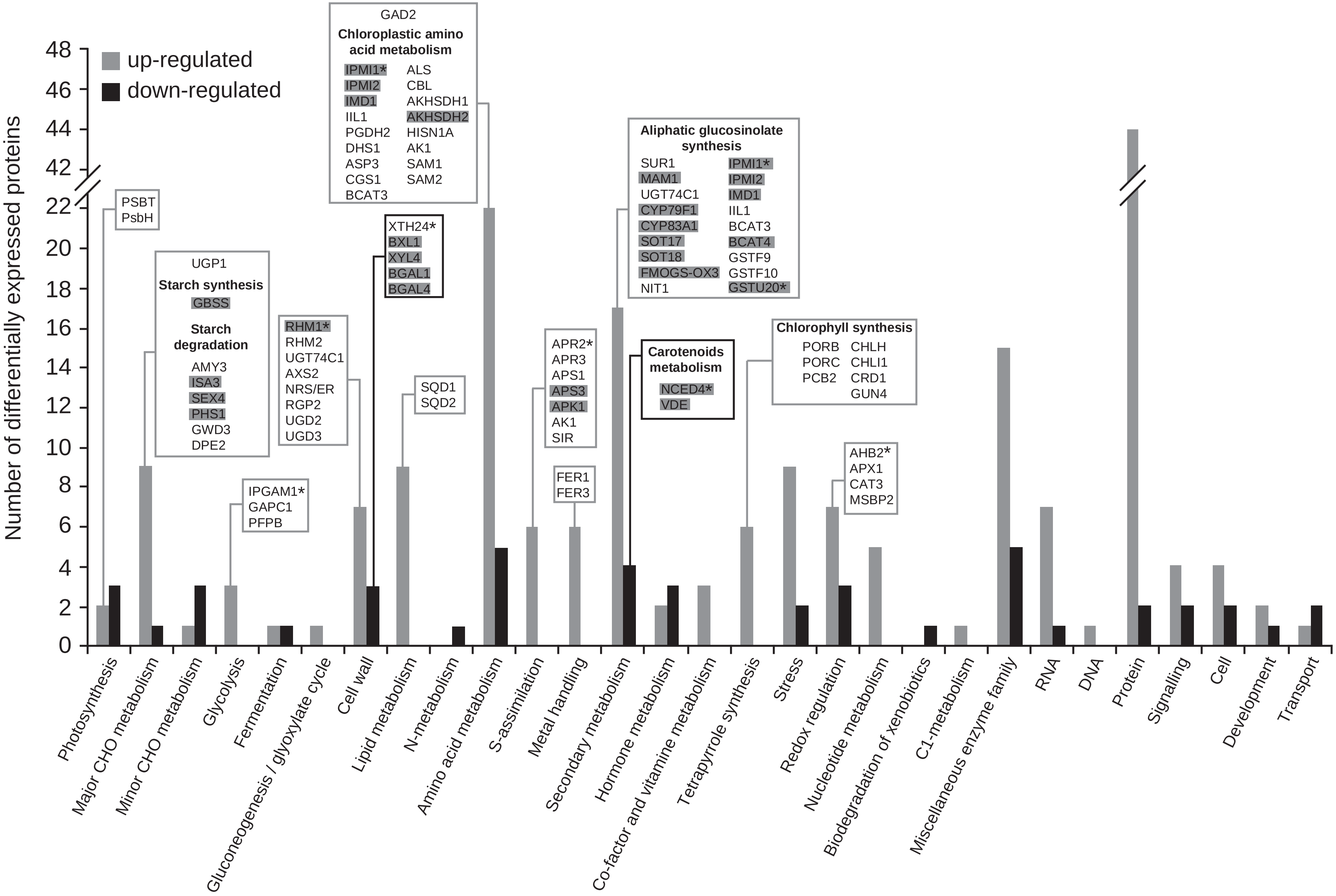

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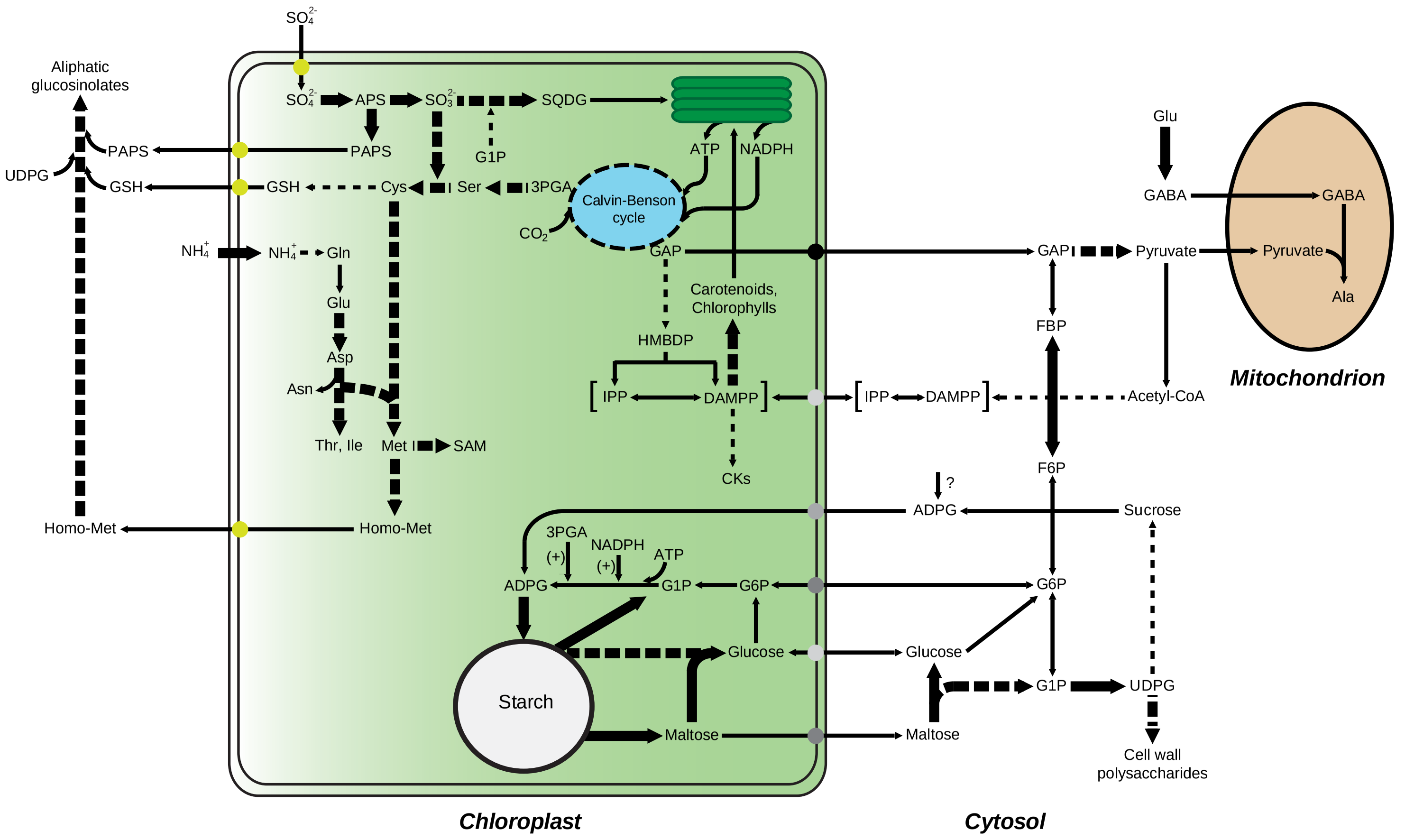

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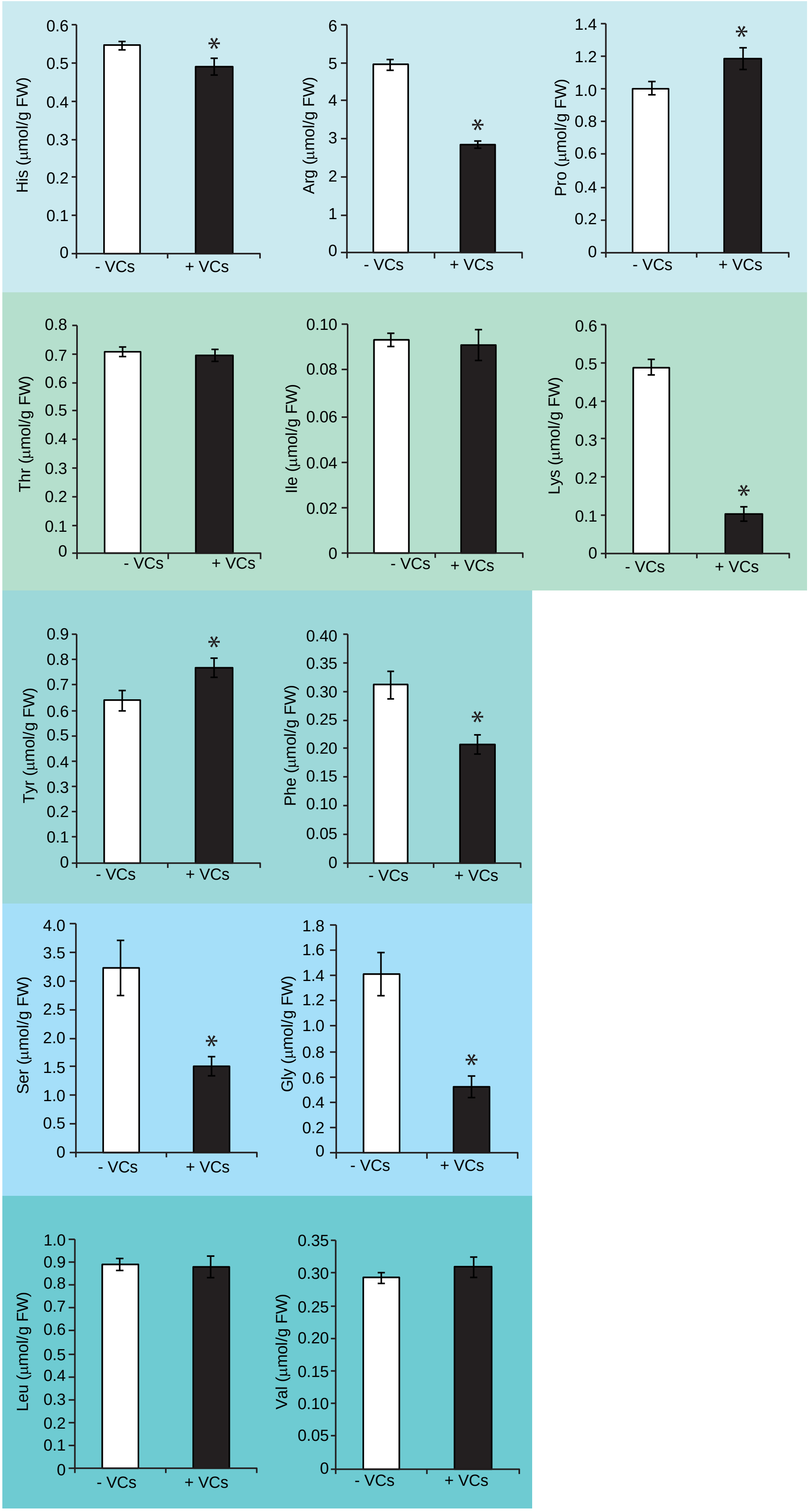
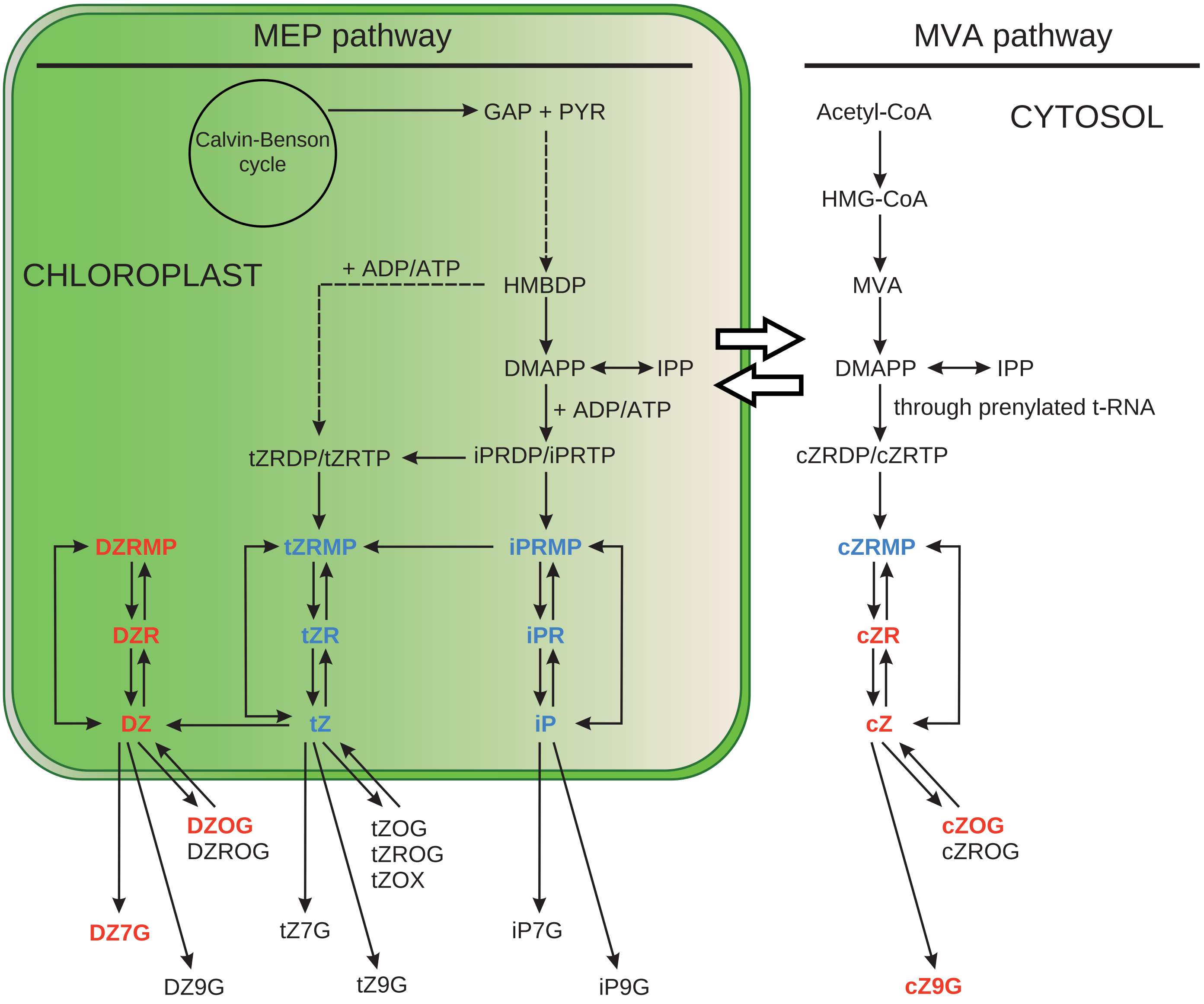
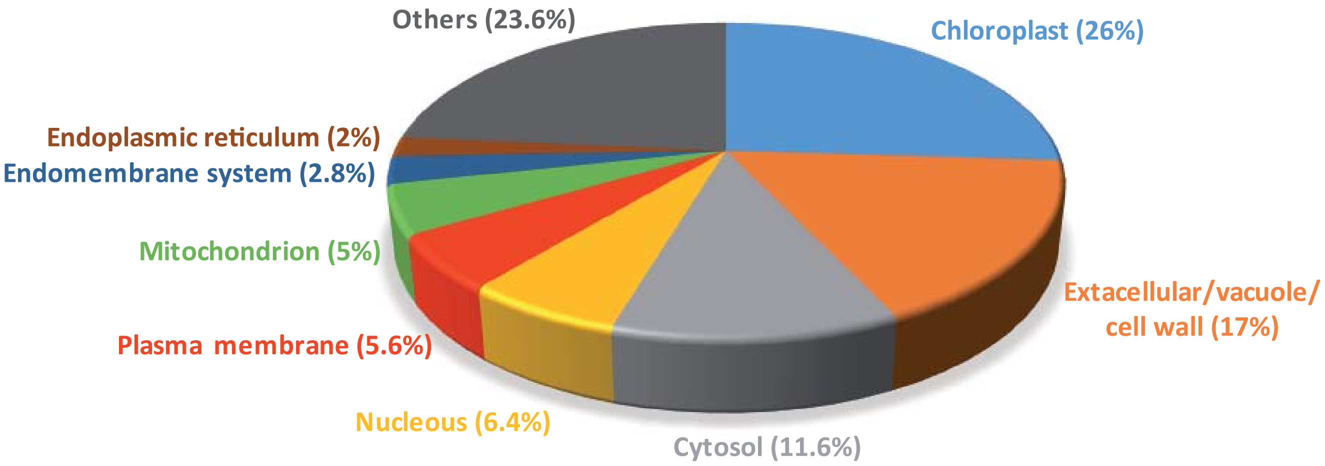


Supplemental Figure S1: Free amino acid contents in the leaves of *pgi1-2* plants cultured in the absence or presence of *A. alternata* VCs for three days. Asterisks indicate significant differences between microbial VC-treated plants and controls (non-treated plants) according to the Student´s t-tests (*p*<0.05). The amino acids are grouped according to their biosynthetic families.



Supplemental Figure S2: VCs emitted by *A. alternata* promote the augmentation of the CK levels in the leaves of *pgi1-2* plants.The presented scheme illustrates pathways of CK biosynthesis within the plastidic MEP and cytosolic MVA pathways in leaves of VC-treated *pgi1-2* plants. Black arrows show the biosynthesis, interconversions and metabolic flow of CKs in an *Arabidopsis* cell (adapted from Spíchal, 2012). Multistep reactions are depicted with hollow arrows. The green arrows indicate a hypothetical exchange of a common precursor(s) between the MEP and MVA pathways (adapted from Kasahara et al., 2004). The CKs with enhanced levels following VC exposure (cf. Table 2) are highlighted in blue, while the CKs with decreased levels following VC exposure (cf. Table 2) are highlighted in red.



Supplemental Figure S3: Categorization of the differentially expressed proteins in the leaves of *pgi1-2* plants cultured in the presence of VCs emitted by *A. alternata* according to their subcellular localization. Data are obtained from Supplemental Table S1.

Supplemental Table S1: list of proteins whose expression is differentially regulated by VOCs emitted by A. alternata. Proteins whose encoding genes are up- or down-regulated by VOCs (Sánchez-López et al. 2016) are highlighted in blue and brown, respectively. Proteins whose encoding genes are regulated by CKs are indicated with asterisks (**)

Down-regulated **Up-regulated**

ID	Locus	Description	# Peptides	Pept. modified	Modification	Ratio_log2	p-value	e-value	FDR
O04130	At1g17745	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2	2	---	----	2,011	1,00E-05	0,03	0,00%
Q9S7C0	At1g79930	Heat shock 70 kDa protein 14 OS=Arabidopsis thaliana GN=HSP70-14 PE=2 SV=1	1	---	----	1,955	1,00E-05	0,03	0,10%
P21218	At4g27440	Protochlorophyllide reductase B, chloroplastic OS=Arabidopsis thaliana GN=PORB PE=1 SV=3	4	---	----	1,789	1,00E-05	0,03	0,00%
Q9MAQ0	At1g32900	Granule-bound starch synthase 1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=GBSS1 PE=1 SV=1	7	---	----	1,621	1,00E-05	0,03	0,00%
Q1H537	At5g18660	Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic OS=Arabidopsis thaliana GN=PCB2 PE=1 SV=1	1	---	----	1,487	1,00E-05	0,03	0,00%
Q9LE06	At3g19710	Methionine aminotransferase BCAT4 OS=Arabidopsis thaliana GN=BCAT4 PE=1 SV=1	8	---	----	1,399	1,00E-05	0,03	0,00%
Q9ZW84	At2g43100	3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1	3	---	----	1,364	1,00E-05	0,03	0,00%
Q9LYT7**	At3g58990	3-isopropylmalate dehydratase small subunit 2 OS=Arabidopsis thaliana GN=IPMI1 PE=1 SV=1	3	---	----	1,357	1,00E-05	0,03	0,00%
O23324;Q9LIK9	At4g14680	ATP-sulfurylase 3, chloroplastic OS=Arabidopsis thaliana GN=APS3 PE=1 SV=1	3	---	----	1,262	1,00E-05	0,03	0,00%
P17562;P23686;Q	At4g01850	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	1	---	----	1,257	1,00E-05	0,03	0,00%
Q94AQ3	At1g48750	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein OS=Arabidopsis thaliana GN=At1g48750 PE=2 SV=1	1	---	----	1,239	0,00401	11,37	2,00%
P92980;P92981	At4g21990	5'-adenylylsulfate reductase 3, chloroplastic OS=Arabidopsis thaliana GN=APR3 PE=2 SV=2	1	---	----	1,199	0,00021	0,60	0,20%
P25858;Q5E924;Q	At3g04120	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	1	AASFNIIPSSTGAAK	none	1,112	1,00E-05	0,03	0,10%
Q9C6B9**	At1g73600	Phosphoethanolamine N-methyltransferase 3 OS=Arabidopsis thaliana GN=NMT3 PE=2 SV=2	4	---	----	1,083	1,00E-05	0,03	0,00%
P48421	At4g13770	Cytochrome P450 83A1 OS=Arabidopsis thaliana GN=CYP83A1 PE=1 SV=2	5	---	----	1,078	1,00E-05	0,03	0,00%
Q9CAX6;Q9SIH0	At3g11510	40S ribosomal protein S14-2 OS=Arabidopsis thaliana GN=RPS14B PE=1 SV=1	2	---	----	1,075	1,00E-05	0,03	0,00%
P19456;P20431	At4g30190	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	1	---	----	1,074	0,00181	5,13	1,00%
Q949U1	At1g16410	Dihomomethionine N-hydroxylase OS=Arabidopsis thaliana GN=CYP79F1 PE=1 SV=1	4	---	----	1,062	1,00E-05	0,03	0,00%
Q9SK84	At1g22410	Class-II DAHP synthetase family protein OS=Arabidopsis thaliana GN=F12K8.24 PE=4 SV=1	3	---	----	1,062	1,00E-05	0,03	0,00%
Q9FMT1	At5g14200	3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMD1 PE=1 SV=1	9	---	----	1,01	1,00E-05	0,03	0,00%
Q94A41	At1g69830	Alpha-amylase 3, chloroplastic OS=Arabidopsis thaliana GN=AMY3 PE=2 SV=1	6	---	----	1,005	1,00E-05	0,03	0,00%
Q8L7C9**	At1g78370	Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1	8	---	----	0,995	1,00E-05	0,03	0,00%
Q43295	At2g14750	Adenylyl-sulfate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=APK1 PE=1 SV=1	1	---	----	0,992	0,00341	9,67	1,70%
Q9M0A7**	At4g30530	AT4g30530/F17I23_130 OS=Arabidopsis thaliana GN=At4g30530 PE=2 SV=1	5	---	----	0,991	1,00E-05	0,03	0,00%
Q9LX31	At3g59400	Tetrapyrrole-binding protein, chloroplastic OS=Arabidopsis thaliana GN=GUN4 PE=1 SV=1	4	---	----	0,985	1,00E-05	0,03	0,00%
P25853	At4g15210	Beta-amylase 5 OS=Arabidopsis thaliana GN=BAM5 PE=2 SV=1	7	---	----	0,984	1,00E-05	0,03	0,00%
F4JGR5;Q8W4M5	At4g04040	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 2 OS=Arabidopsis thaliana GN=PFPB PE=3 SV=1	1	---	----	0,961	0,00401	11,37	1,90%
Q9LV28	At3g18130	Receptor for activated C kinase 1C OS=Arabidopsis thaliana GN=RACK1C PE=1 SV=1	2	---	----	0,96	0,00101	2,86	0,60%
A8MS32;Q9C787	At5g64130	AT5G64130 protein OS=Arabidopsis thaliana GN=At5g64130 PE=1 SV=1	1	---	----	0,949	0,00361	10,23	1,80%
Q9FKC0;Q9LRX8;Q	At5g48760	60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	1	---	----	0,936	1,00E-05	0,03	0,00%
Q8VY86	At4g21830	Peptide methionine sulfoxide reductase B7 OS=Arabidopsis thaliana GN=MSRB7 PE=2 SV=1	1	---	----	0,935	1,00E-05	0,03	0,00%
Q9FG67	At5g23010	Methylthioalkylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=MAM1 PE=1 SV=1	1	---	----	0,934	1,00E-05	0,03	0,00%
Q9LIK9	At3g22890	ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=1 SV=1	8	---	----	0,93	1,00E-05	0,03	0,00%
Q94AR8	At4g13430	3-isopropylmalate dehydratase large subunit OS=Arabidopsis thaliana GN=IIL1 PE=1 SV=1	13	---	----	0,906	1,00E-05	0,03	0,10%
O82392	At2g29630	Phosphomethylpyrimidine synthase, chloroplastic OS=Arabidopsis thaliana GN=THIC PE=1 SV=1	4	---	----	0,904	1,00E-05	0,03	0,00%
Q9LYN2;Q9S756	At3g56090	Ferritin-3, chloroplastic OS=Arabidopsis thaliana GN=FER3 PE=2 SV=1	1	---	----	0,901	0,00481	13,63	2,30%
Q9LUT2	At3g17390	S-adenosylmethionine synthase 4 OS=Arabidopsis thaliana GN=SAMS3 PE=1 SV=1	9	---	----	0,9	1,00E-05	0,03	0,00%
Q38814	At5g54770	Thiamine thiazole synthase, chloroplastic OS=Arabidopsis thaliana GN=THI1 PE=1 SV=1	8	---	----	0,896	1,00E-05	0,03	0,00%
P29976;Q00218;Q	At4g39980	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2	1	---	----	0,894	1,00E-05	0,03	0,50%
O81852;Q9SA18	At4g19710	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH2 PE=1 SV=1	3	---	----	0,89	1,00E-05	0,03	0,00%
Q9LUD4**	At3g14600	60S ribosomal protein L18a-3 OS=Arabidopsis thaliana GN=RPL18AC PE=2 SV=1	1	---	----	0,889	0,00361	10,23	1,80%
Q9LVQ8	At5g66720	Probable protein phosphatase 2C 80 OS=Arabidopsis thaliana GN=At5g66720 PE=2 SV=1	1	---	----	0,876	1,00E-05	0,03	0,10%
Q9ZPZ4	At1g09310	Putative uncharacterized protein At1g09310 OS=Arabidopsis thaliana GN=T31J12.3 PE=2 SV=1	9	---	----	0,874	1,00E-05	0,03	0,00%
O22832;Q9M879	At2g43710	Acyl-[acyl-carrier-protein] desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1	3	---	----	0,871	1,00E-05	0,03	0,00%
Q9ZWC4	At1g04040	At1g04040/F21M11_2 OS=Arabidopsis thaliana GN=F21M11.2 PE=2 SV=1	3	---	----	0,869	1,00E-05	0,03	0,00%
Q8VZ19	At1g77940	60S ribosomal protein L30-2 OS=Arabidopsis thaliana GN=RPL30B PE=3 SV=1	2	---	----	0,86	1,00E-05	0,03	0,00%
Q9SSK7;Q9SSK9**	At1g70850	MLP-like protein 34 OS=Arabidopsis thaliana GN=MLP34 PE=2 SV=1	1	---	----	0,855	0,00441	12,50	2,10%
P49637	At1g70600	60S ribosomal protein L27a-3 OS=Arabidopsis thaliana GN=RPL27AC PE=2 SV=2	5	---	----	0,851	1,00E-05	0,03	0,00%
Q944H0;Q9C6B9;Q	At1g48600	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2	1	---	----	0,837	1,00E-05	0,03	0,00%
Q9M1G8	At3g54600	DJ-1 protein homolog F OS=Arabidopsis thaliana GN=DJ1F PE=1 SV=1	4	---	----	0,836	1,00E-05	0,03	0,00%
O48917	At4g33030	UDP-sulfoquinovose synthase, chloroplastic OS=Arabidopsis thaliana GN=SQD1 PE=1 SV=1	5	---	----	0,83	1,00E-05	0,03	0,00%
Q94K48	At3g62530	E-Z type HEAT repeat-containing protein OS=Arabidopsis thaliana GN=At3g62530 PE=2 SV=1	7	---	----	0,811	1,00E-05	0,03	0,00%
O80852	At2g30860	Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1	10	---	----	0,807	1,00E-05	0,03	0,00%
P92981**	At1g62180	5'-adenylylsulfate reductase 2, chloroplastic OS=Arabidopsis thaliana GN=APR2 PE=1 SV=2	3	---	----	0,8	1,00E-05	0,03	0,00%
Q9FEB5	At3g52180	Phosphoglucan phosphatase DSP4, chloroplastic OS=Arabidopsis thaliana GN=SEX4 PE=1 SV=1	6	---	----	0,779	1,00E-05	0,03	0,00%
Q9SIV0	At2g20610	S-alkyl-thiohydroximate lyase SUR1 OS=Arabidopsis thaliana GN=SUR1 PE=1 SV=1	8	---	----	0,771	1,00E-05	0,03	0,00%
Q93VI3	At1g27400	60S ribosomal protein L17-1 OS=Arabidopsis thaliana GN=RPL17A PE=2 SV=1	1	---	----	0,77	0,00041	1,16	0,30%
O23515	At4g16720	60S ribosomal protein L15-1 OS=Arabidopsis thaliana GN=RPL15A PE=2 SV=1	3	---	----	0,768	1,00E-05	0,03	0,00%
Q9T043	At4g27090	60S ribosomal protein L14-2 OS=Arabidopsis thaliana GN=RPL14B PE=2 SV=1	4	---	----	0,764	1,00E-05	0,03	0,00%
Q9C9C9;Q9FZ80	At1g74090	Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1	2	---	----	0,763	1,00E-05	0,03	0,00%
Q9FF90	At5g23900	60S ribosomal protein L13-3 OS=Arabidopsis thaliana GN=RPL13D PE=1 SV=1	1	---	----	0,763	0,00061	1,73	0,40%
P23686	At1g02500	S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2	1	---	----	0,752	0,00101	2,86	0,60%
Q9C4Z6	At1g48630	Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1	2	---	----	0,751	1,00E-05	0,03	0,00%
Q9LFW1;Q9SRT9	At5g15650	UDP-arabinopyranose mutase 2 OS=Arabidopsis thaliana GN=RGP2 PE=1 SV=1	5	---	----	0,734	1,00E-05	0,03	0,00%
Q9LQQ3	At1g07750	At1g07750/F24B9_13 OS=Arabidopsis thaliana GN=F24B9.13 PE=2 SV=1	3	---	----	0,734	1,00E-05	0,03	0,10%
Q9SJW3	At2g03680	Protein SPIRAL1 OS=Arabidopsis thaliana GN=SPR1 PE=2 SV=1	2	---	----	0,731	0,00041	1,16	0,30%
O04846	At3g52720	Alpha carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=ACA1 PE=1 SV=2	2	---	----	0,727	0,00141	4,00	0,80%
Q9FNB0	At5g13630	Magnesium-chelatase subunit ChlH, chloroplastic OS=Arabidopsis thaliana GN=CHLH PE=1 SV=1	15	---	----	0,723	1,00E-05	0,03	0,00%
P38418	At3g45140	Lipoxygenase 2, chloroplastic OS=Arabidopsis thaliana GN=LOX2 PE=1 SV=1	25	---	----	0,722	1,00E-05	0,03	0,10%
Q8LDQ8	At5g24165	At5g24165 OS=Arabidopsis thaliana GN=At5g24165 PE=2 SV=1	2	---	----	0,722	0,00021	0,60	0,20%

Q8W108	At4g14710	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 3 OS=Arabidopsis thaliana GN=ARD3 PE=2 SV=1	2	---	----	0,722	0,00121	3,43	0,80%
Q9LIB2;Q9SD76	At3g29320	Alpha-glucan phosphorylase 1 OS=Arabidopsis thaliana GN=PHS1 PE=2 SV=1	1	---	----	0,722	0,00161	4,56	1,00%
Q9LF33;Q9LIA8	At5g15490	UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1	5	---	----	0,721	1,00E-05	0,03	0,00%
P46312	At4g30950	Omega-6 fatty acid desaturase, chloroplastic OS=Arabidopsis thaliana GN=FAD6 PE=2 SV=2	2	---	----	0,721	0,00101	2,86	0,70%
Q39195	At3g21055	Photosystem II 5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=PSBT PE=3 SV=2	1	---	----	0,719	0,00061	1,73	0,40%
Q9M2Z4**	At3g48890	Membrane steroid-binding protein 2 OS=Arabidopsis thaliana GN=MSBP2 PE=1 SV=1	2	---	----	0,719	0,00201	5,70	1,10%
Q9LPG6	At1g53500	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM2 OS=Arabidopsis thaliana GN=RHM2 PE=1 SV=1	2	---	----	0,718	0,00161	4,56	1,00%
P46644;P46645	At5g11520	Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1	2	---	----	0,716	0,00081	2,30	0,60%
Q9SE50	At1g52400	Beta-D-glucopyranosyl abscisate beta-glucosidase OS=Arabidopsis thaliana GN=BGLU18 PE=1 SV=2	3	---	----	0,714	0,00021	0,60	0,20%
P68209;Q8LAD2	At5g08300	Succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1	2	---	----	0,711	0,00141	4,00	0,90%
Q9FLF0;Q9LXG1	AT5G39850	40S ribosomal protein S9-2 OS=Arabidopsis thaliana GN=RPS9C PE=2 SV=1	1	---	----	0,703	0,00141	4,00	0,80%
Q9LLR6	AT5G59310	Non-specific lipid-transfer protein 4 OS=Arabidopsis thaliana GN=LTP4 PE=3 SV=1	1	---	----	0,703	0,00261	7,40	1,40%
Q93VT9	AT1G14320	60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1	2	---	----	0,699	1,00E-05	0,03	0,00%
Q42547;Q96528	AT1G20620	Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3	1	---	----	0,698	0,00121	3,43	0,70%
Q9S762	AT1G58080	ATP phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN1A PE=1 SV=1	2	---	----	0,697	1,00E-05	0,03	0,00%
O80626	AT2G39390	60S ribosomal protein L35-2 OS=Arabidopsis thaliana GN=RPL35B PE=2 SV=1	2	---	----	0,692	1,00E-05	0,03	0,00%
P29402	AT5G61790	Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1	8	---	----	0,69	1,00E-05	0,03	0,10%
Q9FZ76	AT1G18540	60S ribosomal protein L6-1 OS=Arabidopsis thaliana GN=RPL6A PE=2 SV=1	2	---	----	0,689	1,00E-05	0,03	0,00%
O48741	AT1G03630	Protochlorophyllide reductase C, chloroplastic OS=Arabidopsis thaliana GN=PORC PE=1 SV=1	6	---	----	0,689	1,00E-05	0,03	0,20%
Q9SF85	AT3G09820	Adenosine kinase 1 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=1	4	---	----	0,689	1,00E-05	0,03	0,20%
Q39101	AT5G01600	Ferritin-1, chloroplastic OS=Arabidopsis thaliana GN=FER1 PE=2 SV=1	6	---	----	0,688	1,00E-05	0,03	0,10%
Q03250	AT2G21660	Glycine-rich RNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1	3	---	----	0,682	1,00E-05	0,03	0,00%
P59230;P59231;Q	AT2G27530	60S ribosomal protein L10a-2 OS=Arabidopsis thaliana GN=RPL10AB PE=1 SV=1	1	---	----	0,682	0,00061	1,73	0,40%
F4JLY4	AT4G22690	Cytochrome P450, family 706, subfamily A, polypeptide 1 OS=Arabidopsis thaliana GN=CYP706A1 PE=3 SV=1	6	---	----	0,679	1,00E-05	0,03	0,00%
Q9M0A5;Q9M0A7	AT4G30550	Gamma-glutamyl peptidase 3 OS=Arabidopsis thaliana GN=At4g30550 PE=4 SV=1	1	---	----	0,677	0,00081	2,30	0,50%
Q9LK36	AT3G23810	Adenosylhomocysteinase 2 OS=Arabidopsis thaliana GN=SAHH2 PE=1 SV=1	4	---	----	0,675	1,00E-05	0,03	0,00%
O24457	AT1G01090	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic OS=Arabidopsis thaliana GN=PDH-E1 ALPHA PE=2 SV=1	8	---	----	0,67	1,00E-05	0,03	0,00%
P51430	AT5G10360	40S ribosomal protein S6-2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=3	2	---	----	0,67	0,00041	1,16	0,30%
P42733**	AT5G23740	40S ribosomal protein S11-3 OS=Arabidopsis thaliana GN=RPS11C PE=2 SV=2	2	---	----	0,669	1,00E-05	0,03	0,10%
Q9SA18	AT1G31230	Bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH1 PE=1 SV=1	8	---	----	0,665	1,00E-05	0,03	0,00%
Q9SXE1	AT1G62560	Flavin-containing monooxygenase FMO GS-OX3 OS=Arabidopsis thaliana GN=FMOGS-OX3 PE=2 SV=1	4	---	----	0,665	1,00E-05	0,03	0,00%
Q9LYU8	AT5G13280	Aspartokinase 1, chloroplastic OS=Arabidopsis thaliana GN=AK1 PE=1 SV=1	2	---	----	0,663	0,00041	1,16	0,30%
Q9SRG3;Q9XI01	AT1G77510	Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1	3	---	----	0,661	1,00E-05	0,03	0,00%
Q38924	AT2G27190	Fe(3+)-Zn(2+) purple acid phosphatase 12 OS=Arabidopsis thaliana GN=PAP12 PE=2 SV=3	1	---	----	0,66	0,00221	6,26	1,20%
F4K6N0	AT5G07350	TUDOR-SN protein 1 OS=Arabidopsis thaliana GN=Tudor1 PE=1 SV=1	5	---	----	0,657	1,00E-05	0,03	0,00%
O24521**	AT3G10520	Non-symbiotic hemoglobin 2 OS=Arabidopsis thaliana GN=AHB2 PE=1 SV=1	4	---	----	0,656	1,00E-05	0,03	0,00%
Q8S4F6	AT5G01220	Sulfoquinovosyl transferase SQD2 OS=Arabidopsis thaliana GN=SQD2 PE=1 SV=1	3	---	----	0,65	1,00E-05	0,03	0,00%
P28185;Q39222;Q	AT1G06400	Ras-related protein RABA1a OS=Arabidopsis thaliana GN=RABA1A PE=1 SV=1	1	---	----	0,649	0,00341	9,67	1,70%
Q9FF55	AT5G60640	Protein disulfide isomerase-like 1-4 OS=Arabidopsis thaliana GN=PDIL1-4 PE=1 SV=1	9	---	----	0,648	1,00E-05	0,03	0,00%
Q9SKC1	AT2G31790	UDP-glycosyltransferase 74C1 OS=Arabidopsis thaliana GN=UGT74C1 PE=2 SV=1	2	---	----	0,645	0,00081	2,30	0,50%
Q8LCT3	AT4G29670	Thioredoxin-like 2-2, chloroplastic OS=Arabidopsis thaliana GN=At4g29670 PE=2 SV=2	2	---	----	0,645	0,00301	8,53	1,60%
F4I1G1	AT1G29350	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g29350 PE=4 SV=1	1	---	----	0,644	0,00341	9,67	1,70%
O49562	AT4G21210	Pyruvate, phosphate dikinase regulatory protein 1, chloroplastic OS=Arabidopsis thaliana GN=RP1 PE=1 SV=1	5	---	----	0,642	1,00E-05	0,03	0,00%
P55217	AT3G01120	Cystathionine gamma-synthase 1, chloroplastic OS=Arabidopsis thaliana GN=CGS1 PE=1 SV=3	12	---	----	0,639	1,00E-05	0,03	0,00%
P25702	AT1G54630	Acyl carrier protein 3, chloroplastic OS=Arabidopsis thaliana GN=ACP3 PE=1 SV=2	2	---	----	0,638	0,00601	17,03	2,70%
Q9SGE0;Q9ZUY6	AT1G08200	UDP-D-apiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1	6	---	----	0,637	1,00E-05	0,03	0,20%
Q9M356	AT3G61820	Aspartyl protease OS=Arabidopsis thaliana GN=F15G16.210 PE=4 SV=1	2	---	----	0,637	0,00601	17,03	2,70%
F4I3B3	AT1G49600	Polyadenylate-binding protein RBP47A OS=Arabidopsis thaliana GN=RBP47A PE=2 SV=1	1	---	----	0,636	0,00281	7,96	1,50%
P42801	AT4G39800	Inositol-3-phosphate synthase isozyme 1 OS=Arabidopsis thaliana GN=IPS1 PE=1 SV=3	5	---	----	0,635	1,00E-05	0,03	0,20%
O04499;Q9M9K1*	AT1G09780	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=IPGAM1 PE=2 SV=3	5	---	----	0,634	1,00E-05	0,03	0,00%
Q8LGG0	AT5G64350	Peptidyl-prolyl cis-trans isomerase FKBP12 OS=Arabidopsis thaliana GN=FKBP12 PE=1 SV=2	2	---	----	0,633	0,00281	7,96	1,50%
Q9SIP7	AT2G31610	40S ribosomal protein S3-1 OS=Arabidopsis thaliana GN=RPS3A PE=1 SV=1	2	---	----	0,632	1,00E-05	0,03	0,00%
Q8VY88	AT1G50900	Protein LHCP TRANSLOCATION DEFECT OS=Arabidopsis thaliana GN=LTD PE=1 SV=1	4	---	----	0,631	1,00E-05	0,03	0,70%
P51418;Q9LUD4	AT2G34480	60S ribosomal protein L18a-2 OS=Arabidopsis thaliana GN=RPL18AB PE=2 SV=2	3	---	----	0,619	0,00021	0,60	0,20%
Q9M0S5	AT4G09020	Isoamylase 3, chloroplastic OS=Arabidopsis thaliana GN=ISA3 PE=2 SV=2	3	---	----	0,617	0,00121	3,43	0,80%
Q9SUQ9;Q9ZVF3	AT4G23680	AT4g23680/F9D16_150 OS=Arabidopsis thaliana GN=F9D16.150 PE=2 SV=1	1	---	----	0,616	0,00021	0,60	0,20%
Q6ZY51	AT5G26570	Phosphoglucan, water dikinase, chloroplastic OS=Arabidopsis thaliana GN=GWD3 PE=1 SV=1	14	---	----	0,615	1,00E-05	0,03	0,10%
Q56YU0	AT3G24503	Aldehyde dehydrogenase family 2 member C4 OS=Arabidopsis thaliana GN=ALDH2C4 PE=1 SV=2	11	---	----	0,613	1,00E-05	0,03	0,00%
Q9C5C8	AT4G21860	Peptide methionine sulfoxide reductase B2, chloroplastic OS=Arabidopsis thaliana GN=MSRB2 PE=1 SV=1	2	---	----	0,612	0,00101	2,86	0,70%
O23684**	AT2G41950	At2g41950/T6D20.26 OS=Arabidopsis thaliana GN=At2g41950 PE=2 SV=1	2	---	----	0,61	0,00541	15,33	2,50%
Q9SJL8	AT2G36880	S-adenosylmethionine synthase 3 OS=Arabidopsis thaliana GN=MAT3 PE=1 SV=1	9	---	----	0,607	1,00E-05	0,03	0,00%
Q9M401	AT3G49680	Branched-chain-amino-acid aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=BCAT3 PE=1 SV=1	9	---	----	0,607	1,00E-05	0,03	0,00%
Q9SRV5	AT3G03780	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 OS=Arabidopsis thaliana GN=MS2 PE=1 SV=1	13	---	----	0,606	1,00E-05	0,03	0,00%
Q8LDP4	AT2G29960	Peptidyl-prolyl cis-trans isomerase CYP19-4 OS=Arabidopsis thaliana GN=CYP19-4 PE=1 SV=2	2	---	----	0,606	0,00201	5,70	1,10%
Q93W34	AT4G27000	Polyadenylate-binding protein RBP45C OS=Arabidopsis thaliana GN=RBP45C PE=2 SV=1	2	---	----	0,605	0,00281	7,96	1,50%
Q9T074	AT4G37870	Phosphoenolpyruvate carboxykinase [ATP] OS=Arabidopsis thaliana GN=PCKA PE=1 SV=1	5	---	----	0,604	0,00021	0,60	0,20%
P17597	AT3G48560	Acetolactate synthase, chloroplastic OS=Arabidopsis thaliana GN=ALS PE=1 SV=1	4	---	----	0,6	1,00E-05	0,03	0,00%
Q9LQ04	AT1G63000	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana GN=NRS/ER PE=1 SV=1	3	---	----	0,6	0,00021	0,60	0,20%
Q9SYM5**	AT1G78570	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 OS=Arabidopsis thaliana GN=RHM1 PE=1 SV=1	6	---	----	0,599	1,00E-05	0,03	0,10%
P57106	AT5G43330	Malate dehydrogenase, cytoplasmic 2 OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1	3	---	----	0,588	1,00E-05	0,03	0,00%
O64688	AT2G34590	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic OS=Arabidopsis thaliana GN=E1-BETA-2 PE=2 SV=1	3	---	----	0,586	0,00221	6,26	1,20%
P51413;Q93VI3	AT1G67430	60S ribosomal protein L17-2 OS=Arabidopsis thaliana GN=RPL17B PE=2 SV=2	5	---	----	0,579	1,00E-05	0,03	0,00%
Q8L9E3	AT5G61220	At5g61220 OS=Arabidopsis thaliana GN=At5g61220 PE=2 SV=1	1	---	----	0,578	0,00521	14,77	2,40%
P32961;P32962	AT3G44310	Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	3	---	----	0,576	1,00E-05	0,03	0,00%
Q9FE58;Q9M9W1	AT5G27770	60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1	2	---	----	0,575	1,00E-05	0,03	0,00%

O04905	AT5G26667	UMP-CMP kinase 3 OS=Arabidopsis thaliana GN=UMK3 PE=1 SV=1	3	---	----	0,575	0,00321	9,10	1,60%
Q8GW48	AT4G15802	At4g15810 OS=Arabidopsis thaliana GN=HSBP PE=2 SV=1	3	---	----	0,573	0,00121	3,43	0,70%
Q9SCX3	AT5G19510	Elongation factor 1-beta 2 OS=Arabidopsis thaliana GN=At5g19510 PE=1 SV=1	5	---	----	0,567	1,00E-05	0,03	0,00%
P49692	AT2G47610	60S ribosomal protein L7a-1 OS=Arabidopsis thaliana GN=RPL7AA PE=1 SV=2	2	---	----	0,567	0,00021	0,60	0,20%
Q941D3	AT5G19940	Probable plastid-lipid-associated protein 8, chloroplastic OS=Arabidopsis thaliana GN=PAP8 PE=2 SV=1	7	---	----	0,566	1,00E-05	0,03	0,00%
Q8VY70	AT1G62780	Putative uncharacterized protein At1g62780 OS=Arabidopsis thaliana GN=At1g62780 PE=2 SV=1	8	---	----	0,562	1,00E-05	0,03	0,00%
Q9FZ80	AT1G18590	Cytosolic sulfotransferase 17 OS=Arabidopsis thaliana GN=SOT17 PE=1 SV=1	3	---	----	0,559	0,00141	4,00	0,90%
Q9XI42	AT1G15270	F9L1.21 protein OS=Arabidopsis thaliana GN=F9L1.21 PE=2 SV=1	2	---	----	0,553	0,00461	13,07	2,20%
O49499	AT4G34050	Caffeoyl-CoA O-methyltransferase 1 OS=Arabidopsis thaliana GN=CCOAOMT1 PE=1 SV=1	7	---	----	0,552	1,00E-05	0,03	0,20%
Q9M352	AT3G53740	60S ribosomal protein L36-2 OS=Arabidopsis thaliana GN=RPL36B PE=2 SV=1	2	---	----	0,55	0,00041	1,16	0,30%
Q39108	AT4G38460	Heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic OS=Arabidopsis thaliana GN=GGR PE=1 SV=2	6	---	----	0,55	0,00041	1,16	0,30%
Q9FVQ1	AT1G48920	Nucleolin 1 OS=Arabidopsis thaliana GN=NUCL1 PE=1 SV=1	12	---	----	0,548	1,00E-05	0,03	0,00%
Q9LIA8	AT3G29360	UDP-glucose 6-dehydrogenase 2 OS=Arabidopsis thaliana GN=UGD2 PE=1 SV=1	4	---	----	0,548	0,00561	15,90	2,60%
Q84WM9**	AT5G12110	Elongation factor 1-beta 1 OS=Arabidopsis thaliana GN=At5g12110 PE=2 SV=2	3	---	----	0,546	0,00021	0,60	0,20%
Q9LZ57;Q9M352	AT5G02450	60S ribosomal protein L36-3 OS=Arabidopsis thaliana GN=RPL36C PE=3 SV=1	1	---	----	0,546	0,00181	5,13	1,00%
Q9FE65;Q9LJW6	AT1G69620	60S ribosomal protein L34-2 OS=Arabidopsis thaliana GN=RPL34B PE=3 SV=1	1	---	----	0,545	1,00E-05	0,03	0,00%
Q9SZI2	AT4G26110	Nucleosome assembly protein 1;1 OS=Arabidopsis thaliana GN=NAP1;1 PE=1 SV=1	4	---	----	0,541	0,00101	2,86	0,70%
Q9M885	AT3G02560	40S ribosomal protein S7-2 OS=Arabidopsis thaliana GN=RPS7B PE=2 SV=1	4	---	----	0,54	0,00041	1,16	0,30%
Q9LZ23	AT5G04740	ACT domain-containing protein ACR12 OS=Arabidopsis thaliana GN=ACR12 PE=2 SV=1	3	---	----	0,539	1,00E-05	0,03	0,00%
P82658	AT3G63540	Thylakoid lumenal 19 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At3g63540 PE=1 SV=2	4	---	----	0,537	0,00081	2,30	0,50%
Q42340;Q9SK22	AT5G18380	40S ribosomal protein S16-3 OS=Arabidopsis thaliana GN=RPS16C PE=2 SV=1	6	---	----	0,534	1,00E-05	0,03	0,00%
O04151;Q38858	AT1G56340	Calreticulin-1 OS=Arabidopsis thaliana GN=CRT1 PE=1 SV=1	5	---	----	0,533	1,00E-05	0,03	0,00%
Q39043;Q9LKR3	AT5G42020	Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	23	---	----	0,531	1,00E-05	0,03	0,00%
Q9LVT8	AT5G47210	At5g47210 OS=Arabidopsis thaliana GN=At5g47210 PE=2 SV=1	11	---	----	0,531	1,00E-05	0,03	0,00%
P60039**	AT2G44120	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	3	---	----	0,529	0,00021	0,60	0,20%
F4KIB2;Q9C5N2	AT5G10840	Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1	4	---	----	0,529	0,00081	2,30	0,50%
P29514;P29515;P2	AT5G12250	Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1	1	---	----	0,529	0,00541	15,33	2,50%
P42761	AT2G30870	Glutathione S-transferase F10 OS=Arabidopsis thaliana GN=GSTF10 PE=1 SV=3	10	---	----	0,527	1,00E-05	0,03	0,00%
P49201	AT5G02960	40S ribosomal protein S23-2 OS=Arabidopsis thaliana GN=RPS23B PE=2 SV=2	3	---	----	0,524	1,00E-05	0,03	0,00%
F4JB05;Q9ASR1	AT3G12915	Ribosomal protein S5/Elongation factor G/III/V family protein OS=Arabidopsis thaliana GN=At3g12915 PE=4 SV=1	12	---	----	0,523	1,00E-05	0,03	0,00%
Q93VP3	AT1G26630	Eukaryotic translation initiation factor 5A-2 OS=Arabidopsis thaliana GN=ELF5A-2 PE=1 SV=1	6	---	----	0,519	1,00E-05	0,03	0,00%
F4JFN3**	AT3G07770	HEAT SHOCK PROTEIN 89.1 OS=Arabidopsis thaliana GN=Hsp89.1 PE=3 SV=1	4	---	----	0,512	0,00181	5,13	1,00%
Q9STX5**	AT4G24190	Endoplasmin homolog OS=Arabidopsis thaliana GN=SHD PE=1 SV=1	20	---	----	0,511	1,00E-05	0,03	0,00%
P29515	AT2G29550	Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	2	---	----	0,511	0,00341	9,67	1,70%
O48549	AT4G31700	40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2	2	---	----	0,504	0,00081	2,30	0,50%
F4ISU2	AT2G32240	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g32240 PE=1 SV=1	23	---	----	0,502	1,00E-05	0,03	0,00%
Q940B0	AT5G27850	60S ribosomal protein L18-3 OS=Arabidopsis thaliana GN=RPL18C PE=2 SV=1	7	---	----	0,501	1,00E-05	0,03	0,00%
Q9LZG0;Q9SF85	AT5G03300	Adenosine kinase 2 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	6	---	----	0,499	1,00E-05	0,03	0,00%
F4JKH6	AT4G28080	Tetratricopeptide repeat domain protein OS=Arabidopsis thaliana GN=At4g28080 PE=1 SV=1	7	---	----	0,498	1,00E-05	0,03	0,00%
Q93VK5	AT1G31800	Protein LUTEIN DEFICIENT 5, chloroplastic OS=Arabidopsis thaliana GN=CYP97A3 PE=1 SV=1	4	---	----	0,497	0,00361	10,23	1,80%
Q05431	AT1G07890	L-ascorbate peroxidase 1, cytosolic OS=Arabidopsis thaliana GN=APX1 PE=1 SV=2	12	---	----	0,495	1,00E-05	0,03	0,10%
Q9SFU1	AT3G07110	60S ribosomal protein L13a-1 OS=Arabidopsis thaliana GN=RPL13AA PE=2 SV=1	5	---	----	0,494	1,00E-05	0,03	0,00%
Q56WH4	AT5G22650	Histone deacetylase HDT2 OS=Arabidopsis thaliana GN=HDT2 PE=1 SV=2	4	---	----	0,492	0,00321	9,10	1,70%
O80585;Q9SE60	AT2G44160	Methylenetetrahydrofolate reductase 2 OS=Arabidopsis thaliana GN=MTHFR2 PE=1 SV=2	4	---	----	0,489	1,00E-05	0,03	0,00%
Q42112	AT3G09200	60S acidic ribosomal protein P0-2 OS=Arabidopsis thaliana GN=RPP0B PE=1 SV=2	8	---	----	0,487	1,00E-05	0,03	0,00%
P22953;Q9LHA8	AT5G02500	Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	3	---	----	0,487	1,00E-05	0,03	0,00%
Q9LY15	AT5G07460	Peptide methionine sulfoxide reductase A2 OS=Arabidopsis thaliana GN=MRSA2 PE=1 SV=1	3	---	----	0,487	0,00081	2,30	0,50%
P59232	AT2G47110	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=1 SV=2	1	---	----	0,486	0,00381	10,80	1,90%
Q9M591	AT3G56940	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic OS=Arabidopsis thaliana GN=CRD1 PE=1 SV=2	13	---	----	0,485	1,00E-05	0,03	0,00%
Q9SUR0	AT4G23670	AT4G23670 protein OS=Arabidopsis thaliana GN=F9D16.140 PE=2 SV=1	7	---	----	0,485	1,00E-05	0,03	0,10%
O82089	AT3G56240	Copper transport protein CCH OS=Arabidopsis thaliana GN=CCH PE=1 SV=1	5	---	----	0,484	1,00E-05	0,03	0,00%
P41127;Q9FF90	AT3G49010	60S ribosomal protein L13-1 OS=Arabidopsis thaliana GN=RPL13B PE=1 SV=1	2	---	----	0,484	0,00221	6,26	1,20%
P53780	AT3G57050	Cystathionine beta-lyase, chloroplastic OS=Arabidopsis thaliana GN=CBL PE=1 SV=1	3	---	----	0,482	0,00281	7,96	1,50%
P56780	AtCg00710	Photosystem II reaction center protein H OS=Arabidopsis thaliana GN=psbH PE=1 SV=2	1	**ATQTVEDSSR**	**Phospho T2**	0,477	0,00461	13,07	2,20%
P46286	AT2G18020	60S ribosomal protein L8-1 OS=Arabidopsis thaliana GN=RPL8A PE=1 SV=2	2	---	----	0,475	0,00401	11,37	1,90%
P16181**	AT3G48930	40S ribosomal protein S11-1 OS=Arabidopsis thaliana GN=RPS11A PE=2 SV=1	3	---	----	0,472	0,00061	1,73	0,40%
Q9SUR6	AT4G23600	Cystine lyase CORI3 OS=Arabidopsis thaliana GN=CORI3 PE=1 SV=1	13	---	----	0,472	1,00E-05	0,03	0,00%
Q9ZWT2	AT5G48810	Cytochrome B5 isoform D OS=Arabidopsis thaliana GN=CYTB5-D PE=1 SV=1	4	---	----	0,468	0,00021	0,60	0,20%
Q9ZUP3	AT2G19480	Nucleosome assembly protein 1;2 OS=Arabidopsis thaliana GN=NAP1;2 PE=1 SV=1	6	---	----	0,468	1,00E-05	0,03	0,00%
Q9SFB1	AT3G08030	F17A17.37 protein OS=Arabidopsis thaliana GN=F17A17.37 PE=2 SV=1	8	---	----	0,463	1,00E-05	0,03	0,00%
P25855;Q9LQL0	AT2G35370	Glycine cleavage system H protein 1, mitochondrial OS=Arabidopsis thaliana GN=GDH1 PE=1 SV=1	3	---	----	0,458	1,00E-05	0,03	0,00%
Q9M9P3	AT3G03250	Probable UTP--glucose-1-phosphate uridylyltransferase 2 OS=Arabidopsis thaliana GN=UGP1 PE=1 SV=1	7	---	----	0,457	1,00E-05	0,03	0,10%
Q9M2F1	AT3G61110	40S ribosomal protein S27-2 OS=Arabidopsis thaliana GN=RPS27B PE=2 SV=2	2	---	----	0,456	1,00E-05	0,03	0,00%
P59223;P59224	AT3G60770	40S ribosomal protein S13-1 OS=Arabidopsis thaliana GN=RPS13A PE=2 SV=1	5	---	----	0,455	1,00E-05	0,03	0,00%
Q9ZUJ3	At1g60000	AT1G60000 protein OS=Arabidopsis thaliana GN=T2K10.5 PE=2 SV=1	3	---	----	0,454	0,00161	4,56	1,00%
P49688;Q8L8Y0	At2g41840	40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2	4	---	----	0,454	1,00E-05	0,03	0,10%
Q6NKS4	At5g47110	At5g47110 OS=Arabidopsis thaliana GN=At5g47110 PE=2 SV=1	5	---	----	0,453	0,00021	0,60	0,20%
P48006	At1g30230	Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2	10	---	----	0,452	1,00E-05	0,03	0,10%
P17094	At1g43170	60S ribosomal protein L3-1 OS=Arabidopsis thaliana GN=ARP1 PE=2 SV=5	17	---	----	0,452	1,00E-05	0,03	0,00%
P16127	At4g18480	Magnesium-chelatase subunit ChlI-1, chloroplastic OS=Arabidopsis thaliana GN=CHLI1 PE=1 SV=1	6	---	----	0,449	1,00E-05	0,03	0,00%
Q6STH5	At3g24430	Fe-S cluster assembly factor HCF101, chloroplastic OS=Arabidopsis thaliana GN=HCF101 PE=1 SV=1	5	---	----	0,448	1,00E-05	0,03	0,00%
Q9LZ66	At5g04590	Sulfite reductase [ferredoxin], chloroplastic OS=Arabidopsis thaliana GN=SIR PE=1 SV=1	12	---	----	0,447	1,00E-05	0,03	0,10%
F4K409	At5g13650	Putative TypA-like translation elongation factor SVR3 OS=Arabidopsis thaliana GN=At5g13650 PE=4 SV=1	8	---	----	0,447	1,00E-05	0,03	0,00%
B9DGT7;B9DHQ0;	At1g50010	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	5	---	----	0,446	1,00E-05	0,03	0,00%
Q8RXD9	At2g40840	4-alpha-glucanotransferase DPE2 OS=Arabidopsis thaliana GN=DPE2 PE=1 SV=1	14	---	----	0,446	1,00E-05	0,03	0,00%

O23255	At4g13940	Adenosylhomocysteinase 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1	8	---	----	0,445	1,00E-05	0,03	0,00%
P51420	At5g56710	60S ribosomal protein L31-3 OS=Arabidopsis thaliana GN=RPL31C PE=2 SV=2	2	---	----	0,443	0,00441	12,50	2,10%
Q43349	At3g53460	29 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP29A PE=2 SV=2	4	---	----	0,442	1,00E-05	0,03	0,00%
Q42547	AT3G45030	Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3	18	---	----	0,441	1,00E-05	0,03	0,00%
Q42472	AT1G65960	Glutamate decarboxylase 2 OS=Arabidopsis thaliana GN=GAD2 PE=1 SV=1	8	---	----	0,438	1,00E-05	0,03	0,00%
Q93XW5	AT5G48180	Nitrile-specifier protein 5 OS=Arabidopsis thaliana GN=NSP5 PE=2 SV=1	7	---	----	-0,435	1,00E-05	0,03	0,30%
Q93W28	AT4G15545	Uncharacterized protein At4g15545 OS=Arabidopsis thaliana GN=At4g15545 PE=1 SV=1	7	---	----	-0,435	1,00E-05	0,03	0,00%
Q9LU85	AT3G26070	Probable plastid-lipid-associated protein 4, chloroplastic OS=Arabidopsis thaliana GN=PAP4 PE=2 SV=1	7	---	----	-0,436	1,00E-05	0,03	0,00%
Q8W585	AT1G06430	ATP-dependent zinc metalloprotease FTSH 8, chloroplastic OS=Arabidopsis thaliana GN=FTSH8 PE=1 SV=1	6	---	----	-0,437	1,00E-05	0,03	0,00%
Q56Z59	AT1G72160	Patellin-3 OS=Arabidopsis thaliana GN=PATL3 PE=1 SV=2	9	---	----	-0,438	1,00E-05	0,03	0,00%
O23629;Q9FFC0;Q	AT3G45980	Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	3	---	----	-0,438	1,00E-05	0,03	0,00%
Q9LX13	AT5G10160	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-like protein OS=Arabidopsis thaliana GN=T31P16_150 PE=2 SV=1	3	---	----	-0,439	0,00041	1,16	0,30%
Q9ZVS4;Q9ZVS5	AT1G03220	Aspartyl protease-like protein OS=Arabidopsis thaliana GN=F15K9.17 PE=2 SV=1	3	---	----	-0,44	0,00061	1,73	0,40%
F4INE2;O03042;P9	AT2G07732	Ribulose bisphosphate carboxylase large chain, catalytic domain OS=Arabidopsis thaliana GN=At2g07732 PE=3 SV=1	1	---	----	-0,457	0,00101	2,86	0,70%
Q96262	AT4G20260	Plasma membrane-associated cation-binding protein 1 OS=Arabidopsis thaliana GN=PCAP1 PE=1 SV=1	10	---	----	-0,466	1,00E-05	0,03	0,00%
P81760	AT5G53490	Thylakoid lumenal 17.4 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At5g53490 PE=1 SV=2	6	---	----	-0,471	1,00E-05	0,03	0,00%
Q38946	AT5G07440	Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1	7	---	----	-0,475	1,00E-05	0,03	0,00%
F4KBJ3	AT5G38520	Alpha/beta-hydrolase-like protein OS=Arabidopsis thaliana GN=At5g38520 PE=4 SV=1	4	---	----	-0,478	0,00381	10,80	1,90%
Q39249	AT1G08550	Violaxanthin de-epoxidase, chloroplastic OS=Arabidopsis thaliana GN=VDE1 PE=1 SV=1	3	---	----	-0,479	0,00521	14,77	2,40%
Q9CAR7;Q9FM19;	AT1G69840	Hypersensitive-induced response protein 2 OS=Arabidopsis thaliana GN=HIR2 PE=1 SV=1	3	---	----	-0,48	0,00401	11,37	2,00%
Q9M2D8	AT3G61260	Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1	6	---	----	-0,483	1,00E-05	0,03	0,00%
Q9FJ95	AT5G51970	Sorbitol dehydrogenase OS=Arabidopsis thaliana GN=SDH PE=1 SV=1	9	---	----	-0,483	1,00E-05	0,03	0,10%
O80533	AT1G09500	Alcohol dehydrogenase-like protein OS=Arabidopsis thaliana GN=F14J9.16 PE=2 SV=1	4	---	----	-0,484	0,00081	2,30	0,50%
Q9SYG7	AT1G54100	Aldehyde dehydrogenase family 7 member B4 OS=Arabidopsis thaliana GN=ALDH7B4 PE=2 SV=3	11	---	----	-0,494	1,00E-05	0,03	0,00%
O49675**	AT4G19170	Probable carotenoid cleavage dioxygenase 4, chloroplastic OS=Arabidopsis thaliana GN=NCED4 PE=1 SV=1	8	---	----	-0,494	1,00E-05	0,03	0,00%
O04922;P52032;Q	AT2G31570	Probable glutathione peroxidase 2 OS=Arabidopsis thaliana GN=GPX2 PE=1 SV=1	2	---	----	-0,501	1,00E-05	0,03	0,00%
F4IAP5	AT1G18270	Ketose-bisphosphate aldolase class-II family protein OS=Arabidopsis thaliana GN=At1g18270 PE=4 SV=1	13	---	----	-0,502	1,00E-05	0,03	0,00%
P42762	AT5G51070	Chaperone protein ClpD, chloroplastic OS=Arabidopsis thaliana GN=CLPD PE=1 SV=1	4	---	----	-0,503	0,00441	12,50	2,10%
P56755	ATCG01090	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic OS=Arabidopsis thaliana GN=ndhI PE=3 SV=1	2	---	----	-0,505	0,00161	4,56	0,90%
Q9FKK7	AT5G57655	Xylose isomerase OS=Arabidopsis thaliana GN=XYLA PE=2 SV=2	19	---	----	-0,525	1,00E-05	0,03	0,00%
Q56Y11	AT5G58770	Dehydrodolichyl diphosphate synthase 2 OS=Arabidopsis thaliana GN=At5g58770 PE=2 SV=2	6	---	----	-0,529	1,00E-05	0,03	0,00%
O49304	AT1G23130	At1g23130/T26J12_10 OS=Arabidopsis thaliana GN=T26J12.10 PE=2 SV=1	3	---	----	-0,53	0,00541	15,33	2,50%
Q9C8L4	AT1G53580	Persulfide dioxygenase ETHE1 homolog, mitochondrial OS=Arabidopsis thaliana GN=GLY3 PE=1 SV=3	5	---	----	-0,531	1,00E-05	0,03	0,00%
P52032	AT2G25080	Phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic OS=Arabidopsis thaliana GN=GPX1 PE=2 SV=2	5	---	----	-0,533	1,00E-05	0,03	0,00%
Q37165	ATCG01100	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ndhA PE=3 SV=2	3	---	----	-0,538	0,00141	4,00	0,90%
Q9FLG1	AT5G64570	Beta-D-xylosidase 4 OS=Arabidopsis thaliana GN=XYL4 PE=1 SV=1	6	---	----	-0,541	1,00E-05	0,03	0,00%
P25819;Q96528	AT4G35090	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=2 SV=3	6	---	----	-0,546	1,00E-05	0,03	0,10%
Q9ZW13**	AT2G29290	Tropinone reductase homolog At2g29290 OS=Arabidopsis thaliana GN=At2g29290 PE=2 SV=1	2	---	----	-0,551	0,00541	15,33	2,50%
Q8RXD5	AT1G73260	Kunitz trypsin inhibitor 1 OS=Arabidopsis thaliana GN=KTI1 PE=2 SV=1	1	---	----	-0,557	0,00401	11,37	1,90%
P32962	AT3G44300	Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1	2	---	----	-0,558	0,00501	14,20	2,30%
Q9SYI5	AT4G01870	Putative uncharacterized protein AT4g01870 OS=Arabidopsis thaliana GN=T7B11.13 PE=2 SV=1	11	---	----	-0,575	1,00E-05	0,03	0,00%
Q9SWG0	AT3G45300	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2	6	---	----	-0,584	1,00E-05	0,03	0,20%
Q9LMJ7	AT1G07040	At1g07040 OS=Arabidopsis thaliana GN=F10K1.25 PE=2 SV=1	6	---	----	-0,598	1,00E-05	0,03	0,00%
F4IRX7	AT2G37970	SOUL heme-binding-like protein OS=Arabidopsis thaliana GN=SOUL-1 PE=1 SV=1	6	---	----	-0,603	1,00E-05	0,03	0,10%
Q7XA63	AT5G19860	At5g19860 OS=Arabidopsis thaliana GN=At5g19860 PE=2 SV=1	2	---	----	-0,61	1,00E-05	0,03	0,00%
O80517	AT2G44790	Uclacyanin-2 OS=Arabidopsis thaliana GN=At2g44790 PE=1 SV=1	1	---	----	-0,628	0,00501	14,20	2,30%
Q42523	AT1G03090	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Arabidopsis thaliana GN=MCCA PE=1 SV=2	12	---	----	-0,635	1,00E-05	0,03	0,00%
Q9LDD8	AT4G34030	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Arabidopsis thaliana GN=MCCB PE=2 SV=1	6	---	----	-0,638	1,00E-05	0,03	0,00%
O22788	AT2G33380	Probable peroxygenase 3 OS=Arabidopsis thaliana GN=PXG3 PE=1 SV=1	3	---	----	-0,652	0,00041	1,16	0,30%
P93836	AT1G06570	4-hydroxyphenylpyruvate dioxygenase OS=Arabidopsis thaliana GN=HPD PE=1 SV=2	2	---	----	-0,652	0,00101	2,86	0,70%
Q9FE06;Q9FY71**	AT5G64260	Protein EXORDIUM-like 2 OS=Arabidopsis thaliana GN=EXL2 PE=2 SV=1	2	---	----	-0,659	0,00121	3,43	0,80%
O80845	AT2G45740	Peroxisomal membrane protein 11D OS=Arabidopsis thaliana GN=PEX11D PE=1 SV=2	4	---	----	-0,679	1,00E-05	0,03	0,00%
O81439	AT4G04020	Probable plastid-lipid-associated protein 1, chloroplastic OS=Arabidopsis thaliana GN=PAP1 PE=1 SV=1	15	---	----	-0,692	1,00E-05	0,03	0,00%
Q9LPL5	AT1G21400	2-oxoisovalerate dehydrogenase subunit alpha 1, mitochondrial OS=Arabidopsis thaliana GN=At1g21400 PE=2 SV=1	5	---	----	-0,727	1,00E-05	0,03	0,00%
Q9SCV8	AT5G56870	Beta-galactosidase 4 OS=Arabidopsis thaliana GN=BGAL4 PE=1 SV=1	13	---	----	-0,752	1,00E-05	0,03	0,00%
O49629	At4g22240	Probable plastid-lipid-associated protein 2, chloroplastic OS=Arabidopsis thaliana GN=PAP2 PE=2 SV=1	12	---	----	-0,788	1,00E-05	0,03	0,00%
Q8RX87	AT5G20250	Probable galactinol--sucrose galactosyltransferase 6 OS=Arabidopsis thaliana GN=RFS6 PE=2 SV=2	9	---	----	-0,803	1,00E-05	0,03	0,30%
Q9SCW1	AT3G13750	Beta-galactosidase 1 OS=Arabidopsis thaliana GN=BGAL1 PE=1 SV=1	9	---	----	-0,82	1,00E-05	0,03	0,10%
P49078	AT3G47340	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Arabidopsis thaliana GN=ASN1 PE=2 SV=2	3	---	----	-0,826	1,00E-05	0,03	0,00%
Q9FGY1	AT5G49360	Beta-D-xylosidase 1 OS=Arabidopsis thaliana GN=BXL1 PE=1 SV=1	16	---	----	-0,844	1,00E-05	0,03	0,00%
Q56WK6	AT1G72150	Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2	19	---	----	-0,908	1,00E-05	0,03	0,10%
Q93V62	AT4G27450	AT4g27450/F27G19_50 OS=Arabidopsis thaliana GN=At4g27450 PE=1 SV=1	2	---	----	-0,994	1,00E-05	0,03	0,00%
P24806;Q38857**	At4g30270	Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2	1	---	----	-1,089	1,00E-05	0,03	0,00%
Q07473	AT5G01530	Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1	1	**NLAGDVIGTRTEAADAK**	**Phospho T9**	-1,181	1,00E-05	0,03	0,00%
P23586	AT1G11260	Sugar transport protein 1 OS=Arabidopsis thaliana GN=STP1 PE=1 SV=2	5	---	----	-1,304	1,00E-05	0,03	0,00%
Q38853	AT4G35770	Rhodanese-like domain-containing protein 15, chloroplastic OS=Arabidopsis thaliana GN=STR15 PE=2 SV=1	1	---	----	-1,496	1,00E-05	0,03	0,00%

Supplemental Table S2: List of proteins identified in the proteomic study

Group	Description	# Peptides	Pept. modified	Modification	Ratio_log2	p-value	e-value	FDR
O04130	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2	2	---	----	2,011	1,00E-05	0,03	0,00%
P21218	Protochlorophyllide reductase B, chloroplastic OS=Arabidopsis thaliana GN=PORB PE=1 SV=3	4	---	----	1,789	1,00E-05	0,03	0,00%
Q9MAQ0	Granule-bound starch synthase 1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=GBSS1 PE=1 SV=1	7	---	----	1,621	1,00E-05	0,03	0,00%
Q1H537	Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic OS=Arabidopsis thaliana GN=DVR PE=1 SV=1	1	---	----	1,487	1,00E-05	0,03	0,00%
Q9LE06	Methionine aminotransferase BCAT4 OS=Arabidopsis thaliana GN=BCAT4 PE=1 SV=1	8	---	----	1,399	1,00E-05	0,03	0,00%
Q9ZW84	3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1	3	---	----	1,364	1,00E-05	0,03	0,00%
Q9LYT7	3-isopropylmalate dehydratase small subunit 2 OS=Arabidopsis thaliana GN=IPMI1 PE=1 SV=1	3	---	----	1,357	1,00E-05	0,03	0,00%
O23324;Q9LIK9	ATP-sulfurylase 3, chloroplastic OS=Arabidopsis thaliana GN=APS3 PE=1 SV=1	3	---	----	1,262	1,00E-05	0,03	0,00%
P17562;P23686;Q9SJL8	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	1	---	----	1,257	1,00E-05	0,03	0,00%
Q9C6B9	Phosphoethanolamine N-methyltransferase 3 OS=Arabidopsis thaliana GN=NMT3 PE=2 SV=2	4	---	----	1,083	1,00E-05	0,03	0,00%
P48421	Cytochrome P450 83A1 OS=Arabidopsis thaliana GN=CYP83A1 PE=1 SV=2	5	---	----	1,078	1,00E-05	0,03	0,00%
Q9CAX6;Q9SIH0	40S ribosomal protein S14-2 OS=Arabidopsis thaliana GN=RPS14B PE=1 SV=1	2	---	----	1,075	1,00E-05	0,03	0,00%
Q9SK84	Class-II DAHP synthetase family protein OS=Arabidopsis thaliana GN=F12K8.24 PE=4 SV=1	3	---	----	1,062	1,00E-05	0,03	0,00%
Q949U1	Dihomomethionine N-hydroxylase OS=Arabidopsis thaliana GN=CYP79F1 PE=1 SV=1	4	---	----	1,062	1,00E-05	0,03	0,00%
Q9FMT1	3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMDH3 PE=1 SV=1	9	---	----	1,01	1,00E-05	0,03	0,00%
Q94A41	Alpha-amylase 3, chloroplastic OS=Arabidopsis thaliana GN=AMY3 PE=2 SV=1	6	---	----	1,005	1,00E-05	0,03	0,00%
Q8L7C9	Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1	8	---	----	0,995	1,00E-05	0,03	0,00%
Q9M0A7	AT4g30530/F17I23_130 OS=Arabidopsis thaliana GN=At4g30530 PE=2 SV=1	5	---	----	0,991	1,00E-05	0,03	0,00%
Q9LX31	Tetrapyrrole-binding protein, chloroplastic OS=Arabidopsis thaliana GN=GUN4 PE=1 SV=1	4	---	----	0,985	1,00E-05	0,03	0,00%
P25853	Beta-amylase 5 OS=Arabidopsis thaliana GN=BAM5 PE=2 SV=1	7	---	----	0,984	1,00E-05	0,03	0,00%
O23324	ATP-sulfurylase 3, chloroplastic OS=Arabidopsis thaliana GN=APS3 PE=1 SV=1	3	---	----	0,942	1,00E-05	0,03	0,00%
Q9FKC0;Q9LRX8;Q9SFU1	60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	1	---	----	0,936	1,00E-05	0,03	0,00%
Q8VY86	Peptide methionine sulfoxide reductase B7 OS=Arabidopsis thaliana GN=MSRB7 PE=2 SV=1	1	---	----	0,935	1,00E-05	0,03	0,00%
Q9FG67	Methylthioalkylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=MAM1 PE=1 SV=1	1	---	----	0,934	1,00E-05	0,03	0,00%
Q9LIK9	ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=1 SV=1	8	---	----	0,93	1,00E-05	0,03	0,00%
O82392	Phosphomethylpyrimidine synthase, chloroplastic OS=Arabidopsis thaliana GN=THIC PE=1 SV=1	4	---	----	0,904	1,00E-05	0,03	0,00%
Q9LUT2	S-adenosylmethionine synthase 4 OS=Arabidopsis thaliana GN=METK4 PE=1 SV=1	9	---	----	0,9	1,00E-05	0,03	0,00%
Q38814	Thiamine thiazole synthase, chloroplastic OS=Arabidopsis thaliana GN=THI1 PE=1 SV=1	8	---	----	0,896	1,00E-05	0,03	0,00%
O81852;Q9SA18	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH2 PE=1 S	3	---	----	0,89	1,00E-05	0,03	0,00%
Q9ZPZ4	Putative uncharacterized protein At1g09310 OS=Arabidopsis thaliana GN=T31J12.3 PE=2 SV=1	9	---	----	0,874	1,00E-05	0,03	0,00%
O22832;Q9M879	Acyl-[acyl-carrier-protein] desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1	3	---	----	0,871	1,00E-05	0,03	0,00%
Q9ZWC4	At1g04040/F21M11_2 OS=Arabidopsis thaliana GN=F21M11.2 PE=2 SV=1	3	---	----	0,869	1,00E-05	0,03	0,00%
Q8VZ19	60S ribosomal protein L30-2 OS=Arabidopsis thaliana GN=RPL30B PE=3 SV=1	2	---	----	0,86	1,00E-05	0,03	0,00%
P49637	60S ribosomal protein L27a-3 OS=Arabidopsis thaliana GN=RPL27AC PE=2 SV=2	5	---	----	0,851	1,00E-05	0,03	0,00%
Q9FKC0;Q9LRX8	60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	1	---	----	0,839	1,00E-05	0,03	0,00%
Q944H0;Q9C6B9;Q9FR44	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2	1	---	----	0,837	1,00E-05	0,03	0,00%
Q9M1G8	DJ-1 protein homolog F OS=Arabidopsis thaliana GN=DJ1F PE=1 SV=1	4	---	----	0,836	1,00E-05	0,03	0,00%
P17562;P23686;Q9LUT2;	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	4	---	----	0,831	1,00E-05	0,03	0,00%
O48917	UDP-sulfoquinovose synthase, chloroplastic OS=Arabidopsis thaliana GN=SQD1 PE=1 SV=1	5	---	----	0,83	1,00E-05	0,03	0,00%
Q94K48	E-Z type HEAT repeat-containing protein OS=Arabidopsis thaliana GN=At3g62530 PE=2 SV=1	7	---	----	0,811	1,00E-05	0,03	0,00%
O80852	Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1	10	---	----	0,807	1,00E-05	0,03	0,00%
P92981	5'-adenylylsulfate reductase 2, chloroplastic OS=Arabidopsis thaliana GN=APR2 PE=1 SV=2	3	---	----	0,8	1,00E-05	0,03	0,00%
P25858	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	3	---	----	0,791	1,00E-05	0,03	0,00%
Q9FEB5	Phosphoglucan phosphatase DSP4, chloroplastic OS=Arabidopsis thaliana GN=DSP4 PE=1 SV=1	6	---	----	0,779	1,00E-05	0,03	0,00%
P17562;P23686;Q9LUT2	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	2	---	----	0,776	1,00E-05	0,03	0,00%
Q9SIV0	S-alkyl-thiohydroximate lyase SUR1 OS=Arabidopsis thaliana GN=SUR1 PE=1 SV=1	8	---	----	0,771	1,00E-05	0,03	0,00%
O23515	60S ribosomal protein L15-1 OS=Arabidopsis thaliana GN=RPL15A PE=2 SV=1	3	---	----	0,768	1,00E-05	0,03	0,00%
Q9T043	60S ribosomal protein L14-2 OS=Arabidopsis thaliana GN=RPL14B PE=2 SV=1	4	---	----	0,764	1,00E-05	0,03	0,00%
Q9C9C9;Q9FZ80	Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1	2	---	----	0,763	1,00E-05	0,03	0,00%
Q9C4Z6	Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1	2	---	----	0,751	1,00E-05	0,03	0,00%
Q9LFW1;Q9SRT9	UDP-arabinopyranose mutase 2 OS=Arabidopsis thaliana GN=RGP2 PE=1 SV=1	5	---	----	0,734	1,00E-05	0,03	0,00%
Q9FNB0	Magnesium-chelatase subunit ChlH, chloroplastic OS=Arabidopsis thaliana GN=CHLH PE=1 SV=1	15	---	----	0,723	1,00E-05	0,03	0,00%

Q9LF33;Q9LIA8	UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1	5	---	----	0,721	1,00E-05	0,03	0,00%
Q9C9C9	Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1	3	---	----	0,714	1,00E-05	0,03	0,00%
O80852;P42761	Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1	1	---	----	0,703	1,00E-05	0,03	0,00%
Q93VT9	60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1	2	---	----	0,699	1,00E-05	0,03	0,00%
Q9S762	ATP phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN1A PE=1 SV=1	2	---	----	0,697	1,00E-05	0,03	0,00%
O80626	60S ribosomal protein L35-2 OS=Arabidopsis thaliana GN=RPL35B PE=2 SV=1	2	---	----	0,692	1,00E-05	0,03	0,00%
Q9FZ76	60S ribosomal protein L6-1 OS=Arabidopsis thaliana GN=RPL6A PE=2 SV=1	2	---	----	0,689	1,00E-05	0,03	0,00%
Q03250	Glycine-rich RNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1	3	---	----	0,682	1,00E-05	0,03	0,00%
F4JLY4	Cytochrome P450, family 706, subfamily A, polypeptide 1 OS=Arabidopsis thaliana GN=CYP706A1 PE=3 SV=1	6	---	----	0,679	1,00E-05	0,03	0,00%
Q9LK36	Adenosylhomocysteinase 2 OS=Arabidopsis thaliana GN=SAHH2 PE=1 SV=1	4	---	----	0,675	1,00E-05	0,03	0,00%
Q9C4Z6;Q9LV28	Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1	3	---	----	0,671	1,00E-05	0,03	0,00%
O24457	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic OS=Arabidopsis thaliana GN=PDH-E1 ALPHA PE=	8	---	----	0,67	1,00E-05	0,03	0,00%
Q9SXE1	Flavin-containing monooxygenase FMO GS-OX3 OS=Arabidopsis thaliana GN=FMOGS-OX3 PE=2 SV=1	4	---	----	0,665	1,00E-05	0,03	0,00%
Q9SA18	Bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH1 PE=1 SV	8	---	----	0,665	1,00E-05	0,03	0,00%
Q9SRG3;Q9XI01	Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1	3	---	----	0,661	1,00E-05	0,03	0,00%
F4K6N0	TUDOR-SN protein 1 OS=Arabidopsis thaliana GN=Tudor1 PE=1 SV=1	5	---	----	0,657	1,00E-05	0,03	0,00%
O24521	Non-symbiotic hemoglobin 2 OS=Arabidopsis thaliana GN=AHB2 PE=1 SV=1	4	---	----	0,656	1,00E-05	0,03	0,00%
Q8S4F6	Sulfoquinovosyl transferase SQD2 OS=Arabidopsis thaliana GN=SQD2 PE=1 SV=1	3	---	----	0,65	1,00E-05	0,03	0,00%
Q9FF55	Protein disulfide isomerase-like 1-4 OS=Arabidopsis thaliana GN=PDIL1-4 PE=1 SV=1	9	---	----	0,648	1,00E-05	0,03	0,00%
O49562	Pyruvate, phosphate dikinase regulatory protein 1, chloroplastic OS=Arabidopsis thaliana GN=RP1 PE=1 SV=1	5	---	----	0,642	1,00E-05	0,03	0,00%
P55217	Cystathionine gamma-synthase 1, chloroplastic OS=Arabidopsis thaliana GN=CGS1 PE=1 SV=3	12	---	----	0,639	1,00E-05	0,03	0,00%
O04499;Q9M9K1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=PGM1 PE=2 SV=3	5	---	----	0,634	1,00E-05	0,03	0,00%
Q9SIP7	40S ribosomal protein S3-1 OS=Arabidopsis thaliana GN=RPS3A PE=1 SV=1	2	---	----	0,632	1,00E-05	0,03	0,00%
Q56YU0	Aldehyde dehydrogenase family 2 member C4 OS=Arabidopsis thaliana GN=ALDH2C4 PE=1 SV=2	11	---	----	0,613	1,00E-05	0,03	0,00%
Q9M401	Branched-chain-amino-acid aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=BCAT3 PE=1 SV=1	9	---	----	0,607	1,00E-05	0,03	0,00%
Q9SJL8	S-adenosylmethionine synthase 3 OS=Arabidopsis thaliana GN=METK3 PE=1 SV=1	9	---	----	0,607	1,00E-05	0,03	0,00%
Q9SRV5	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 OS=Arabidopsis thaliana GN=MS2 PE=1 SV	13	---	----	0,606	1,00E-05	0,03	0,00%
P17597	Acetolactate synthase, chloroplastic OS=Arabidopsis thaliana GN=ALS PE=1 SV=1	4	---	----	0,6	1,00E-05	0,03	0,00%
P57106	Malate dehydrogenase, cytoplasmic 2 OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1	3	---	----	0,588	1,00E-05	0,03	0,00%
P51413;Q93VI3	60S ribosomal protein L17-2 OS=Arabidopsis thaliana GN=RPL17B PE=2 SV=2	5	---	----	0,579	1,00E-05	0,03	0,00%
P32961;P32962	Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	3	---	----	0,576	1,00E-05	0,03	0,00%
Q9FE58;Q9M9W1	60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1	2	---	----	0,575	1,00E-05	0,03	0,00%
O22832	Acyl-[acyl-carrier-protein] desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1	8	---	----	0,572	1,00E-05	0,03	0,00%
Q9SCX3	Elongation factor 1-beta 2 OS=Arabidopsis thaliana GN=At5g19510 PE=1 SV=1	5	---	----	0,567	1,00E-05	0,03	0,00%
Q941D3	Probable plastid-lipid-associated protein 8, chloroplastic OS=Arabidopsis thaliana GN=PAP8 PE=2 SV=1	7	---	----	0,566	1,00E-05	0,03	0,00%
Q8VY70	Putative uncharacterized protein At1g62780 OS=Arabidopsis thaliana GN=At1g62780 PE=2 SV=1	8	---	----	0,562	1,00E-05	0,03	0,00%
Q9SRG3	Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1	12	---	----	0,561	1,00E-05	0,03	0,00%
Q9FVQ1	Nucleolin 1 OS=Arabidopsis thaliana GN=NUCL1 PE=1 SV=1	12	---	----	0,548	1,00E-05	0,03	0,00%
Q9FE65;Q9LJW6	60S ribosomal protein L34-2 OS=Arabidopsis thaliana GN=RPL34B PE=3 SV=1	1	---	----	0,545	1,00E-05	0,03	0,00%
Q9LZ23	ACT domain-containing protein ACR12 OS=Arabidopsis thaliana GN=ACR12 PE=2 SV=1	3	---	----	0,539	1,00E-05	0,03	0,00%
Q9FE65	60S ribosomal protein L34-2 OS=Arabidopsis thaliana GN=RPL34B PE=3 SV=1	2	---	----	0,536	1,00E-05	0,03	0,00%
Q42340;Q9SK22	40S ribosomal protein S16-3 OS=Arabidopsis thaliana GN=RPS16C PE=2 SV=1	6	---	----	0,534	1,00E-05	0,03	0,00%
O04151;Q38858	Calreticulin-1 OS=Arabidopsis thaliana GN=CRT1 PE=1 SV=1	5	---	----	0,533	1,00E-05	0,03	0,00%
Q39043;Q9LKR3	Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	23	---	----	0,531	1,00E-05	0,03	0,00%
Q9LVT8	At5g47210 OS=Arabidopsis thaliana GN=At5g47210 PE=2 SV=1	11	---	----	0,531	1,00E-05	0,03	0,00%
O04499	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=PGM1 PE=2 SV=3	10	---	----	0,528	1,00E-05	0,03	0,00%
P42761	Glutathione S-transferase F10 OS=Arabidopsis thaliana GN=GSTF10 PE=1 SV=3	10	---	----	0,527	1,00E-05	0,03	0,00%
O04151	Calreticulin-1 OS=Arabidopsis thaliana GN=CRT1 PE=1 SV=1	8	---	----	0,527	1,00E-05	0,03	0,00%
P49201	40S ribosomal protein S23-2 OS=Arabidopsis thaliana GN=RPS23B PE=2 SV=2	3	---	----	0,524	1,00E-05	0,03	0,00%
F4JB05;Q9ASR1	Ribosomal protein S5/Elongation factor G/III/V family protein OS=Arabidopsis thaliana GN=At3g12915 PE=4 SV=1	12	---	----	0,523	1,00E-05	0,03	0,00%
Q93VP3	Eukaryotic translation initiation factor 5A-2 OS=Arabidopsis thaliana GN=ELF5A-2 PE=1 SV=1	6	---	----	0,519	1,00E-05	0,03	0,00%
Q9STX5	Endoplasmin homolog OS=Arabidopsis thaliana GN=SHD PE=1 SV=1	20	---	----	0,511	1,00E-05	0,03	0,00%
F4ISU2	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g32240 PE=1 SV=1	23	---	----	0,502	1,00E-05	0,03	0,00%
Q940B0	60S ribosomal protein L18-3 OS=Arabidopsis thaliana GN=RPL18C PE=2 SV=1	7	---	----	0,501	1,00E-05	0,03	0,00%
Q9LZG0;Q9SF85	Adenosine kinase 2 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	6	---	----	0,499	1,00E-05	0,03	0,00%

F4JKH6	Tetratricopeptide repeat domain protein OS=Arabidopsis thaliana GN=At4g28080 PE=1 SV=1	7	---	----	0,498	1,00E-05	0,03	0,00%
Q9SFU1	60S ribosomal protein L13a-1 OS=Arabidopsis thaliana GN=RPL13AA PE=2 SV=1	5	---	----	0,494	1,00E-05	0,03	0,00%
O80585;Q9SE60	Methylenetetrahydrofolate reductase 2 OS=Arabidopsis thaliana GN=MTHFR2 PE=1 SV=2	4	---	----	0,489	1,00E-05	0,03	0,00%
Q42112	60S acidic ribosomal protein P0-2 OS=Arabidopsis thaliana GN=RPP0B PE=1 SV=2	8	---	----	0,487	1,00E-05	0,03	0,00%
P22953;Q9LHA8	Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	3	---	----	0,487	1,00E-05	0,03	0,00%
Q9M591	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic OS=Arabidopsis thaliana GN=CRD1	13	---	----	0,485	1,00E-05	0,03	0,00%
P29976	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2	4	---	----	0,484	1,00E-05	0,03	0,00%
O82089	Copper transport protein CCH OS=Arabidopsis thaliana GN=CCH PE=1 SV=1	5	---	----	0,484	1,00E-05	0,03	0,00%
Q9SUR6	Cystine lyase CORI3 OS=Arabidopsis thaliana GN=CORI3 PE=1 SV=1	13	---	----	0,472	1,00E-05	0,03	0,00%
Q9ZUP3	Nucleosome assembly protein 1;2 OS=Arabidopsis thaliana GN=NAP1;2 PE=1 SV=1	6	---	----	0,468	1,00E-05	0,03	0,00%
Q9SFB1	F17A17.37 protein OS=Arabidopsis thaliana GN=F17A17.37 PE=2 SV=1	8	---	----	0,463	1,00E-05	0,03	0,00%
P25855;Q9LQL0	Glycine cleavage system H protein 1, mitochondrial OS=Arabidopsis thaliana GN=GDH1 PE=1 SV=1	3	---	----	0,458	1,00E-05	0,03	0,00%
Q9M2F1	40S ribosomal protein S27-2 OS=Arabidopsis thaliana GN=RPS27B PE=2 SV=2	2	---	----	0,456	1,00E-05	0,03	0,00%
P59223;P59224	40S ribosomal protein S13-1 OS=Arabidopsis thaliana GN=RPS13A PE=2 SV=1	5	---	----	0,455	1,00E-05	0,03	0,00%
O80626;Q9M3D2;Q9SF53	60S ribosomal protein L35-2 OS=Arabidopsis thaliana GN=RPL35B PE=2 SV=1	2	---	----	0,453	1,00E-05	0,03	0,00%
P17094	60S ribosomal protein L3-1 OS=Arabidopsis thaliana GN=ARP1 PE=2 SV=5	17	---	----	0,452	1,00E-05	0,03	0,00%
P16127	Magnesium-chelatase subunit ChlI-1, chloroplastic OS=Arabidopsis thaliana GN=CHLI1 PE=1 SV=1	6	---	----	0,449	1,00E-05	0,03	0,00%
Q6STH5	Fe-S cluster assembly factor HCF101, chloroplastic OS=Arabidopsis thaliana GN=HCF101 PE=1 SV=1	5	---	----	0,448	1,00E-05	0,03	0,00%
F4K409	Putative TypA-like translation elongation factor SVR3 OS=Arabidopsis thaliana GN=At5g13650 PE=4 SV=1	8	---	----	0,447	1,00E-05	0,03	0,00%
B9DGT7;B9DHQ0;P11139	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	5	---	----	0,446	1,00E-05	0,03	0,00%
Q8RXD9	4-alpha-glucanotransferase DPE2 OS=Arabidopsis thaliana GN=DPE2 PE=1 SV=1	14	---	----	0,446	1,00E-05	0,03	0,00%
O23255	Adenosylhomocysteinase 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1	8	---	----	0,445	1,00E-05	0,03	0,00%
Q43349	29 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP29A PE=2 SV=2	4	---	----	0,442	1,00E-05	0,03	0,00%
Q42547	Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3	18	---	----	0,441	1,00E-05	0,03	0,00%
Q42472	Glutamate decarboxylase 2 OS=Arabidopsis thaliana GN=GAD2 PE=1 SV=1	8	---	----	0,438	1,00E-05	0,03	0,00%
P22953	Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	9	---	----	0,433	1,00E-05	0,03	0,00%
Q8L7S8	DEAD-box ATP-dependent RNA helicase 3, chloroplastic OS=Arabidopsis thaliana GN=RH3 PE=1 SV=2	20	---	----	0,428	1,00E-05	0,03	0,00%
Q9ZW85	3-isopropylmalate dehydratase small subunit 3 OS=Arabidopsis thaliana GN=At2g43090 PE=1 SV=1	7	---	----	0,423	1,00E-05	0,03	0,00%
A8MSC5;O22263	AT2G47470 protein OS=Arabidopsis thaliana GN=UNE5 PE=2 SV=1	7	---	----	0,418	1,00E-05	0,03	0,00%
P0DH99	Elongation factor 1-alpha 1 OS=Arabidopsis thaliana GN=A1 PE=1 SV=1	15	---	----	0,414	1,00E-05	0,03	0,00%
Q9LVM3	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g58250 PE=4 SV=1	5	---	----	0,413	1,00E-05	0,03	0,00%
Q9LFH5	60S ribosomal protein L12-2 OS=Arabidopsis thaliana GN=RPL12B PE=1 SV=1	5	---	----	0,405	1,00E-05	0,03	0,00%
Q9FXA2	Polyadenylate-binding protein 8 OS=Arabidopsis thaliana GN=PAB8 PE=1 SV=1	12	---	----	0,405	1,00E-05	0,03	0,00%
Q9FRL8	Glutathione S-transferase DHAR2 OS=Arabidopsis thaliana GN=DHAR2 PE=1 SV=1	8	---	----	0,402	1,00E-05	0,03	0,00%
P25858;Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	1	AASFNIIPSSTGAAK	none	0,401	1,00E-05	0,03	0,00%
Q9SAC6	Alpha-glucan water dikinase 1, chloroplastic OS=Arabidopsis thaliana GN=GWD1 PE=1 SV=2	21	---	----	0,393	1,00E-05	0,03	0,00%
Q9C9C5;Q9FZ76	60S ribosomal protein L6-3 OS=Arabidopsis thaliana GN=RPL6C PE=2 SV=1	5	---	----	0,392	1,00E-05	0,03	0,00%
Q9FWR4	Glutathione S-transferase DHAR1, mitochondrial OS=Arabidopsis thaliana GN=DHAR1 PE=1 SV=1	12	---	----	0,391	1,00E-05	0,03	0,00%
P53492;Q96292	Actin-7 OS=Arabidopsis thaliana GN=ACT7 PE=1 SV=1	2	---	----	0,388	1,00E-05	0,03	0,00%
Q08682	40S ribosomal protein Sa-1 OS=Arabidopsis thaliana GN=RPSaA PE=1 SV=3	11	---	----	0,388	1,00E-05	0,03	0,00%
Q94KE3;Q9SJQ0	Pyruvate kinase OS=Arabidopsis thaliana GN=At3g52990 PE=2 SV=1	7	---	----	0,383	1,00E-05	0,03	0,00%
P32961	Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	5	---	----	0,381	1,00E-05	0,03	0,00%
Q9SJQ9	Fructose-bisphosphate aldolase OS=Arabidopsis thaliana GN=At2g36460 PE=2 SV=1	11	---	----	0,381	1,00E-05	0,03	0,00%
Q9SJE1	Magnesium-chelatase subunit ChlD, chloroplastic OS=Arabidopsis thaliana GN=CHLD PE=1 SV=3	15	---	----	0,381	1,00E-05	0,03	0,00%
P42644	14-3-3-like protein GF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2	10	---	----	0,379	1,00E-05	0,03	0,00%
Q9FJA6;Q9M339;Q9SIP7	40S ribosomal protein S3-3 OS=Arabidopsis thaliana GN=RPS3C PE=1 SV=1	10	---	----	0,379	1,00E-05	0,03	0,00%
Q9SZY1	Nascent polypeptide-associated complex subunit alpha-like protein 4 OS=Arabidopsis thaliana GN=At4g10480 PE=2 SV	4	---	----	0,378	1,00E-05	0,03	0,00%
P31265	Translationally-controlled tumor protein homolog OS=Arabidopsis thaliana GN=TCTP PE=2 SV=2	8	---	----	0,376	1,00E-05	0,03	0,00%
Q9SW18	Magnesium protoporphyrin IX methyltransferase, chloroplastic OS=Arabidopsis thaliana GN=CHLM PE=1 SV=1	10	---	----	0,373	1,00E-05	0,03	0,00%
O65351	Subtilisin-like protease SBT1.7 OS=Arabidopsis thaliana GN=SBT1.7 PE=1 SV=1	7	---	----	0,373	1,00E-05	0,03	0,00%
P51419;Q8LCL3	60S ribosomal protein L27-3 OS=Arabidopsis thaliana GN=RPL27C PE=2 SV=2	3	---	----	0,373	1,00E-05	0,03	0,00%
P49692;Q9LZH9	60S ribosomal protein L7a-1 OS=Arabidopsis thaliana GN=RPL7AA PE=1 SV=2	7	---	----	0,371	1,00E-05	0,03	0,00%
Q944H0	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2	8	---	----	0,369	1,00E-05	0,03	0,00%
F4K0E8	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic OS=Arabidopsis thaliana GN=ISPG P	26	---	----	0,369	1,00E-05	0,03	0,00%
O04309	Jacalin-related lectin 35 OS=Arabidopsis thaliana GN=JAL35 PE=1 SV=1	7	---	----	0,357	2,00E-05	0,06	0,00%

Q38884	Eukaryotic translation initiation factor 3 subunit I OS=Arabidopsis thaliana GN=TIF3I1 PE=2 SV=2	7	---	----	0,356	1,00E-05	0,03	0,00%
P25858;Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	15	---	----	0,356	1,00E-05	0,03	0,00%
P51818;P55737	Heat shock protein 90-3 OS=Arabidopsis thaliana GN=HSP90-3 PE=1 SV=2	20	---	----	0,351	1,00E-05	0,03	0,00%
P42643	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	8	---	----	0,347	1,00E-05	0,03	0,00%
F4K6N0;Q9FLT0	TUDOR-SN protein 1 OS=Arabidopsis thaliana GN=Tudor1 PE=1 SV=1	9	---	----	0,346	1,00E-05	0,03	0,00%
O24456	Receptor for activated C kinase 1A OS=Arabidopsis thaliana GN=RACK1A PE=1 SV=2	10	---	----	0,344	1,00E-05	0,03	0,00%
Q9LYR4	Aldolase-type TIM barrel family protein OS=Arabidopsis thaliana GN=T22N19_70 PE=2 SV=1	12	---	----	0,344	1,00E-05	0,03	0,00%
O23255;Q9LK36	Adenosylhomocysteinase 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1	12	---	----	0,343	1,00E-05	0,03	0,00%
O50008;Q9SRV5	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV	12	---	----	0,336	1,00E-05	0,03	0,00%
Q9C9C5	60S ribosomal protein L6-3 OS=Arabidopsis thaliana GN=RPL6C PE=2 SV=1	6	---	----	0,331	1,00E-05	0,03	0,00%
P49204	40S ribosomal protein S4-2 OS=Arabidopsis thaliana GN=RPS4B PE=2 SV=4	11	---	----	0,329	1,00E-05	0,03	0,00%
Q41932	Oxygen-evolving enhancer protein 3-2, chloroplastic OS=Arabidopsis thaliana GN=PSBQ2 PE=1 SV=2	7	---	----	0,327	1,00E-05	0,03	0,00%
Q8GUM2	Heat shock 70 kDa protein 9, mitochondrial OS=Arabidopsis thaliana GN=HSP70-9 PE=2 SV=1	13	---	----	0,326	1,00E-05	0,03	0,00%
P30184	Leucine aminopeptidase 1 OS=Arabidopsis thaliana GN=PM25 PE=1 SV=1	12	---	----	0,306	1,00E-05	0,03	0,00%
Q9ASR1	At1g56070/T6H22_13 OS=Arabidopsis thaliana GN=T6H22.13 PE=1 SV=1	23	---	----	0,293	1,00E-05	0,03	0,00%
P57751;Q9M9P3	UTP--glucose-1-phosphate uridylyltransferase 1 OS=Arabidopsis thaliana GN=At5g17310 PE=2 SV=1	11	---	----	0,291	1,00E-05	0,03	0,00%
O04487;Q9FVT2	Probable elongation factor 1-gamma 1 OS=Arabidopsis thaliana GN=At1g09640 PE=2 SV=1	8	---	----	0,277	1,00E-05	0,03	0,00%
Q9SYT0	Annexin D1 OS=Arabidopsis thaliana GN=ANN1 PE=1 SV=1	18	---	----	0,272	1,00E-05	0,03	0,00%
P48491	Triosephosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=CTIMC PE=1 SV=2	12	---	----	0,269	1,00E-05	0,03	0,00%
Q9SIF2	At2g04030/F3C11.14 OS=Arabidopsis thaliana GN=CR88 PE=1 SV=1	27	---	----	0,255	1,00E-05	0,03	0,00%
P31167	ADP,ATP carrier protein 1, mitochondrial OS=Arabidopsis thaliana GN=AAC1 PE=1 SV=2	7	---	----	0,237	1,00E-05	0,03	0,00%
Q9SAJ4	Phosphoglycerate kinase OS=Arabidopsis thaliana GN=T8K14.3 PE=1 SV=1	14	---	----	0,228	1,00E-05	0,03	0,00%
Q8RY71	Epithiospecifier protein OS=Arabidopsis thaliana GN=ESP PE=1 SV=2	29	---	----	0,182	1,00E-05	0,03	0,00%
O65282	20 kDa chaperonin, chloroplastic OS=Arabidopsis thaliana GN=CPN21 PE=1 SV=2	15	---	----	0,174	1,00E-05	0,03	0,00%
Q9FI56;Q9SXJ7	Chaperone protein ClpC1, chloroplastic OS=Arabidopsis thaliana GN=CLPC1 PE=1 SV=1	26	---	----	0,158	1,00E-05	0,03	0,00%
P10896;P10896-2	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RCA PE=1 SV=2	23	---	----	-0,119	1,00E-05	0,03	0,00%
P56757	ATP synthase subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=atpA PE=1 SV=1	21	---	----	-0,14	1,00E-05	0,03	0,00%
P34791	Peptidyl-prolyl cis-trans isomerase CYP20-3, chloroplastic OS=Arabidopsis thaliana GN=CYP20-3 PE=1 SV=1	8	---	----	-0,204	1,00E-05	0,03	0,00%
Q39102;Q9FH02	ATP-dependent zinc metalloprotease FTSH 1, chloroplastic OS=Arabidopsis thaliana GN=FTSH1 PE=1 SV=2	19	---	----	-0,211	1,00E-05	0,03	0,00%
Q9LRR9	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1 OS=Arabidopsis thaliana GN=GLO1 PE=1 SV=1	6	---	----	-0,218	1,00E-05	0,03	0,00%
O80934	Uncharacterized protein At2g37660, chloroplastic OS=Arabidopsis thaliana GN=At2g37660 PE=2 SV=2	12	---	----	-0,222	1,00E-05	0,03	0,00%
Q949U7	Peroxiredoxin-2E, chloroplastic OS=Arabidopsis thaliana GN=PRXIIE PE=1 SV=2	10	---	----	-0,233	2,00E-05	0,06	0,00%
Q9ZVL6	UPF0603 protein At1g54780, chloroplastic OS=Arabidopsis thaliana GN=At1g54780 PE=1 SV=1	10	---	----	-0,234	1,00E-05	0,03	0,00%
P37702	Myrosinase 1 OS=Arabidopsis thaliana GN=TGG1 PE=1 SV=1	16	---	----	-0,235	1,00E-05	0,03	0,00%
Q9LW57	Probable plastid-lipid-associated protein 6, chloroplastic OS=Arabidopsis thaliana GN=PAP6 PE=1 SV=1	9	---	----	-0,239	1,00E-05	0,03	0,00%
Q9SHE8	Photosystem I reaction center subunit III, chloroplastic OS=Arabidopsis thaliana GN=PSAF PE=1 SV=1	6	---	----	-0,248	1,00E-05	0,03	0,00%
Q9SY97	PSI type III chlorophyll a/b-binding protein OS=Arabidopsis thaliana GN=T25B24.12 PE=1 SV=1	7	---	----	-0,25	1,00E-05	0,03	0,00%
P04778;P0CJ48	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1	3	---	----	-0,251	1,00E-05	0,03	0,00%
Q9SLA8	Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic OS=Arabidopsis thaliana GN=MOD1 PE=1 SV=1	10	---	----	-0,252	1,00E-05	0,03	0,00%
Q56WD9	3-ketoacyl-CoA thiolase 2, peroxisomal OS=Arabidopsis thaliana GN=PED1 PE=1 SV=2	14	---	----	-0,253	1,00E-05	0,03	0,00%
Q9STF2	Protein plastid transcriptionally active 16 OS=Arabidopsis thaliana GN=T6H20.190 PE=1 SV=1	26	---	----	-0,261	1,00E-05	0,03	0,00%
Q9XF91	Photosystem II 22 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=PSBS PE=2 SV=1	8	---	----	-0,268	1,00E-05	0,03	0,00%
Q56YA5	Serine--glyoxylate aminotransferase OS=Arabidopsis thaliana GN=AGT1 PE=1 SV=2	17	---	----	-0,276	1,00E-05	0,03	0,00%
O50061	50S ribosomal protein L4, chloroplastic OS=Arabidopsis thaliana GN=RPL4 PE=2 SV=2	11	---	----	-0,286	1,00E-05	0,03	0,00%
O23049	50S ribosomal protein L6, chloroplastic OS=Arabidopsis thaliana GN=RPL6 PE=2 SV=1	13	---	----	-0,289	1,00E-05	0,03	0,00%
Q94CE5	Gamma-aminobutyrate transaminase POP2, mitochondrial OS=Arabidopsis thaliana GN=POP2 PE=1 SV=1	11	---	----	-0,296	1,00E-05	0,03	0,00%
Q9LR30	Glutamate--glyoxylate aminotransferase 1 OS=Arabidopsis thaliana GN=GGAT1 PE=1 SV=1	13	---	----	-0,298	1,00E-05	0,03	0,00%
Q9C8G5	CSC1-like protein ERD4 OS=Arabidopsis thaliana GN=ERD4 PE=2 SV=1	15	---	----	-0,312	1,00E-05	0,03	0,00%
Q9S7J7;Q9XF87	At2g05070/F1O13.20 OS=Arabidopsis thaliana GN=LHCB2.2 PE=2 SV=1	4	---	----	-0,312	1,00E-05	0,03	0,00%
Q9C9W5	Glycerate dehydrogenase HPR, peroxisomal OS=Arabidopsis thaliana GN=HPR PE=1 SV=1	24	---	----	-0,313	1,00E-05	0,03	0,00%
F4K5B9	Aspartyl protease family protein OS=Arabidopsis thaliana GN=At5g07030 PE=4 SV=1	8	---	----	-0,321	1,00E-05	0,03	0,00%
P43297	Cysteine proteinase RD21a OS=Arabidopsis thaliana GN=RD21A PE=1 SV=1	7	---	----	-0,329	1,00E-05	0,03	0,00%
Q56ZI2	Patellin-2 OS=Arabidopsis thaliana GN=PATL2 PE=1 SV=2	19	---	----	-0,336	1,00E-05	0,03	0,00%
Q9SGS4	Thioredoxin-like protein CDSP32, chloroplastic OS=Arabidopsis thaliana GN=CDSP32 PE=1 SV=1	8	---	----	-0,34	1,00E-05	0,03	0,00%
Q9SSL0	At1g70820 OS=Arabidopsis thaliana GN=F15H11.7 PE=2 SV=1	10	---	----	-0,34	1,00E-05	0,03	0,00%

Q8S9M1-3	Isoform 3 of Probable plastid-lipid-associated protein 13, chloroplastic OS=Arabidopsis thaliana GN=PAP13	11	---	----	-0,347	1,00E-05	0,03	0,00%
P43286	Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1	5	---	----	-0,349	1,00E-05	0,03	0,00%
Q9S726	Probable ribose-5-phosphate isomerase 3, chloroplastic OS=Arabidopsis thaliana GN=RPI3 PE=1 SV=1	11	---	----	-0,359	1,00E-05	0,03	0,00%
Q9LRR9;Q9LRS0	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1 OS=Arabidopsis thaliana GN=GLO1 PE=1 SV=1	9	---	----	-0,362	1,00E-05	0,03	0,00%
Q8W4F1	Probable plastid-lipid-associated protein 10, chloroplastic OS=Arabidopsis thaliana GN=PAP10 PE=2 SV=1	9	---	----	-0,389	1,00E-05	0,03	0,00%
O65581	Fructose-bisphosphate aldolase OS=Arabidopsis thaliana GN=M3E9.40 PE=2 SV=1	11	---	----	-0,413	1,00E-05	0,03	0,00%
Q9LRS0	Peroxisomal (S)-2-hydroxy-acid oxidase GLO2 OS=Arabidopsis thaliana GN=GLO2 PE=1 SV=1	7	---	----	-0,421	1,00E-05	0,03	0,00%
P27140-2;P27140-3	Isoform 2 of Beta carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=BCA1	8	---	----	-0,428	1,00E-05	0,03	0,00%
Q9LU10	Protease Do-like 8, chloroplastic OS=Arabidopsis thaliana GN=DEGP8 PE=1 SV=1	8	---	----	-0,434	1,00E-05	0,03	0,00%
Q93W28	Uncharacterized protein At4g15545 OS=Arabidopsis thaliana GN=At4g15545 PE=1 SV=1	7	---	----	-0,435	1,00E-05	0,03	0,00%
Q9LU85	Probable plastid-lipid-associated protein 4, chloroplastic OS=Arabidopsis thaliana GN=PAP4 PE=2 SV=1	7	---	----	-0,436	1,00E-05	0,03	0,00%
Q8W585	ATP-dependent zinc metalloprotease FTSH 8, chloroplastic OS=Arabidopsis thaliana GN=FTSH8 PE=1 SV=1	6	---	----	-0,437	1,00E-05	0,03	0,00%
O23629;Q9FFC0;Q9SI96;C	Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	3	---	----	-0,438	1,00E-05	0,03	0,00%
Q56Z59	Patellin-3 OS=Arabidopsis thaliana GN=PATL3 PE=1 SV=2	9	---	----	-0,438	1,00E-05	0,03	0,00%
Q96262	Plasma membrane-associated cation-binding protein 1 OS=Arabidopsis thaliana GN=PCAP1 PE=1 SV=1	10	---	----	-0,466	1,00E-05	0,03	0,00%
P81760	Thylakoid lumenal 17.4 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At5g53490 PE=1 SV=2	6	---	----	-0,471	1,00E-05	0,03	0,00%
Q38946	Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1	7	---	----	-0,475	1,00E-05	0,03	0,00%
Q9M2D8	Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1	6	---	----	-0,483	1,00E-05	0,03	0,00%
O49675	Probable carotenoid cleavage dioxygenase 4, chloroplastic OS=Arabidopsis thaliana GN=CCD4 PE=1 SV=1	8	---	----	-0,494	1,00E-05	0,03	0,00%
Q9SYG7	Aldehyde dehydrogenase family 7 member B4 OS=Arabidopsis thaliana GN=ALDH7B4 PE=2 SV=3	11	---	----	-0,494	1,00E-05	0,03	0,00%
P25819	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=2 SV=3	10	---	----	-0,501	1,00E-05	0,03	0,00%
O04922;P52032;Q9SZ54	Probable glutathione peroxidase 2 OS=Arabidopsis thaliana GN=GPX2 PE=1 SV=1	2	---	----	-0,501	1,00E-05	0,03	0,00%
F4IAP5	Ketose-bisphosphate aldolase class-II family protein OS=Arabidopsis thaliana GN=At1g18270 PE=4 SV=1	13	---	----	-0,502	1,00E-05	0,03	0,00%
Q9FKK7	Xylose isomerase OS=Arabidopsis thaliana GN=XYLA PE=2 SV=2	19	---	----	-0,525	1,00E-05	0,03	0,00%
Q56Y11	Dehydrodolichyl diphosphate synthase 2 OS=Arabidopsis thaliana GN=At5g58770 PE=2 SV=2	6	---	----	-0,529	1,00E-05	0,03	0,00%
Q9C8L4	Persulfide dioxygenase ETHE1 homolog, mitochondrial OS=Arabidopsis thaliana GN=GLY3 PE=1 SV=3	5	---	----	-0,531	1,00E-05	0,03	0,00%
P52032	Phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic OS=Arabidopsis thaliana GN=GPX1 PE=2 SV=2	5	---	----	-0,533	1,00E-05	0,03	0,00%
Q9FLG1	Beta-D-xylosidase 4 OS=Arabidopsis thaliana GN=BXL4 PE=1 SV=1	6	---	----	-0,541	1,00E-05	0,03	0,00%
P24806	Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2	4	---	----	-0,57	1,00E-05	0,03	0,00%
Q9SYI5	Putative uncharacterized protein AT4g01870 OS=Arabidopsis thaliana GN=T7B11.13 PE=2 SV=1	11	---	----	-0,575	1,00E-05	0,03	0,00%
Q9LMJ7	At1g07040 OS=Arabidopsis thaliana GN=F10K1.25 PE=2 SV=1	6	---	----	-0,598	1,00E-05	0,03	0,00%
Q7XA63	At5g19860 OS=Arabidopsis thaliana GN=At5g19860 PE=2 SV=1	2	---	----	-0,61	1,00E-05	0,03	0,00%
O49629;O81439	Probable plastid-lipid-associated protein 2, chloroplastic OS=Arabidopsis thaliana GN=PAP2 PE=2 SV=1	1	---	----	-0,622	1,00E-05	0,03	0,00%
Q42523	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Arabidopsis thaliana GN=MCCA PE=1 SV=2	12	---	----	-0,635	1,00E-05	0,03	0,00%
Q9LDD8	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Arabidopsis thaliana GN=MCCB PE=2 SV=1	6	---	----	-0,638	1,00E-05	0,03	0,00%
O80845	Peroxisomal membrane protein 11D OS=Arabidopsis thaliana GN=PEX11D PE=1 SV=2	4	---	----	-0,679	1,00E-05	0,03	0,00%
O81439	Probable plastid-lipid-associated protein 1, chloroplastic OS=Arabidopsis thaliana GN=PAP1 PE=1 SV=1	15	---	----	-0,692	1,00E-05	0,03	0,00%
Q9LPL5	2-oxoisovalerate dehydrogenase subunit alpha 1, mitochondrial OS=Arabidopsis thaliana GN=At1g21400 PE=2 SV=1	5	---	----	-0,727	1,00E-05	0,03	0,00%
Q9SCV8	Beta-galactosidase 4 OS=Arabidopsis thaliana GN=BGAL4 PE=1 SV=1	13	---	----	-0,752	1,00E-05	0,03	0,00%
O49629	Probable plastid-lipid-associated protein 2, chloroplastic OS=Arabidopsis thaliana GN=PAP2 PE=2 SV=1	12	---	----	-0,788	1,00E-05	0,03	0,00%
P49078	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Arabidopsis thaliana GN=ASN1 PE=2 SV=2	3	---	----	-0,826	1,00E-05	0,03	0,00%
Q9FGY1	Beta-D-xylosidase 1 OS=Arabidopsis thaliana GN=BXL1 PE=1 SV=1	16	---	----	-0,844	1,00E-05	0,03	0,00%
Q93V62	AT4g27450/F27G19_50 OS=Arabidopsis thaliana GN=At4g27450 PE=1 SV=1	2	---	----	-0,994	1,00E-05	0,03	0,00%
P24806;Q38857	Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2	1	---	----	-1,089	1,00E-05	0,03	0,00%
Q07473	Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1	1	LAGDVIGTRTEAAD/	Phospho T9	-1,181	1,00E-05	0,03	0,00%
P23586	Sugar transport protein 1 OS=Arabidopsis thaliana GN=STP1 PE=1 SV=2	5	---	----	-1,304	1,00E-05	0,03	0,00%
Q38853	Rhodanese-like domain-containing protein 15, chloroplastic OS=Arabidopsis thaliana GN=STR15 PE=2 SV=1	1	---	----	-1,496	1,00E-05	0,03	0,00%
Q9S7C0	Heat shock 70 kDa protein 14 OS=Arabidopsis thaliana GN=HSP70-14 PE=2 SV=1	1	---	----	1,955	1,00E-05	0,03	0,10%
P25858;Q5E924;Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	1	---	----	1,112	1,00E-05	0,03	0,10%
Q94AR8	3-isopropylmalate dehydratase large subunit OS=Arabidopsis thaliana GN=IIL1 PE=1 SV=1	13	---	----	0,906	1,00E-05	0,03	0,10%
Q9LVQ8	Probable protein phosphatase 2C 80 OS=Arabidopsis thaliana GN=At5g66720 PE=2 SV=1	1	---	----	0,876	1,00E-05	0,03	0,10%
P56780	Photosystem II reaction center protein H OS=Arabidopsis thaliana GN=psbH PE=1 SV=2	1	ATQTVEDSSR	none	0,844	1,00E-05	0,03	0,10%
Q9LQQ3	At1g07750/F24B9_13 OS=Arabidopsis thaliana GN=F24B9.13 PE=2 SV=1	3	---	----	0,734	1,00E-05	0,03	0,10%
P38418	Lipoxygenase 2, chloroplastic OS=Arabidopsis thaliana GN=LOX2 PE=1 SV=1	25	---	----	0,722	1,00E-05	0,03	0,10%
P29402	Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1	8	---	----	0,69	1,00E-05	0,03	0,10%

Q39101	Ferritin-1, chloroplastic OS=Arabidopsis thaliana GN=FER1 PE=2 SV=1	6	---	----	0,688	1,00E-05	0,03	0,10%
P42733	40S ribosomal protein S11-3 OS=Arabidopsis thaliana GN=RPS11C PE=2 SV=2	2	---	----	0,669	1,00E-05	0,03	0,10%
Q6ZY51	Phosphoglucan, water dikinase, chloroplastic OS=Arabidopsis thaliana GN=GWD3 PE=1 SV=1	14	---	----	0,615	1,00E-05	0,03	0,10%
Q9SYM5	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-red	6	---	----	0,599	1,00E-05	0,03	0,10%
Q05431	L-ascorbate peroxidase 1, cytosolic OS=Arabidopsis thaliana GN=APX1 PE=1 SV=2	12	---	----	0,495	1,00E-05	0,03	0,10%
Q9SUR0	AT4G23670 protein OS=Arabidopsis thaliana GN=F9D16.140 PE=2 SV=1	7	---	----	0,485	1,00E-05	0,03	0,10%
Q9M9P3	Probable UTP--glucose-1-phosphate uridylyltransferase 2 OS=Arabidopsis thaliana GN=At3g03250 PE=1 SV=1	7	---	----	0,457	1,00E-05	0,03	0,10%
P49688;Q8L8Y0	40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2	4	---	----	0,454	1,00E-05	0,03	0,10%
P48006	Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2	10	---	----	0,452	1,00E-05	0,03	0,10%
Q9LZ66	Sulfite reductase [ferredoxin], chloroplastic OS=Arabidopsis thaliana GN=SIR PE=1 SV=1	12	---	----	0,447	1,00E-05	0,03	0,10%
Q8LAH7	12-oxophytodienoate reductase 1 OS=Arabidopsis thaliana GN=OPR1 PE=1 SV=2	13	---	----	0,418	1,00E-05	0,03	0,10%
Q9CAV0	40S ribosomal protein S3a-1 OS=Arabidopsis thaliana GN=RPS3AA PE=1 SV=3	5	---	----	0,382	1,00E-05	0,03	0,10%
P49691;Q9SF40	60S ribosomal protein L4-2 OS=Arabidopsis thaliana GN=RPL4D PE=2 SV=2	9	---	----	0,382	1,00E-05	0,03	0,10%
Q9LF98	Fructose-bisphosphate aldolase OS=Arabidopsis thaliana GN=F8J2_100 PE=2 SV=1	13	---	----	0,366	1,00E-05	0,03	0,10%
Q9SD76	Alpha-glucan phosphorylase 2, cytosolic OS=Arabidopsis thaliana GN=PHS2 PE=1 SV=1	22	---	----	0,341	1,00E-05	0,03	0,10%
P25696	Bifunctional enolase 2/transcriptional activator OS=Arabidopsis thaliana GN=ENO2 PE=1 SV=1	15	---	----	0,336	1,00E-05	0,03	0,10%
O65398	Lactoylglutathione lyase OS=Arabidopsis thaliana GN=F12F1.32 PE=2 SV=1	8	---	----	0,331	1,00E-05	0,03	0,10%
Q39061	RNA-binding protein CP33, chloroplastic OS=Arabidopsis thaliana GN=CP33 PE=2 SV=1	9	---	----	0,325	1,00E-05	0,03	0,10%
Q9SA73	Obg-like ATPase 1 OS=Arabidopsis thaliana GN=T5I8.3 PE=2 SV=1	17	---	----	0,284	1,00E-05	0,03	0,10%
P27521	Chlorophyll a-b binding protein 4, chloroplastic OS=Arabidopsis thaliana GN=LHCA4 PE=1 SV=1	10	---	----	-0,208	1,00E-05	0,03	0,10%
P17745	Elongation factor Tu, chloroplastic OS=Arabidopsis thaliana GN=TUFA PE=1 SV=1	16	---	----	-0,241	1,00E-05	0,03	0,10%
O82291	Probable plastid-lipid-associated protein 3, chloroplastic OS=Arabidopsis thaliana GN=PAP3 PE=2 SV=1	10	---	----	-0,248	1,00E-05	0,03	0,10%
O82660	Photosystem II stability/assembly factor HCF136, chloroplastic OS=Arabidopsis thaliana GN=HCF136 PE=1 SV=1	15	---	----	-0,256	1,00E-05	0,03	0,10%
O22160	Thylakoid lumenal 15 kDa protein 1, chloroplastic OS=Arabidopsis thaliana GN=At2g44920 PE=1 SV=2	8	---	----	-0,382	1,00E-05	0,03	0,10%
Q9SXE9	At1g62480/T3P18_4 OS=Arabidopsis thaliana GN=At1g62480 PE=2 SV=1	4	---	----	-0,422	1,00E-05	0,03	0,10%
Q9FJ95	Sorbitol dehydrogenase OS=Arabidopsis thaliana GN=SDH PE=1 SV=1	9	---	----	-0,483	1,00E-05	0,03	0,10%
P25819;Q96528	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=2 SV=3	6	---	----	-0,546	1,00E-05	0,03	0,10%
F4IRX7	SOUL heme-binding-like protein OS=Arabidopsis thaliana GN=SOUL-1 PE=1 SV=1	6	---	----	-0,603	1,00E-05	0,03	0,10%
Q9SCW1	Beta-galactosidase 1 OS=Arabidopsis thaliana GN=BGAL1 PE=1 SV=1	9	---	----	-0,82	1,00E-05	0,03	0,10%
Q56WK6	Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2	19	---	----	-0,908	1,00E-05	0,03	0,10%
P92980;P92981	5'-adenylylsulfate reductase 3, chloroplastic OS=Arabidopsis thaliana GN=APR3 PE=2 SV=2	1	---	----	1,199	0,00021	0,60	0,20%
P92980	5'-adenylylsulfate reductase 3, chloroplastic OS=Arabidopsis thaliana GN=APR3 PE=2 SV=2	2	---	----	0,999	0,00021	0,60	0,20%
Q8LDQ8	At5g24165 OS=Arabidopsis thaliana GN=At5g24165 PE=2 SV=1	2	---	----	0,722	0,00021	0,60	0,20%
Q9SE50	Beta-D-glucopyranosyl abscisate beta-glucosidase OS=Arabidopsis thaliana GN=BGLU18 PE=1 SV=2	3	---	----	0,714	0,00021	0,60	0,20%
O48741	Protochlorophyllide reductase C, chloroplastic OS=Arabidopsis thaliana GN=PORC PE=1 SV=1	6	---	----	0,689	1,00E-05	0,03	0,20%
Q9SF85	Adenosine kinase 1 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=1	4	---	----	0,689	1,00E-05	0,03	0,20%
Q9SGE0;Q9ZUY6	UDP-D-apiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1	6	---	----	0,637	1,00E-05	0,03	0,20%
P42801	Inositol-3-phosphate synthase isozyme 1 OS=Arabidopsis thaliana GN=IPS1 PE=1 SV=3	5	---	----	0,635	1,00E-05	0,03	0,20%
P51418;Q9LUD4	60S ribosomal protein L18a-2 OS=Arabidopsis thaliana GN=RPL18AB PE=2 SV=2	3	---	----	0,619	0,00021	0,60	0,20%
Q9SUQ9;Q9ZVF3	AT4g23680/F9D16_150 OS=Arabidopsis thaliana GN=F9D16.150 PE=2 SV=1	1	---	----	0,616	0,00021	0,60	0,20%
Q9T074	Phosphoenolpyruvate carboxykinase [ATP] OS=Arabidopsis thaliana GN=PCKA PE=1 SV=1	5	---	----	0,604	0,00021	0,60	0,20%
Q9LQ04	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana G	3	---	----	0,6	0,00021	0,60	0,20%
P49692	60S ribosomal protein L7a-1 OS=Arabidopsis thaliana GN=RPL7AA PE=1 SV=2	2	---	----	0,567	0,00021	0,60	0,20%
O49499	Caffeoyl-CoA O-methyltransferase 1 OS=Arabidopsis thaliana GN=CCOAOMT1 PE=1 SV=1	7	---	----	0,552	1,00E-05	0,03	0,20%
Q84WM9	Elongation factor 1-beta 1 OS=Arabidopsis thaliana GN=At5g12110 PE=2 SV=2	3	---	----	0,546	0,00021	0,60	0,20%
P60039	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	3	---	----	0,529	0,00021	0,60	0,20%
Q9ZWT2	Cytochrome B5 isoform D OS=Arabidopsis thaliana GN=CYTB5-D PE=1 SV=1	4	---	----	0,468	0,00021	0,60	0,20%
Q6NKS4	At5g47110 OS=Arabidopsis thaliana GN=At5g47110 PE=2 SV=1	5	---	----	0,453	0,00021	0,60	0,20%
Q42262;Q9CAV0	40S ribosomal protein S3a-2 OS=Arabidopsis thaliana GN=RPS3AB PE=2 SV=3	4	---	----	0,407	0,00021	0,60	0,20%
Q9C7N5	GDSL esterase/lipase At1g29660 OS=Arabidopsis thaliana GN=At1g29660 PE=2 SV=1	8	---	----	0,402	0,00021	0,60	0,20%
P60039;P60040;Q9LHP1	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	5	---	----	0,399	0,00021	0,60	0,20%
Q9LF98;Q9SJQ9	Fructose-bisphosphate aldolase OS=Arabidopsis thaliana GN=F8J2_100 PE=2 SV=1	3	---	----	0,389	0,00021	0,60	0,20%
Q9LZ17;Q9SJ36	40S ribosomal protein S17-4 OS=Arabidopsis thaliana GN=RPS17D PE=2 SV=3	6	---	----	0,38	1,00E-05	0,03	0,20%
Q42347	60S ribosomal protein L24-1 OS=Arabidopsis thaliana GN=RPL24A PE=1 SV=2	4	---	----	0,363	0,00021	0,60	0,20%
Q9LV21	T-complex protein 1 subunit delta OS=Arabidopsis thaliana GN=CCT4 PE=1 SV=1	11	---	----	0,349	0,00021	0,60	0,20%

Q9LXG1	40S ribosomal protein S9-1 OS=Arabidopsis thaliana GN=RPS9B PE=1 SV=1	10	---	----	0,346	0,00021	0,60	0,20%
P28769	T-complex protein 1 subunit alpha OS=Arabidopsis thaliana GN=CCT1 PE=1 SV=1	11	---	----	0,336	0,00021	0,60	0,20%
Q03251	Glycine-rich RNA-binding protein 8 OS=Arabidopsis thaliana GN=RBG8 PE=1 SV=1	6	---	----	0,314	0,00022	0,62	0,20%
O49299	Probable phosphoglucomutase, cytoplasmic 1 OS=Arabidopsis thaliana GN=At1g23190 PE=2 SV=2	12	---	----	0,306	0,00021	0,60	0,20%
F4JTK8	Aminoacylase-1 OS=Arabidopsis thaliana GN=At4g38220 PE=3 SV=1	14	---	----	0,306	0,00021	0,60	0,20%
P54609;Q9LZF6	Cell division control protein 48 homolog A OS=Arabidopsis thaliana GN=CDC48A PE=1 SV=1	12	---	----	0,301	0,00021	0,60	0,20%
Q42403	Thioredoxin H3 OS=Arabidopsis thaliana GN=TRX3 PE=1 SV=1	7	---	----	0,301	0,00021	0,60	0,20%
P52577	Isoflavone reductase homolog P3 OS=Arabidopsis thaliana GN=At1g75280 PE=2 SV=1	12	---	----	0,253	0,00021	0,60	0,20%
P93028	Ubiquitin-activating enzyme E1 1 OS=Arabidopsis thaliana GN=UBA1 PE=1 SV=1	17	---	----	0,243	0,00021	0,60	0,20%
Q9FVT2	Probable elongation factor 1-gamma 2 OS=Arabidopsis thaliana GN=At1g57720 PE=2 SV=1	9	---	----	0,242	0,00021	0,60	0,20%
Q0WW26	Coatomer subunit gamma OS=Arabidopsis thaliana GN=At4g34450 PE=1 SV=2	22	---	----	0,23	0,00021	0,60	0,20%
Q8RWV0	Transketolase-1, chloroplastic OS=Arabidopsis thaliana GN=TKL-1 PE=1 SV=1	19	---	----	-0,137	0,00021	0,60	0,20%
P25697	Phosphoribulokinase, chloroplastic OS=Arabidopsis thaliana GN=At1g32060 PE=2 SV=1	13	---	----	-0,163	0,00021	0,60	0,20%
P25856;Q9LPW0	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3	7	---	----	-0,171	0,00022	0,62	0,20%
O49506;Q9LRR9;Q9LRS0	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 OS=Arabidopsis thaliana GN=GLO5 PE=1 SV=1	5	---	----	-0,202	0,00021	0,60	0,20%
O23404	Pyruvate, phosphate dikinase 1, chloroplastic OS=Arabidopsis thaliana GN=PPDK PE=1 SV=2	16	---	----	-0,223	0,00021	0,60	0,20%
Q9LT39	Leucine-rich repeat-containing protein OS=Arabidopsis thaliana GN=At3g20820 PE=2 SV=1	11	---	----	-0,245	0,00021	0,60	0,20%
Q9FJY6	Aldose 1-epimerase family protein OS=Arabidopsis thaliana GN=At5g66530 PE=2 SV=1	9	---	----	-0,276	0,00021	0,60	0,20%
Q0WM29	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Arabidopsis thaliana GN=ALDH6B2 PE=2	9	---	----	-0,337	0,00021	0,60	0,20%
Q94K97	Putative 30S ribosomal protein OS=Arabidopsis thaliana GN=At5g24490 PE=1 SV=1	7	---	----	-0,401	0,00021	0,60	0,20%
Q9SWG0	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2	6	---	----	-0,584	1,00E-05	0,03	0,20%
Q93VI3	60S ribosomal protein L17-1 OS=Arabidopsis thaliana GN=RPL17A PE=2 SV=1	1	---	----	0,77	0,00041	1,16	0,30%
Q9SJW3	Protein SPIRAL1 OS=Arabidopsis thaliana GN=SPR1 PE=2 SV=1	2	---	----	0,731	0,00041	1,16	0,30%
P51430	40S ribosomal protein S6-2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=3	2	---	----	0,67	0,00041	1,16	0,30%
Q9LYU8	Aspartokinase 1, chloroplastic OS=Arabidopsis thaliana GN=AK1 PE=1 SV=1	2	---	----	0,663	0,00041	1,16	0,30%
Q9M352	60S ribosomal protein L36-2 OS=Arabidopsis thaliana GN=RPL36B PE=2 SV=1	2	---	----	0,55	0,00041	1,16	0,30%
Q39108	Heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic OS=Arabidopsis thaliana GN=GGR P	6	---	----	0,55	0,00041	1,16	0,30%
Q9M885	40S ribosomal protein S7-2 OS=Arabidopsis thaliana GN=RPS7B PE=2 SV=1	4	---	----	0,54	0,00041	1,16	0,30%
Q9LIN0	Major latex protein, putative OS=Arabidopsis thaliana GN=At3g26450 PE=2 SV=1	4	---	----	0,434	1,00E-05	0,03	0,30%
Q9C5Z2	Eukaryotic translation initiation factor 3 subunit H OS=Arabidopsis thaliana GN=TIF3H1 PE=1 SV=2	5	---	----	0,421	0,00041	1,16	0,30%
Q8LER3	Probable xyloglucan endotransglucosylase/hydrolase protein 7 OS=Arabidopsis thaliana GN=XTH7 PE=2 SV=2	7	---	----	0,401	0,00041	1,16	0,30%
P42763	Dehydrin ERD14 OS=Arabidopsis thaliana GN=ERD14 PE=1 SV=1	4	---	----	0,363	0,00041	1,16	0,30%
Q43291	60S ribosomal protein L21-1 OS=Arabidopsis thaliana GN=RPL21A PE=2 SV=2	5	---	----	0,357	0,00041	1,16	0,30%
Q42522	Glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplastic OS=Arabidopsis thaliana GN=GSA2 PE=2 SV=2	6	---	----	0,34	0,00041	1,16	0,30%
O65719;P22953;Q39043;	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	2	---	----	0,339	0,00041	1,16	0,30%
Q8VYV7	3-dehydroquinate synthase, chloroplastic OS=Arabidopsis thaliana GN=DHQS PE=2 SV=1	10	---	----	0,322	0,00041	1,16	0,30%
Q93VG5	40S ribosomal protein S8-1 OS=Arabidopsis thaliana GN=RPS8A PE=2 SV=1	8	---	----	0,248	0,00041	1,16	0,30%
O80576	At2g44060 OS=Arabidopsis thaliana GN=At2g44060 PE=2 SV=1	17	---	----	0,246	0,00041	1,16	0,30%
O82662	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Arabidopsis thaliana GN=At2g20420 PE=1 SV=1	17	---	----	0,235	0,00042	1,19	0,30%
Q9SE60	Methylenetetrahydrofolate reductase 1 OS=Arabidopsis thaliana GN=MTHFR1 PE=1 SV=1	15	---	----	0,228	0,00041	1,16	0,30%
O23254	Serine hydroxymethyltransferase 4 OS=Arabidopsis thaliana GN=SHM4 PE=1 SV=1	12	---	----	0,228	0,00041	1,16	0,30%
F4KHD5	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g40450 PE=1 SV=1	27	---	----	0,186	0,00041	1,16	0,30%
Q0WLB5;Q0WNJ6	Clathrin heavy chain 2 OS=Arabidopsis thaliana GN=CHC2 PE=1 SV=1	32	---	----	0,166	0,00041	1,16	0,30%
Q9LTX9;Q9STW6	Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana GN=HSP70-7 PE=2 SV=1	18	---	----	-0,151	0,00041	1,16	0,30%
P0DKC3	Phosphoglycolate phosphatase 1A, chloroplastic OS=Arabidopsis thaliana GN=PGLP1A PE=1 SV=1	15	---	----	-0,155	0,00041	1,16	0,30%
B3H5S2;P10795;P10796;	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=At5g38410 PE=3 SV=1	2	---	----	-0,163	0,00041	1,16	0,30%
Q07473	Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1	8	---	----	-0,185	0,00041	1,16	0,30%
Q9MA79	Fructose-1,6-bisphosphatase, cytosolic OS=Arabidopsis thaliana GN=At1g43670 PE=2 SV=1	14	---	----	-0,224	0,00041	1,16	0,30%
Q9S9M7	Putative uncharacterized protein At1g16080 OS=Arabidopsis thaliana GN=T24D18.18 PE=2 SV=1	14	---	----	-0,251	0,00041	1,16	0,30%
Q9FVR6	Uncharacterized protein At1g32220, chloroplastic OS=Arabidopsis thaliana GN=At1g32220 PE=2 SV=1	6	---	----	-0,333	0,00041	1,16	0,30%
Q93XW5	Nitrile-specifier protein 5 OS=Arabidopsis thaliana GN=NSP5 PE=2 SV=1	7	---	----	-0,435	1,00E-05	0,03	0,30%
Q9LX13	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-like protein OS=Arabidopsis thaliana GN=T31P16_150 PE=2 S	3	---	----	-0,439	0,00041	1,16	0,30%
O22788	Probable peroxygenase 3 OS=Arabidopsis thaliana GN=PXG3 PE=1 SV=1	3	---	----	-0,652	0,00041	1,16	0,30%
Q8RX87	Probable galactinol--sucrose galactosyltransferase 6 OS=Arabidopsis thaliana GN=RFS6 PE=2 SV=2	9	---	----	-0,803	1,00E-05	0,03	0,30%
Q9FF90	60S ribosomal protein L13-3 OS=Arabidopsis thaliana GN=RPL13D PE=1 SV=1	1	---	----	0,763	0,00061	1,73	0,40%

A8MS32	AT5G64130 protein OS=Arabidopsis thaliana GN=At5g64130 PE=1 SV=1	2	---	----	0,737	0,00061	1,73	0,40%
Q39195	Photosystem II 5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=PSBT PE=3 SV=2	1	---	----	0,719	0,00061	1,73	0,40%
P59230;P59231;Q8VZB9	60S ribosomal protein L10a-2 OS=Arabidopsis thaliana GN=RPL10AB PE=1 SV=1	1	---	----	0,682	0,00061	1,73	0,40%
Q93VT9;Q93W22	60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1	2	---	----	0,509	0,00061	1,73	0,40%
P16181	40S ribosomal protein S11-1 OS=Arabidopsis thaliana GN=RPS11A PE=2 SV=1	3	---	----	0,472	0,00061	1,73	0,40%
P59230	60S ribosomal protein L10a-2 OS=Arabidopsis thaliana GN=RPL10AB PE=1 SV=1	3	---	----	0,468	0,00061	1,73	0,40%
Q9M9K1	Probable 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 2 OS=Arabidopsis thaliana GN=At3g08590 P	9	---	----	0,347	1,00E-05	0,03	0,40%
P39207	Nucleoside diphosphate kinase 1 OS=Arabidopsis thaliana GN=NDK1 PE=1 SV=1	6	---	----	0,31	0,00061	1,73	0,40%
P27323;P51818;P55737	Heat shock protein 90-1 OS=Arabidopsis thaliana GN=HSP90-1 PE=1 SV=3	6	---	----	0,291	0,00061	1,73	0,40%
F4JHJ0	HSP20-like chaperone OS=Arabidopsis thaliana GN=At4g02450 PE=1 SV=1	8	---	----	0,257	0,00061	1,73	0,40%
Q9XI01	Protein disulfide isomerase-like 1-1 OS=Arabidopsis thaliana GN=PDIL1-1 PE=1 SV=1	13	---	----	0,231	0,00061	1,73	0,40%
P29197;Q8L7B5	Chaperonin CPN60, mitochondrial OS=Arabidopsis thaliana GN=CPN60 PE=2 SV=2	10	---	----	0,228	0,00061	1,73	0,40%
O03042;P93292	Ribulose bisphosphate carboxylase large chain OS=Arabidopsis thaliana GN=rbcL PE=1 SV=1	3	---	----	0,212	0,00062	1,76	0,40%
P04778;P0CJ48;Q39142;C	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1	3	---	----	-0,16	0,00061	1,73	0,40%
Q42139	AT4g32260/F10M6_100 OS=Arabidopsis thaliana GN=F10M6.100 PE=1 SV=2	12	---	----	-0,183	0,00061	1,73	0,40%
Q9S7Y7	Alpha-xylosidase 1 OS=Arabidopsis thaliana GN=XYL1 PE=1 SV=1	15	---	----	-0,203	0,00061	1,73	0,40%
P46422	Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3	10	---	----	-0,207	0,00061	1,73	0,40%
Q8W4S4	V-type proton ATPase subunit a3 OS=Arabidopsis thaliana GN=VHA-a3 PE=1 SV=1	10	---	----	-0,251	0,00061	1,73	0,40%
O65202	Peroxisomal acyl-coenzyme A oxidase 1 OS=Arabidopsis thaliana GN=ACX1 PE=1 SV=1	11	---	----	-0,328	0,00061	1,73	0,40%
P25819;Q42547	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=2 SV=3	1	---	----	-0,347	0,00061	1,73	0,40%
Q8L636	Putative uncharacterized protein At1g53210 OS=Arabidopsis thaliana GN=At1g53210 PE=2 SV=1	5	---	----	-0,386	0,00061	1,73	0,40%
Q9ZP05	Malate dehydrogenase, glyoxysomal OS=Arabidopsis thaliana GN=At5g09660 PE=2 SV=1	9	---	----	-0,399	1,00E-05	0,03	0,40%
Q9ZVS4;Q9ZVS5	Aspartyl protease-like protein OS=Arabidopsis thaliana GN=F15K9.17 PE=2 SV=1	3	---	----	-0,44	0,00061	1,73	0,40%
P29976;Q00218;Q9SK84	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2	1	---	----	0,894	1,00E-05	0,03	0,50%
Q9M0A5;Q9M0A7	Gamma-glutamyl peptidase 3 OS=Arabidopsis thaliana GN=At4g30550 PE=4 SV=1	1	---	----	0,677	0,00081	2,30	0,50%
Q9SKC1	UDP-glycosyltransferase 74C1 OS=Arabidopsis thaliana GN=UGT74C1 PE=2 SV=1	2	---	----	0,645	0,00081	2,30	0,50%
P82658	Thylakoid lumenal 19 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At3g63540 PE=1 SV=2	4	---	----	0,537	0,00081	2,30	0,50%
F4KIB2;Q9C5N2	Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1	4	---	----	0,529	0,00081	2,30	0,50%
O48549	40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2	2	---	----	0,504	0,00081	2,30	0,50%
Q9LY15	Peptide methionine sulfoxide reductase A2 OS=Arabidopsis thaliana GN=MRSA2 PE=1 SV=1	3	---	----	0,487	0,00081	2,30	0,50%
Q9LF30;Q9SGA6	40S ribosomal protein S19-2 OS=Arabidopsis thaliana GN=RPS19B PE=2 SV=1	4	---	----	0,411	0,00081	2,30	0,50%
F4I893	Protein ILITYHIA OS=Arabidopsis thaliana GN=ILA PE=1 SV=1	7	---	----	0,408	0,00081	2,30	0,50%
Q8L940	Pyridoxal 5'-phosphate synthase subunit PDX1.3 OS=Arabidopsis thaliana GN=PDX13 PE=1 SV=2	3	---	----	0,4	0,00081	2,30	0,50%
Q9MAH0	Phosphoenolpyruvate carboxylase 1 OS=Arabidopsis thaliana GN=PPC1 PE=1 SV=1	11	---	----	0,324	0,00081	2,30	0,50%
Q9LIB2	Alpha-glucan phosphorylase 1 OS=Arabidopsis thaliana GN=PHS1 PE=2 SV=1	26	---	----	0,211	0,00081	2,30	0,50%
Q8W493	Ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic OS=Arabidopsis thaliana GN=LFNR2 PE=1 SV=1	13	---	----	-0,173	0,00082	2,32	0,50%
Q39041	Acid beta-fructofuranosidase 4, vacuolar OS=Arabidopsis thaliana GN=BFRUCT4 PE=2 SV=2	6	---	----	-0,282	0,00081	2,30	0,50%
Q9M2P7	Probable plastid-lipid-associated protein 9, chloroplastic OS=Arabidopsis thaliana GN=PAP9 PE=2 SV=1	7	---	----	-0,346	0,00081	2,30	0,50%
O80533	Alcohol dehydrogenase-like protein OS=Arabidopsis thaliana GN=F14J9.16 PE=2 SV=1	4	---	----	-0,484	0,00081	2,30	0,50%
Q9LV28	Receptor for activated C kinase 1C OS=Arabidopsis thaliana GN=RACK1C PE=1 SV=1	2	---	----	0,96	0,00101	2,86	0,60%
P23686	S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2	1	---	----	0,752	0,00101	2,86	0,60%
P46644;P46645	Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1	2	---	----	0,716	0,00081	2,30	0,60%
Q9FMT1;Q9SA14	3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMDH3 PE=1 SV=1	2	---	----	0,447	0,00101	2,86	0,60%
Q9LUG8	AT3g23600/MDB19_9 OS=Arabidopsis thaliana GN=At3g23600 PE=2 SV=1	6	---	----	0,376	0,00101	2,86	0,60%
P46645	Aspartate aminotransferase, cytoplasmic isozyme 1 OS=Arabidopsis thaliana GN=ASP2 PE=1 SV=2	8	---	----	0,324	0,00101	2,86	0,60%
P41916	GTP-binding nuclear protein Ran-1 OS=Arabidopsis thaliana GN=RAN1 PE=1 SV=1	6	---	----	0,299	0,00101	2,86	0,60%
F4HQD4;Q9S7C0	Heat shock 70 kDa protein 15 OS=Arabidopsis thaliana GN=HSP70-15 PE=1 SV=1	21	---	----	0,287	1,00E-05	0,03	0,60%
P53492	Actin-7 OS=Arabidopsis thaliana GN=ACT7 PE=1 SV=1	6	---	----	0,286	0,00081	2,30	0,60%
P21276	Superoxide dismutase [Fe] 1, chloroplastic OS=Arabidopsis thaliana GN=FSD1 PE=1 SV=4	4	---	----	0,281	0,00081	2,30	0,60%
P16127;Q5XF33	Magnesium-chelatase subunit ChlI-1, chloroplastic OS=Arabidopsis thaliana GN=CHLI1 PE=1 SV=1	6	---	----	0,27	0,00081	2,30	0,60%
P48347	14-3-3-like protein GF14 epsilon OS=Arabidopsis thaliana GN=GRF10 PE=1 SV=1	9	---	----	0,262	0,00101	2,86	0,60%
P0DH91	ADP-ribosylation factor 2-B OS=Arabidopsis thaliana GN=ARF2-B PE=2 SV=1	7	---	----	0,25	0,00081	2,30	0,60%
P56759	ATP synthase subunit b, chloroplastic OS=Arabidopsis thaliana GN=atpF PE=3 SV=1	12	---	----	-0,153	0,00101	2,86	0,60%
B3H5S2;P10797	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=At5g38410 PE=3 SV=1	1	---	----	-0,248	0,00101	2,86	0,60%
Q9FPF0	Protein DJ-1 homolog A OS=Arabidopsis thaliana GN=DJ1A PE=1 SV=1	8	---	----	-0,271	0,00101	2,86	0,60%

O65220	Peptidyl-prolyl cis-trans isomerase CYP28, chloroplastic OS=Arabidopsis thaliana GN=CYP28 PE=1 SV=1	8	---	----	-0,325	0,00081	2,30	0,60%
P46312	Omega-6 fatty acid desaturase, chloroplastic OS=Arabidopsis thaliana GN=FAD6 PE=2 SV=2	2	---	----	0,721	0,00101	2,86	0,70%
Q42547;Q96528	Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3	1	---	----	0,698	0,00121	3,43	0,70%
Q8VY88	Protein LHCP TRANSLOCATION DEFECT OS=Arabidopsis thaliana GN=LTD PE=1 SV=1	4	---	----	0,631	1,00E-05	0,03	0,70%
Q9C5C8	Peptide methionine sulfoxide reductase B2, chloroplastic OS=Arabidopsis thaliana GN=MSRB2 PE=1 SV=1	2	---	----	0,612	0,00101	2,86	0,70%
Q8GW48	At4g15810 OS=Arabidopsis thaliana GN=HSBP PE=2 SV=1	3	---	----	0,573	0,00121	3,43	0,70%
Q9SZI2	Nucleosome assembly protein 1;1 OS=Arabidopsis thaliana GN=NAP1;1 PE=1 SV=1	4	---	----	0,541	0,00101	2,86	0,70%
Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase GAPC2, cytosolic OS=Arabidopsis thaliana GN=GAPC2 PE=1 SV=1	3	---	----	0,412	0,00101	2,86	0,70%
Q8VYM4	Putative uncharacterized protein At3g52150 OS=Arabidopsis thaliana GN=At3g52150 PE=2 SV=1	9	---	----	0,205	0,00121	3,43	0,70%
Q9M1X0	Ribosome-recycling factor, chloroplastic OS=Arabidopsis thaliana GN=RRF PE=2 SV=2	8	---	----	-0,2	0,00101	2,86	0,70%
Q9FZ47	ACT domain-containing protein ACR11 OS=Arabidopsis thaliana GN=ACR11 PE=1 SV=1	7	---	----	-0,234	0,00101	2,86	0,70%
F4INE2;O03042;P93292	Ribulose bisphosphate carboxylase large chain, catalytic domain OS=Arabidopsis thaliana GN=At2g07732 PE=3 SV=1	1	---	----	-0,457	0,00101	2,86	0,70%
P93836	4-hydroxyphenylpyruvate dioxygenase OS=Arabidopsis thaliana GN=HPD PE=1 SV=2	2	---	----	-0,652	0,00101	2,86	0,70%
O04846	Alpha carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=ACA1 PE=1 SV=2	2	---	----	0,727	0,00141	4,00	0,80%
Q8W108	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 3 OS=Arabidopsis thaliana GN=ARD3 PE=2 SV=1	2	---	----	0,722	0,00121	3,43	0,80%
Q9FLF0;Q9LXG1	40S ribosomal protein S9-2 OS=Arabidopsis thaliana GN=RPS9C PE=2 SV=1	1	---	----	0,703	0,00141	4,00	0,80%
Q9M0S5	Isoamylase 3, chloroplastic OS=Arabidopsis thaliana GN=ISA3 PE=2 SV=2	3	---	----	0,617	0,00121	3,43	0,80%
P19456	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	4	---	----	0,478	0,00121	3,43	0,80%
Q9S791	AT1G70770 protein OS=Arabidopsis thaliana GN=F5A18.5 PE=1 SV=1	8	---	----	0,358	0,00121	3,43	0,80%
O04834;Q8VYP7	GTP-binding protein SAR1A OS=Arabidopsis thaliana GN=SAR1A PE=2 SV=1	5	---	----	0,346	0,00141	4,00	0,80%
Q8LD46	60S ribosomal protein L23a-1 OS=Arabidopsis thaliana GN=RPL23AA PE=2 SV=2	4	---	----	0,338	0,00121	3,43	0,80%
Q94BS2	GAN OS=Arabidopsis thaliana GN=ZKT PE=2 SV=1	14	---	----	-0,196	0,00122	3,46	0,80%
Q9LXX5	PsbP domain-containing protein 6, chloroplastic OS=Arabidopsis thaliana GN=PPD6 PE=1 SV=1	10	---	----	-0,329	0,00121	3,43	0,80%
Q9FE06;Q9FY71	Protein EXORDIUM-like 2 OS=Arabidopsis thaliana GN=EXL2 PE=2 SV=1	2	---	----	-0,659	0,00121	3,43	0,80%
P68209;Q8LAD2	Succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1	2	---	----	0,711	0,00141	4,00	0,90%
Q9FZ80	Cytosolic sulfotransferase 17 OS=Arabidopsis thaliana GN=SOT17 PE=1 SV=1	3	---	----	0,559	0,00141	4,00	0,90%
O65719;P22953;Q9LHA8	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	6	---	----	0,265	0,00141	4,00	0,90%
Q9SFH9	Delta-aminolevulinic acid dehydratase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMB1 PE=2 SV=1	10	---	----	0,219	0,00141	4,00	0,90%
O80988;Q94B78	Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana GN=GLDP2 PE=2 SV=1	12	---	----	0,169	0,00161	4,56	0,90%
P82281	Thylakoid lumenal 29 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=TL29 PE=1 SV=2	14	---	----	-0,181	0,00141	4,00	0,90%
P09468	ATP synthase epsilon chain, chloroplastic OS=Arabidopsis thaliana GN=atpE PE=1 SV=2	8	---	----	-0,193	0,00141	4,00	0,90%
P50318	Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=2 SV=3	10	---	----	-0,198	0,00161	4,56	0,90%
Q8W4D6	High chlorophyll fluorescence phenotype 173 protein OS=Arabidopsis thaliana GN=F17F16.7 PE=2 SV=1	17	---	----	-0,231	0,00161	4,56	0,90%
P10896;P10896-2	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RCA PE=1 SV=2	1	GLAYDTSDDQQDITF	none	-0,235	0,00161	4,56	0,90%
P27140-2;P27140-3;P427	Isoform 2 of Beta carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=BCA1	7	---	----	-0,237	1,00E-05	0,03	0,90%
Q9SEU8	Thioredoxin M2, chloroplastic OS=Arabidopsis thaliana GN=At4g03520 PE=2 SV=2	5	---	----	-0,243	0,00141	4,00	0,90%
Q93Y07	Beta-glucosidase-like SFR2, chloroplastic OS=Arabidopsis thaliana GN=SFR2 PE=1 SV=1	7	---	----	-0,363	0,00161	4,56	0,90%
Q8W4Q4	AT4g24800/F6I7_10 OS=Arabidopsis thaliana GN=At4g24800 PE=2 SV=1	7	---	----	-0,398	0,00161	4,56	0,90%
O80532	Alcohol dehydrogenase OS=Arabidopsis thaliana GN=F14J9.15 PE=2 SV=1	6	---	----	-0,408	0,00161	4,56	0,90%
Q9FVR9	FAD/NAD(P)-binding oxidoreductase domain-containing protein OS=Arabidopsis thaliana GN=F12K22.18 PE=2 SV=1	4	---	----	-0,415	0,00141	4,00	0,90%
P56755	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic OS=Arabidopsis thaliana GN=ndhI PE=3 SV=1	2	---	----	-0,505	0,00161	4,56	0,90%
Q37165	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ndhA PE=3 SV=2	3	---	----	-0,538	0,00141	4,00	0,90%
P19456;P20431	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	1	---	----	1,074	0,00181	5,13	1,00%
Q9LIB2;Q9SD76	Alpha-glucan phosphorylase 1 OS=Arabidopsis thaliana GN=PHS1 PE=2 SV=1	1	---	----	0,722	0,00161	4,56	1,00%
O81852	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH2 PE=1 SV	3	---	----	0,722	0,00181	5,13	1,00%
Q9LPG6	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-red	2	---	----	0,718	0,00161	4,56	1,00%
Q9LZ57;Q9M352	60S ribosomal protein L36-3 OS=Arabidopsis thaliana GN=RPL36C PE=3 SV=1	1	---	----	0,546	0,00181	5,13	1,00%
F4JFN3	HEAT SHOCK PROTEIN 89.1 OS=Arabidopsis thaliana GN=Hsp89.1 PE=3 SV=1	4	---	----	0,512	0,00181	5,13	1,00%
Q39043;Q8GUM2;Q9LDZ	Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	2	---	----	0,5	0,00181	5,13	1,00%
Q9ZUJ3	AT1G60000 protein OS=Arabidopsis thaliana GN=T2K10.5 PE=2 SV=1	3	---	----	0,454	0,00161	4,56	1,00%
O82204	60S ribosomal protein L28-1 OS=Arabidopsis thaliana GN=RPL28A PE=2 SV=1	3	---	----	0,421	0,00181	5,13	1,00%
P56780	Photosystem II reaction center protein H OS=Arabidopsis thaliana GN=psbH PE=1 SV=2	1	---	----	0,371	0,00181	5,13	1,00%
P42734	Probable cinnamyl alcohol dehydrogenase 9 OS=Arabidopsis thaliana GN=CAD9 PE=2 SV=2	12	---	----	0,241	0,00181	5,13	1,00%
Q9FMU6	Mitochondrial phosphate carrier protein 3, mitochondrial OS=Arabidopsis thaliana GN=MPT3 PE=2 SV=1	13	---	----	0,192	0,00161	4,56	1,00%
Q9SA52	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic OS=Arabidopsis thaliana GN=CSP41B PE=1 SV=1	18	---	----	-0,116	0,00181	5,13	1,00%

Q93VC7	Putative ribosomal protein S1 OS=Arabidopsis thaliana GN=RPS1 PE=2 SV=1	13	---	----	-0,171	0,00181	5,13	1,00%
P25864	50S ribosomal protein L9, chloroplastic OS=Arabidopsis thaliana GN=RPL9 PE=2 SV=1	10	---	----	-0,184	0,00181	5,13	1,00%
Q9SCY2	Peptidyl-prolyl cis-trans isomerase FKBP13, chloroplastic OS=Arabidopsis thaliana GN=FKBP13 PE=1 SV=2	5	---	----	-0,223	0,00181	5,13	1,00%
Q9LU86	Peroxiredoxin Q, chloroplastic OS=Arabidopsis thaliana GN=PRXQ PE=1 SV=1	6	---	----	-0,238	0,00161	4,56	1,00%
Q8H112	PGR5-like protein 1A, chloroplastic OS=Arabidopsis thaliana GN=PGRL1A PE=1 SV=1	6	---	----	-0,304	0,00161	4,56	1,00%
P52032;Q9SZ54	Phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic OS=Arabidopsis thaliana GN=GPX1 PE=2 SV=2	1	---	----	-0,459	0,00161	4,56	1,00%
Q9M2Z4	Membrane steroid-binding protein 2 OS=Arabidopsis thaliana GN=MSBP2 PE=1 SV=1	2	---	----	0,719	0,00201	5,70	1,10%
Q8LDP4	Peptidyl-prolyl cis-trans isomerase CYP19-4 OS=Arabidopsis thaliana GN=CYP19-4 PE=1 SV=2	2	---	----	0,606	0,00201	5,70	1,10%
Q9SR19	Rubisco accumulation factor 2, chloroplastic OS=Arabidopsis thaliana GN=RAF2 PE=2 SV=1	6	---	----	0,393	0,00201	5,70	1,10%
O23593	AT4g17520/dl4795w OS=Arabidopsis thaliana GN=dl4795w PE=1 SV=1	9	---	----	0,342	0,00201	5,70	1,10%
Q9LTF2	40S ribosomal protein S10-3 OS=Arabidopsis thaliana GN=RPS10C PE=2 SV=2	4	---	----	0,337	0,00201	5,70	1,10%
Q00218	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=DHS2 PE=2 SV=2	8	---	----	0,282	0,00202	5,73	1,10%
Q94A40;Q9SJT9	Coatomer subunit alpha-1 OS=Arabidopsis thaliana GN=At1g62020 PE=2 SV=2	11	---	----	0,239	0,00201	5,70	1,10%
Q9FWA3	6-phosphogluconate dehydrogenase, decarboxylating 3 OS=Arabidopsis thaliana GN=At3g02360 PE=2 SV=1	11	---	----	0,233	0,00201	5,70	1,10%
Q8VZM7	Putative ion channel POLLUX-like 1 OS=Arabidopsis thaliana GN=At5g02940 PE=2 SV=1	9	---	----	-0,367	0,00201	5,70	1,10%
Q9XI36	Methyl-CpG-binding domain-containing protein 10 OS=Arabidopsis thaliana GN=MBD10 PE=1 SV=1	6	---	----	-0,406	0,00201	5,70	1,10%
Q38924	Fe(3+)-Zn(2+) purple acid phosphatase 12 OS=Arabidopsis thaliana GN=PAP12 PE=2 SV=3	1	---	----	0,66	0,00221	6,26	1,20%
O64688	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic OS=Arabidopsis thaliana GN=E1-BETA-2 PE=2 SV=	3	---	----	0,586	0,00221	6,26	1,20%
P41127;Q9FF90	60S ribosomal protein L13-1 OS=Arabidopsis thaliana GN=RPL13B PE=1 SV=1	2	---	----	0,484	0,00221	6,26	1,20%
P49211	60S ribosomal protein L32-1 OS=Arabidopsis thaliana GN=RPL32A PE=2 SV=2	4	---	----	0,313	0,00221	6,26	1,20%
P51427;Q9ZUT9	40S ribosomal protein S5-2 OS=Arabidopsis thaliana GN=RPS5B PE=1 SV=2	5	---	----	0,259	0,00221	6,26	1,20%
P24636;P29513;P29514;P	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	7	---	----	0,233	0,00221	6,26	1,20%
P25856	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3	6	---	----	-0,165	0,00221	6,26	1,20%
Q9LR30;Q9S7E9	Glutamate--glyoxylate aminotransferase 1 OS=Arabidopsis thaliana GN=GGAT1 PE=1 SV=1	9	---	----	-0,199	0,00221	6,26	1,20%
P04778	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1	1	---	----	0,706	0,00241	6,83	1,30%
Q8LD03;Q9M885	40S ribosomal protein S7-3 OS=Arabidopsis thaliana GN=RPS7C PE=1 SV=2	2	---	----	0,417	0,00241	6,83	1,30%
Q9FK81	Uncharacterized protein At5g22580 OS=Arabidopsis thaliana GN=At5g22580 PE=1 SV=1	2	---	----	0,384	0,00241	6,83	1,30%
Q93ZT6	Eukaryotic translation initiation factor isoform 4G-1 OS=Arabidopsis thaliana GN=EIF(ISO)4G1 PE=1 SV=1	12	---	----	0,238	0,00241	6,83	1,30%
O80503	Expressed protein OS=Arabidopsis thaliana GN=At2g44640 PE=4 SV=2	9	---	----	-0,26	0,00241	6,83	1,30%
Q9LLR6	Non-specific lipid-transfer protein 4 OS=Arabidopsis thaliana GN=LTP4 PE=3 SV=1	1	---	----	0,703	0,00261	7,40	1,40%
O50008	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV	18	---	----	0,346	1,00E-05	0,03	1,40%
P41127	60S ribosomal protein L13-1 OS=Arabidopsis thaliana GN=RPL13B PE=1 SV=1	4	---	----	0,343	0,00261	7,40	1,40%
Q9SSS9	ATP synthase subunit delta, chloroplastic OS=Arabidopsis thaliana GN=ATPD PE=1 SV=1	13	---	----	-0,141	0,00261	7,40	1,40%
Q9SKX4	50S ribosomal protein L3-1, chloroplastic OS=Arabidopsis thaliana GN=RPL3A PE=2 SV=1	13	---	----	-0,185	0,00261	7,40	1,40%
Q8LDL0	Protein HHL1, chloroplastic OS=Arabidopsis thaliana GN=HHL1 PE=1 SV=1	6	---	----	-0,287	0,00261	7,40	1,40%
F4I3B3	Polyadenylate-binding protein RBP47A OS=Arabidopsis thaliana GN=RBP47A PE=2 SV=1	1	---	----	0,636	0,00281	7,96	1,50%
Q8LGG0	Peptidyl-prolyl cis-trans isomerase FKBP12 OS=Arabidopsis thaliana GN=FKBP12 PE=1 SV=2	2	---	----	0,633	0,00281	7,96	1,50%
Q93W34	Polyadenylate-binding protein RBP45C OS=Arabidopsis thaliana GN=RBP45C PE=2 SV=1	2	---	----	0,605	0,00281	7,96	1,50%
P29976;Q00218	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2	1	---	----	0,566	0,00281	7,96	1,50%
P53780	Cystathionine beta-lyase, chloroplastic OS=Arabidopsis thaliana GN=At3g57050 PE=1 SV=1	3	---	----	0,482	0,00281	7,96	1,50%
Q9S7E4	Formate dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=FDH1 PE=1 SV=1	13	---	----	-0,164	0,00281	7,96	1,50%
P10796	Ribulose bisphosphate carboxylase small chain 1B, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1B PE=2 SV=1	1	---	----	-0,232	0,00281	7,96	1,50%
O22773	Thylakoid lumenal 16.5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At4g02530 PE=1 SV=3	8	---	----	-0,239	0,00282	7,99	1,50%
P93004	Aquaporin PIP2-7 OS=Arabidopsis thaliana GN=PIP2-7 PE=1 SV=2	4	---	----	-0,305	0,00281	7,96	1,50%
Q8W0Y8	Photosystem II reaction center PSB28 protein, chloroplastic OS=Arabidopsis thaliana GN=PSB28 PE=2 SV=1	2	---	----	-0,325	0,00281	7,96	1,50%
Q56WK6;Q56ZI2	Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2	2	---	----	-0,443	0,00281	7,96	1,50%
Q8LCT3	Thioredoxin-like 2-2, chloroplastic OS=Arabidopsis thaliana GN=At4g29670 PE=2 SV=2	2	---	----	0,645	0,00301	8,53	1,60%
O04905	UMP-CMP kinase 3 OS=Arabidopsis thaliana GN=UMK3 PE=1 SV=1	3	---	----	0,575	0,00321	9,10	1,60%
O48549;P51430	40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2	4	---	----	0,341	0,00301	8,53	1,60%
Q7DLR9	Proteasome subunit beta type-4 OS=Arabidopsis thaliana GN=PBG1 PE=1 SV=2	6	---	----	0,339	0,00301	8,53	1,60%
Q9SRZ6	Cytosolic isocitrate dehydrogenase [NADP] OS=Arabidopsis thaliana GN=CICDH PE=2 SV=1	19	---	----	0,146	0,00301	8,53	1,60%
Q9FIS4	At5g62140 OS=Arabidopsis thaliana GN=At5g62140 PE=2 SV=1	4	---	----	-0,388	0,00301	8,53	1,60%
Q43295	Adenylyl-sulfate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=APK1 PE=1 SV=1	1	---	----	0,992	0,00341	9,67	1,70%
P17562	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	1	---	----	0,662	0,00321	9,10	1,70%
P28185;Q39222;Q96283;	Ras-related protein RABA1a OS=Arabidopsis thaliana GN=RABA1A PE=1 SV=1	1	---	----	0,649	0,00341	9,67	1,70%

F4I1G1	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g29350 PE=4 SV=1	1	---	----	0,644	0,00341	9,67	1,70%
P29515	Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	2	---	----	0,511	0,00341	9,67	1,70%
Q56WH4	Histone deacetylase HDT2 OS=Arabidopsis thaliana GN=HDT2 PE=1 SV=2	4	---	----	0,492	0,00321	9,10	1,70%
O80889	At2g32520 OS=Arabidopsis thaliana GN=At2g32520 PE=2 SV=1	5	---	----	0,393	0,00321	9,10	1,70%
Q38858	Calreticulin-2 OS=Arabidopsis thaliana GN=CRT2 PE=1 SV=3	7	---	----	0,377	0,00341	9,67	1,70%
Q9LU63	AT5g51110/MWD22_5 OS=Arabidopsis thaliana GN=pdl1 PE=2 SV=1	3	---	----	0,365	0,00341	9,67	1,70%
P42036;Q9CAX6;Q9SIH0	40S ribosomal protein S14-3 OS=Arabidopsis thaliana GN=RPS14C PE=2 SV=2	4	---	----	0,317	0,00321	9,10	1,70%
Q9XEX2	Peroxiredoxin-2B OS=Arabidopsis thaliana GN=PRXIIB PE=1 SV=1	5	---	----	0,287	0,00341	9,67	1,70%
O04487	Probable elongation factor 1-gamma 1 OS=Arabidopsis thaliana GN=At1g09640 PE=2 SV=1	9	---	----	0,271	0,00321	9,10	1,70%
F4J912;Q8LBI1	60S ribosomal protein L5-1 OS=Arabidopsis thaliana GN=ATL5 PE=4 SV=1	7	---	----	0,266	0,00341	9,67	1,70%
Q93WN0	Selenium-binding protein 2 OS=Arabidopsis thaliana GN=SBP2 PE=1 SV=1	10	---	----	0,227	0,00341	9,67	1,70%
P46643	Aspartate aminotransferase, mitochondrial OS=Arabidopsis thaliana GN=ASP1 PE=1 SV=1	9	---	----	0,213	0,00341	9,67	1,70%
Q05758	Ketol-acid reductoisomerase, chloroplastic OS=Arabidopsis thaliana GN=At3g58610 PE=2 SV=2	13	---	----	0,198	0,00321	9,10	1,70%
Q9FR37	Amidase 1 OS=Arabidopsis thaliana GN=AMI1 PE=1 SV=1	7	---	----	-0,326	0,00321	9,10	1,70%
A8MS32;Q9C787	AT5G64130 protein OS=Arabidopsis thaliana GN=At5g64130 PE=1 SV=1	1	---	----	0,949	0,00361	10,23	1,80%
Q9LUD4	60S ribosomal protein L18a-3 OS=Arabidopsis thaliana GN=RPL18AC PE=2 SV=1	1	---	----	0,889	0,00361	10,23	1,80%
Q93VK5	Protein LUTEIN DEFICIENT 5, chloroplastic OS=Arabidopsis thaliana GN=CYP97A3 PE=1 SV=1	4	---	----	0,497	0,00361	10,23	1,80%
Q9SI75	Elongation factor G, chloroplastic OS=Arabidopsis thaliana GN=CPEFG PE=1 SV=1	26	---	----	0,138	0,00362	10,26	1,80%
O22126	Fasciclin-like arabinogalactan protein 8 OS=Arabidopsis thaliana GN=FLA8 PE=1 SV=1	7	---	----	-0,236	0,00361	10,23	1,80%
F4HTT6	Peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic OS=Arabidopsis thaliana GN=CYP26-2 PE=2 SV=1	9	---	----	-0,285	0,00361	10,23	1,80%
Q9ZVS5	Aspartyl protease-like protein OS=Arabidopsis thaliana GN=F15K9.16 PE=2 SV=1	6	---	----	-0,334	0,00362	10,26	1,80%
F4JGR5;Q8W4M5	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 2 OS=Arabidopsis thaliana GN=PFP-BETA2 P	1	---	----	0,961	0,00401	11,37	1,90%
P59232	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=1 SV=2	1	---	----	0,486	0,00381	10,80	1,90%
P46286	60S ribosomal protein L8-1 OS=Arabidopsis thaliana GN=RPL8A PE=1 SV=2	2	---	----	0,475	0,00401	11,37	1,90%
P51419	60S ribosomal protein L27-3 OS=Arabidopsis thaliana GN=RPL27C PE=2 SV=2	1	---	----	0,426	0,00401	11,37	1,90%
Q9SS17	40S ribosomal protein S24-1 OS=Arabidopsis thaliana GN=RPS24A PE=2 SV=1	2	---	----	0,397	0,00381	10,80	1,90%
P42643;P42644;P42645;P	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	2	---	----	0,369	0,00381	10,80	1,90%
O04350	Tubulin-folding cofactor A OS=Arabidopsis thaliana GN=TFCA PE=1 SV=2	4	---	----	0,365	0,00381	10,80	1,90%
Q9FJX3	Mitochondrial outer membrane protein porin 2 OS=Arabidopsis thaliana GN=VDAC2 PE=1 SV=1	9	---	----	0,241	0,00381	10,80	1,90%
Q9LF37	Chaperone protein ClpB3, chloroplastic OS=Arabidopsis thaliana GN=CLPB3 PE=2 SV=1	21	---	----	0,193	0,00381	10,80	1,90%
F4KBJ3	Alpha/beta-hydrolase-like protein OS=Arabidopsis thaliana GN=At5g38520 PE=4 SV=1	4	---	----	-0,478	0,00381	10,80	1,90%
Q8RXD5	Kunitz trypsin inhibitor 1 OS=Arabidopsis thaliana GN=KTI1 PE=2 SV=1	1	---	----	-0,557	0,00401	11,37	1,90%
Q94AQ3	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein OS=Arabidopsis thaliana GN=At1g487	1	---	----	1,239	0,00401	11,37	2,00%
Q9SX77	Succinate dehydrogenase subunit 5, mitochondrial OS=Arabidopsis thaliana GN=SDH5 PE=1 SV=1	4	---	----	0,351	0,00401	11,37	2,00%
P36428	Alanine--tRNA ligase OS=Arabidopsis thaliana GN=ALATS PE=1 SV=3	17	---	----	0,204	0,00421	11,93	2,00%
O81283	Translocase of chloroplast 159, chloroplastic OS=Arabidopsis thaliana GN=TOC159 PE=1 SV=1	19	---	----	0,193	0,00401	11,37	2,00%
P25857	Glyceraldehyde-3-phosphate dehydrogenase GAPB, chloroplastic OS=Arabidopsis thaliana GN=GAPB PE=1 SV=2	19	---	----	-0,106	0,00401	11,37	2,00%
Q8H0S9	Puromycin-sensitive aminopeptidase OS=Arabidopsis thaliana GN=MPA1 PE=2 SV=1	29	---	----	-0,145	0,00401	11,37	2,00%
Q9ZVS4	Aspartyl protease-like protein OS=Arabidopsis thaliana GN=F15K9.17 PE=2 SV=1	5	---	----	-0,341	0,00422	11,96	2,00%
Q9CAR7;Q9FM19;Q9SRH	Hypersensitive-induced response protein 2 OS=Arabidopsis thaliana GN=HIR2 PE=1 SV=1	3	---	----	-0,48	0,00401	11,37	2,00%
Q9SSK7;Q9SSK9	MLP-like protein 34 OS=Arabidopsis thaliana GN=MLP34 PE=2 SV=1	1	---	----	0,855	0,00441	12,50	2,10%
P51420	60S ribosomal protein L31-3 OS=Arabidopsis thaliana GN=RPL31C PE=2 SV=2	2	---	----	0,443	0,00441	12,50	2,10%
Q8H0X6-2	Isoform 2 of Cysteine proteinase inhibitor 6 OS=Arabidopsis thaliana GN=CYS6	6	---	----	0,353	0,00441	12,50	2,10%
Q9LD57	Phosphoglycerate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=PGK1 PE=1 SV=1	12	---	----	-0,104	0,00441	12,50	2,10%
Q8VYL1	Adenylate kinase 5, chloroplastic OS=Arabidopsis thaliana GN=At5g35170 PE=1 SV=1	14	---	----	-0,234	0,00441	12,50	2,10%
O80837	Remorin OS=Arabidopsis thaliana GN=DBP PE=1 SV=1	7	---	----	-0,278	0,00441	12,50	2,10%
P42762	Chaperone protein ClpD, chloroplastic OS=Arabidopsis thaliana GN=CLPD PE=1 SV=1	4	---	----	-0,503	0,00441	12,50	2,10%
Q9XI42	F9L1.21 protein OS=Arabidopsis thaliana GN=F9L1.21 PE=2 SV=1	2	---	----	0,553	0,00461	13,07	2,20%
P56780	Photosystem II reaction center protein H OS=Arabidopsis thaliana GN=psbH PE=1 SV=2	1	ATQTVEDSSR	Phospho T2	0,477	0,00461	13,07	2,20%
Q84WV1	T-complex protein 1 subunit gamma OS=Arabidopsis thaliana GN=CCT3 PE=1 SV=1	8	---	----	0,257	0,00461	13,07	2,20%
Q8H0X5	Putative uncharacterized protein At5g16660 OS=Arabidopsis thaliana GN=At5g16660 PE=2 SV=1	3	---	----	-0,337	0,00461	13,07	2,20%
Q9LYN2;Q9S756	Ferritin-3, chloroplastic OS=Arabidopsis thaliana GN=FER3 PE=2 SV=1	1	---	----	0,901	0,00481	13,63	2,30%
Q9FNN1	Pyruvate kinase OS=Arabidopsis thaliana GN=At5g08570 PE=2 SV=1	5	---	----	0,38	0,00501	14,20	2,30%
Q96252	ATP synthase subunit delta', mitochondrial OS=Arabidopsis thaliana GN=At5g47030 PE=1 SV=1	3	---	----	0,351	0,00481	13,63	2,30%
Q42553	Isopentenyl-diphosphate Delta-isomerase II, chloroplastic OS=Arabidopsis thaliana GN=IPP2 PE=2 SV=1	5	---	----	0,336	0,00481	13,63	2,30%

Q9C9I7	Putative uncharacterized protein At1g71500 OS=Arabidopsis thaliana GN=F26A9.12 PE=2 SV=1	9	---	----	-0,182	0,00481	13,63	2,30%
Q42564	L-ascorbate peroxidase 3, peroxisomal OS=Arabidopsis thaliana GN=APX3 PE=1 SV=1	9	---	----	-0,239	0,00501	14,20	2,30%
Q6NQE2;Q9LSQ5	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 1 OS=Arabidopsis thaliana GN=At4g27270 PE=2 SV=1	2	---	----	-0,348	0,00501	14,20	2,30%
Q9SRX5	F22D16.19 protein OS=Arabidopsis thaliana GN=F22D16.19 PE=2 SV=1	2	---	----	-0,406	0,00481	13,63	2,30%
P32962	Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1	2	---	----	-0,558	0,00501	14,20	2,30%
O80517	Uclacyanin-2 OS=Arabidopsis thaliana GN=At2g44790 PE=1 SV=1	1	---	----	-0,628	0,00501	14,20	2,30%
Q8L9E3	At5g61220 OS=Arabidopsis thaliana GN=At5g61220 PE=2 SV=1	1	---	----	0,578	0,00521	14,77	2,40%
Q96533	Alcohol dehydrogenase class-3 OS=Arabidopsis thaliana GN=ADH2 PE=1 SV=2	10	---	----	0,188	0,00521	14,77	2,40%
P31168	Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2	6	---	----	-0,3	0,00522	14,80	2,40%
Q9SG80	Alpha-L-arabinofuranosidase 1 OS=Arabidopsis thaliana GN=ASD1 PE=1 SV=1	5	---	----	-0,361	0,00521	14,77	2,40%
Q39249	Violaxanthin de-epoxidase, chloroplastic OS=Arabidopsis thaliana GN=VDE1 PE=1 SV=1	3	---	----	-0,479	0,00521	14,77	2,40%
O23684	At2g41950/T6D20.26 OS=Arabidopsis thaliana GN=At2g41950 PE=2 SV=1	2	---	----	0,61	0,00541	15,33	2,50%
P29514;P29515;P29516;C	Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1	1	---	----	0,529	0,00541	15,33	2,50%
P49688	40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2	6	---	----	0,306	0,00561	15,90	2,50%
Q9SV21	Coatomer subunit beta-1 OS=Arabidopsis thaliana GN=At4g31480 PE=2 SV=2	14	---	----	0,23	0,00561	15,90	2,50%
P41376;P41377	Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	13	---	----	0,185	0,00541	15,33	2,50%
Q9ZNZ7	Ferredoxin-dependent glutamate synthase 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLU1 PE=1 SV=	51	---	----	0,082	0,00561	15,90	2,50%
P19366	ATP synthase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=atpB PE=1 SV=2	37	---	----	-0,065	0,00542	15,36	2,50%
Q8H124	Uncharacterized protein At2g34460, chloroplastic OS=Arabidopsis thaliana GN=At2g34460 PE=2 SV=1	9	---	----	-0,235	0,00541	15,33	2,50%
P43287	Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2	4	---	----	-0,381	0,00541	15,33	2,50%
O49304	At1g23130/T26J12_10 OS=Arabidopsis thaliana GN=T26J12.10 PE=2 SV=1	3	---	----	-0,53	0,00541	15,33	2,50%
Q9ZW13	Tropinone reductase homolog At2g29290 OS=Arabidopsis thaliana GN=At2g29290 PE=2 SV=1	2	---	----	-0,551	0,00541	15,33	2,50%
Q9LIA8	UDP-glucose 6-dehydrogenase 2 OS=Arabidopsis thaliana GN=UGD2 PE=1 SV=1	4	---	----	0,548	0,00561	15,90	2,60%
Q96254	Guanosine nucleotide diphosphate dissociation inhibitor 1 OS=Arabidopsis thaliana GN=GDI1 PE=1 SV=1	3	---	----	0,419	0,00581	16,47	2,60%
Q9LMK7	Ran-binding protein 1 homolog a OS=Arabidopsis thaliana GN=RANBP1A PE=1 SV=1	5	---	----	0,309	0,00581	16,47	2,60%
Q43127	Glutamine synthetase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLN2 PE=1 SV=1	18	---	----	-0,113	0,00581	16,47	2,60%
Q9LJL3	Presequence protease 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=PREP1 PE=1 SV=2	33	---	----	-0,127	0,00581	16,47	2,60%
Q9C5D0	CBS domain-containing protein CBSX2, chloroplastic OS=Arabidopsis thaliana GN=CBSX2 PE=1 SV=1	5	---	----	-0,321	0,00581	16,47	2,60%
P25702	Acyl carrier protein 3, chloroplastic OS=Arabidopsis thaliana GN=ACP3 PE=1 SV=2	2	---	----	0,638	0,00601	17,03	2,70%
Q9M356	Aspartyl protease OS=Arabidopsis thaliana GN=F15G16.210 PE=4 SV=1	2	---	----	0,637	0,00601	17,03	2,70%
Q84WM9;Q9SCX3	Elongation factor 1-beta 1 OS=Arabidopsis thaliana GN=At5g12110 PE=2 SV=2	1	---	----	0,431	0,00621	17,60	2,70%
Q9SIB9	Aconitate hydratase 2, mitochondrial OS=Arabidopsis thaliana GN=ACO2 PE=1 SV=2	11	---	----	0,292	0,00601	17,03	2,70%
O80448	Pyridoxal 5'-phosphate synthase subunit PDX1.1 OS=Arabidopsis thaliana GN=PDX11 PE=1 SV=1	6	---	----	-0,246	0,00622	17,63	2,70%
Q8GUK4	Subtilase family protein OS=Arabidopsis thaliana GN=At4g21650 PE=2 SV=1	9	---	----	-0,261	0,00601	17,03	2,70%
P49200;Q9STY6	40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2	1	---	----	0,441	0,00621	17,60	2,80%
P49209	60S ribosomal protein L9-1 OS=Arabidopsis thaliana GN=RPL9B PE=1 SV=3	8	---	----	0,413	1,00E-05	0,03	2,80%
P93032;Q8LFC0	Isocitrate dehydrogenase [NAD] regulatory subunit 2, mitochondrial OS=Arabidopsis thaliana GN=IDH2 PE=2 SV=2	3	---	----	0,382	0,00641	18,17	2,80%
Q9FFS8	40S ribosomal protein S10-2 OS=Arabidopsis thaliana GN=RPS10B PE=2 SV=1	3	---	----	0,336	0,00641	18,17	2,80%
Q9SAR5	Ankyrin repeat domain-containing protein 2 OS=Arabidopsis thaliana GN=AKR2 PE=1 SV=2	7	---	----	0,305	0,00641	18,17	2,80%
O22173	Polyadenylate-binding protein 4 OS=Arabidopsis thaliana GN=PAB4 PE=1 SV=1	7	---	----	0,279	0,00621	17,60	2,80%
Q94K05	T-complex protein 1 subunit theta OS=Arabidopsis thaliana GN=CCT8 PE=1 SV=1	8	---	----	0,256	0,00621	17,60	2,80%
P34788	40S ribosomal protein S18 OS=Arabidopsis thaliana GN=RPS18A PE=1 SV=1	5	---	----	0,191	0,00641	18,17	2,80%
P94072	Germin-like protein subfamily 3 member 3 OS=Arabidopsis thaliana GN=GER3 PE=1 SV=1	3	---	----	-0,188	0,00621	17,60	2,80%
O04616	Protein CURVATURE THYLAKOID 1A, chloroplastic OS=Arabidopsis thaliana GN=CURT1A PE=1 SV=1	5	---	----	-0,235	0,00621	17,60	2,80%
Q42525	Hexokinase-1 OS=Arabidopsis thaliana GN=HXK1 PE=1 SV=2	7	---	----	0,301	0,00661	18,74	2,90%
P55228	Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=2 SV=2	12	---	----	0,175	0,00681	19,30	3,00%
O65686	AT4g34620/T4L20_200 OS=Arabidopsis thaliana GN=T4L20.200 PE=2 SV=1	5	---	----	-0,23	0,00701	19,87	3,00%
Q8VZC0	UDP-glucuronic acid decarboxylase 1 OS=Arabidopsis thaliana GN=UXS1 PE=1 SV=1	1	---	----	1,494	0,00701	19,87	3,10%
Q9SB81	Peroxidase 42 OS=Arabidopsis thaliana GN=PER42 PE=1 SV=2	1	---	----	0,966	0,00701	19,87	3,10%
Q42560	Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2	14	---	----	0,195	0,00721	20,44	3,10%
Q94K74	Putative uncharacterized protein At3g25805 OS=Arabidopsis thaliana GN=At3g25805 PE=2 SV=1	1	---	----	-0,833	0,00701	19,87	3,10%
Q03250;Q03251	Glycine-rich RNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1	2	---	----	0,402	0,00741	21,00	3,20%
P52901;Q8H1Y0	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=E1 ALPHA PE=2 S	4	---	----	0,346	0,00741	21,00	3,20%
O24456;Q9C4Z6;Q9LV28	Receptor for activated C kinase 1A OS=Arabidopsis thaliana GN=RACK1A PE=1 SV=2	1	---	----	0,869	0,00781	22,14	3,30%
P93031	GDP-mannose 4,6 dehydratase 2 OS=Arabidopsis thaliana GN=MUR1 PE=1 SV=3	2	---	----	0,465	0,00761	21,57	3,30%

Q9C5Z3	Eukaryotic translation initiation factor 3 subunit E OS=Arabidopsis thaliana GN=TIF3E1 PE=2 SV=1	6	---	----	0,339	0,00781	22,14	3,30%
Q42342	Cytochrome b5 isoform E OS=Arabidopsis thaliana GN=CYTB5-E PE=1 SV=2	4	---	----	0,327	0,00761	21,57	3,30%
Q9S714	Photosystem I reaction center subunit IV B, chloroplastic OS=Arabidopsis thaliana GN=PSAE2 PE=2 SV=1	3	---	----	-0,241	0,00781	22,14	3,30%
O49292	PsbP domain-containing protein 4, chloroplastic OS=Arabidopsis thaliana GN=PPD4 PE=1 SV=2	8	---	----	-0,249	0,00761	21,57	3,30%
Q41951	Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2	1	---	----	-0,363	0,00761	21,57	3,30%
Q9M339;Q9SIP7	40S ribosomal protein S3-2 OS=Arabidopsis thaliana GN=RPS3B PE=1 SV=1	2	---	----	0,494	0,00801	22,70	3,40%
Q9SN73	DnaJ/Hsp40 cysteine-rich domain-containing protein OS=Arabidopsis thaliana GN=F1P2.200 PE=2 SV=1	1	---	----	0,482	0,00781	22,14	3,40%
Q9ZUY6	UDP-D-apiose/UDP-D-xylose synthase 1 OS=Arabidopsis thaliana GN=AXS1 PE=1 SV=1	3	---	----	0,476	0,00801	22,70	3,40%
Q9C912	60S ribosomal protein L35a-3 OS=Arabidopsis thaliana GN=RPL35AC PE=3 SV=1	2	---	----	0,406	0,00801	22,70	3,40%
P92994	Trans-cinnamate 4-monooxygenase OS=Arabidopsis thaliana GN=CYP73A5 PE=2 SV=1	8	---	----	0,27	0,00801	22,70	3,40%
O49299;Q9SGC1	Probable phosphoglucomutase, cytoplasmic 1 OS=Arabidopsis thaliana GN=At1g23190 PE=2 SV=2	8	---	----	0,194	0,00801	22,70	3,40%
Q94AH9	Mediator of RNA polymerase II transcription subunit 36a OS=Arabidopsis thaliana GN=MED36A PE=1 SV=2	4	---	----	0,384	0,00841	23,84	3,50%
P49691	60S ribosomal protein L4-2 OS=Arabidopsis thaliana GN=RPL4D PE=2 SV=2	3	---	----	0,346	0,00821	23,27	3,50%
Q9SZJ5	Serine hydroxymethyltransferase 1, mitochondrial OS=Arabidopsis thaliana GN=SHM1 PE=1 SV=1	16	---	----	0,108	0,00821	23,27	3,50%
Q8GYL5;Q9SIK2	40S ribosomal protein S25-3 OS=Arabidopsis thaliana GN=RPS25D PE=3 SV=2	1	---	----	0,596	0,00861	24,40	3,60%
Q9LVC9	60S acidic ribosomal protein P3-2 OS=Arabidopsis thaliana GN=RPP3B PE=2 SV=1	2	---	----	0,523	0,00841	23,84	3,60%
Q9LZ57	60S ribosomal protein L36-3 OS=Arabidopsis thaliana GN=RPL36C PE=3 SV=1	2	---	----	0,492	0,00861	24,40	3,60%
P42825	Chaperone protein dnaJ 2 OS=Arabidopsis thaliana GN=ATJ2 PE=1 SV=2	2	---	----	0,773	0,00881	24,97	3,70%
B9DGT7;P29511	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	4	---	----	0,354	0,00881	24,97	3,70%
rev_Q9LSS5	reversed Interactor of constitutive active ROPs 3 OS=Arabidopsis thaliana GN=ICR3 PE=1 SV=1	1	---	----	-0,833	0,00881	24,97	3,70%
Q570C8	3-ketoacyl-CoA thiolase 5, peroxisomal OS=Arabidopsis thaliana GN=KAT5 PE=2 SV=2	2	---	----	0,643	0,00921	26,10	3,80%
P24636;P29515;P29516;P	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	2	---	----	0,385	0,00901	25,54	3,80%
Q38845	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Arabidopsis thaliana GN=PP2	7	---	----	0,289	0,00922	26,13	3,80%
Q9XIE2	ABC transporter G family member 36 OS=Arabidopsis thaliana GN=ABCG36 PE=1 SV=1	17	---	----	-0,198	0,00901	25,54	3,80%
Q9FIJ5	AT5g47860/MCA23_20 OS=Arabidopsis thaliana GN=At5g47860 PE=2 SV=1	6	---	----	-0,383	0,00921	26,10	3,80%
Q9SKZ3	40S ribosomal protein S12-2 OS=Arabidopsis thaliana GN=RPS12C PE=1 SV=1	1	---	----	0,59	0,00941	26,67	3,90%
Q94KI8	Two pore calcium channel protein 1 OS=Arabidopsis thaliana GN=TPC1 PE=1 SV=1	4	---	----	-0,362	0,00941	26,67	3,90%
Q9SI96	Histone H2B.3 OS=Arabidopsis thaliana GN=At2g28720 PE=1 SV=3	1	---	----	-0,589	0,00941	26,67	3,90%
F4HXY8	Ubiquinol-cytochrome C reductase hinge protein OS=Arabidopsis thaliana GN=At1g15120 PE=1 SV=1	1	---	----	0,827	0,00961	27,24	4,00%
Q93VP3;Q9C505	Eukaryotic translation initiation factor 5A-2 OS=Arabidopsis thaliana GN=ELF5A-2 PE=1 SV=1	1	---	----	0,455	0,00961	27,24	4,00%
F4J6A1	Eukaryotic translation initiation factor 3 subunit G OS=Arabidopsis thaliana GN=EIF3G1 PE=3 SV=1	6	---	----	0,301	0,00981	27,81	4,00%
Q9LR44	UDP-glycosyltransferase 75B1 OS=Arabidopsis thaliana GN=UGT75B1 PE=1 SV=1	6	---	----	-0,27	0,00981	27,81	4,00%
F4J6T7;Q9S7Y7	Putative alpha-xylosidase 2 OS=Arabidopsis thaliana GN=XYL2 PE=5 SV=1	4	---	----	-0,331	0,00981	27,81	4,00%
O22711	Peroxiredoxin-2D OS=Arabidopsis thaliana GN=PRXIID PE=1 SV=2	1	---	----	-0,877	0,00961	27,24	4,00%
O80948	Jacalin-related lectin 23 OS=Arabidopsis thaliana GN=JAL23 PE=1 SV=1	1	---	----	0,562	0,01001	28,37	4,10%
P47192	Vesicle-associated membrane protein 722 OS=Arabidopsis thaliana GN=VAMP722 PE=2 SV=2	4	---	----	0,343	0,01001	28,37	4,10%
Q94EG6	Uncharacterized protein At5g02240 OS=Arabidopsis thaliana GN=At5g02240 PE=1 SV=1	7	---	----	0,324	0,01001	28,37	4,10%
Q9LD43	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=CAC3 PE	21	---	----	-0,169	0,01001	28,37	4,10%
Q9LT69	D-3-phosphoglycerate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=PGDH3 PE=1 SV=1	11	---	----	-0,23	0,01001	28,37	4,10%
Q9FFJ2	Putative uncharacterized protein At5g17170 OS=Arabidopsis thaliana GN=ENH1 PE=2 SV=1	3	---	----	-0,274	0,01021	28,94	4,10%
Q6NLR2	At1g64650 OS=Arabidopsis thaliana GN=At1g64650 PE=2 SV=1	1	---	----	0,579	0,01021	28,94	4,20%
O23264;Q93WN0	Selenium-binding protein 1 OS=Arabidopsis thaliana GN=SBP1 PE=1 SV=1	4	---	----	0,331	0,01041	29,51	4,20%
Q9LV77	Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Arabidopsis thaliana GN=ASN2 PE=2 SV=1	12	---	----	0,209	0,01041	29,51	4,20%
P93819	Malate dehydrogenase, cytoplasmic 1 OS=Arabidopsis thaliana GN=MDH1 PE=1 SV=2	9	---	----	0,14	0,01041	29,51	4,20%
Q9SSA5	Peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic OS=Arabidopsis thaliana GN=CYP38 PE=1 SV=1	13	---	----	-0,167	0,01041	29,51	4,20%
Q9SKU1	Clathrin light chain 1 OS=Arabidopsis thaliana GN=At2g20760 PE=2 SV=1	3	---	----	0,419	0,01061	30,07	4,30%
P83291	NADH-cytochrome b5 reductase-like protein OS=Arabidopsis thaliana GN=CBR2 PE=1 SV=2	6	---	----	0,33	0,01081	30,64	4,30%
P20115	Citrate synthase 4, mitochondrial OS=Arabidopsis thaliana GN=CSY4 PE=1 SV=3	12	---	----	0,214	0,01081	30,64	4,30%
F4HR88	Leucine-rich repeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33590 PE=4 SV=1	13	---	----	-0,175	0,01061	30,07	4,30%
Q9SKT0	Protein THYLAKOID FORMATION 1, chloroplastic OS=Arabidopsis thaliana GN=THF1 PE=1 SV=1	7	---	----	-0,177	0,01061	30,07	4,30%
O22870	Peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-3 PE=1 SV=2	6	---	----	-0,241	0,01081	30,64	4,30%
Q39241	Thioredoxin H5 OS=Arabidopsis thaliana GN=TRX5 PE=1 SV=1	3	---	----	-0,441	0,01081	30,64	4,30%
Q9LEW8	Protein-ribulosamine 3-kinase, chloroplastic OS=Arabidopsis thaliana GN=At3g61080 PE=1 SV=2	2	---	----	-0,661	0,01061	30,07	4,30%
Q9FE29	CASP-like protein 1D1 OS=Arabidopsis thaliana GN=At4g15610 PE=2 SV=1	1	---	----	-0,798	0,01081	30,64	4,30%
Q9C9P3	ADP-glucose pyrophosphorylase family protein OS=Arabidopsis thaliana GN=F9E10.24 PE=1 SV=1	1	VSSFEALQPATR	Phospho S3	-2,096	0,01061	30,07	4,30%

P42643;P46077	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	---	----	0,576	0,01101	31,21	4,40%
Q9ZV07	Probable aquaporin PIP2-6 OS=Arabidopsis thaliana GN=PIP2-6 PE=1 SV=1	2	---	----	-0,489	0,01101	31,21	4,40%
Q56YW9	Tubulin beta-2 chain OS=Arabidopsis thaliana GN=TUBB2 PE=2 SV=2	2	---	----	0,38	0,01141	32,34	4,50%
P55229	Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ADG2 PE=1 SV=3	17	---	----	0,162	0,01141	32,34	4,50%
Q8RUW5	Serine carboxypeptidase-like 8 OS=Arabidopsis thaliana GN=SCPL8 PE=1 SV=2	3	---	----	-0,401	0,01141	32,34	4,50%
P61837;Q39196;Q8LAA6	Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1	1	---	----	-0,425	0,01141	32,34	4,50%
Q94EH2	Mitochondrial import inner membrane translocase subunit TIM22-2 OS=Arabidopsis thaliana GN=TIM22-2 PE=1 SV=1	2	---	----	0,8	0,01161	32,91	4,60%
Q9M0E2	60S ribosomal protein L28-2 OS=Arabidopsis thaliana GN=RPL28C PE=2 SV=1	3	---	----	0,365	0,01161	32,91	4,60%
Q9M011	Light-inducible protein ATLS1 OS=Arabidopsis thaliana GN=F7A7_170 PE=2 SV=1	5	---	----	-0,29	0,01161	32,91	4,60%
O22126;Q9LZX4	Fasciclin-like arabinogalactan protein 8 OS=Arabidopsis thaliana GN=FLA8 PE=1 SV=1	2	---	----	-0,348	0,01181	33,47	4,60%
O23629	Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	2	---	----	-0,382	0,01181	33,47	4,60%
Q9LYG3	NADP-dependent malic enzyme 2 OS=Arabidopsis thaliana GN=NADP-ME2 PE=1 SV=1	11	---	----	0,205	0,01241	35,18	4,80%
P92549	ATP synthase subunit alpha, mitochondrial OS=Arabidopsis thaliana GN=ATPA PE=1 SV=2	15	---	----	-0,14	0,01242	35,20	4,80%
Q9LW85	MAR-binding filament-like protein 1 OS=Arabidopsis thaliana GN=MFP1 PE=2 SV=2	16	---	----	-0,161	0,01221	34,61	4,80%
O65502	AT4g35250/F23E12_190 OS=Arabidopsis thaliana GN=F23E12.190 PE=2 SV=1	11	---	----	-0,189	0,01241	35,18	4,80%
Q94FY7	Tocopherol cyclase, chloroplastic OS=Arabidopsis thaliana GN=VTE1 PE=2 SV=1	4	---	----	-0,305	0,01221	34,61	4,80%
P43286;P43287	Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1	1	---	----	-0,351	0,01221	34,61	4,80%
F4KIB2	Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1	1	---	----	0,893	0,01261	35,74	4,90%
Q9LTP9	Genomic DNA, chromosome 3, P1 clone: MQC12 OS=Arabidopsis thaliana GN=At3g20430 PE=2 SV=1	1	---	----	0,867	0,01281	36,31	4,90%
Q3E902;Q9M337	40S ribosomal protein S21-2 OS=Arabidopsis thaliana GN=RPS21C PE=1 SV=2	1	---	----	0,53	0,01261	35,74	4,90%
Q9C9D0	Cytosolic sulfotransferase 16 OS=Arabidopsis thaliana GN=SOT16 PE=1 SV=1	3	---	----	0,425	0,01261	35,74	4,90%
Q29Q26;Q9SAR5	Ankyrin repeat-containing 2B OS=Arabidopsis thaliana GN=AKR2B PE=2 SV=1	2	---	----	0,391	0,01261	35,74	4,90%
Q944K2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Arabidopsis thaliana GN=OST48 PE	5	---	----	0,362	0,01281	36,31	4,90%
Q9SR77	Heme-binding-like protein At3g10130, chloroplastic OS=Arabidopsis thaliana GN=At3g10130 PE=2 SV=1	3	---	----	-0,495	0,01261	35,74	4,90%
P48347;Q9S9Z8-2	14-3-3-like protein GF14 epsilon OS=Arabidopsis thaliana GN=GRF10 PE=1 SV=1	2	---	----	0,555	0,01301	36,88	5,00%
O49485	D-3-phosphoglycerate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=PGDH1 PE=1 SV=1	12	---	----	0,179	0,01301	36,88	5,00%
Q9LQ04;Q9SYM5	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana G	1	---	----	0,81	0,01321	37,44	5,10%
Q9M8S8	Inositol-phosphate phosphatase OS=Arabidopsis thaliana GN=VTC4 PE=1 SV=1	7	---	----	0,265	0,01322	37,47	5,10%
Q9LTV6	Peroxisomal 2,4-dienoyl-CoA reductase OS=Arabidopsis thaliana GN=At3g12800 PE=2 SV=1	5	---	----	-0,237	0,01341	38,01	5,10%
F4JJY7	Uncharacterized protein OS=Arabidopsis thaliana GN=At4g34090 PE=4 SV=1	7	---	----	-0,279	0,01361	38,58	5,20%
Q9SH59	Reticulon-like protein B3 OS=Arabidopsis thaliana GN=RTNLB3 PE=2 SV=1	1	---	----	0,814	0,01381	39,14	5,30%
Q38935	Peptidyl-prolyl cis-trans isomerase FKBP15-1 OS=Arabidopsis thaliana GN=FKBP15-1 PE=2 SV=2	2	---	----	0,481	0,01381	39,14	5,30%
O65423	AT4g21580/F18E5_200 OS=Arabidopsis thaliana GN=F18E5.200 PE=2 SV=1	5	---	----	-0,235	0,01401	39,71	5,30%
P04778;P0CJ48;Q39142	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1	2	---	----	-0,313	0,01381	39,14	5,30%
O65782	Cytochrome P450 83B1 OS=Arabidopsis thaliana GN=CYP83B1 PE=1 SV=1	2	---	----	0,683	0,01441	40,84	5,40%
Q38845;Q38950;Q38951	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Arabidopsis thaliana GN=PP2	1	---	----	0,567	0,01421	40,28	5,40%
Q9SGE0	UDP-D-apiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1	3	---	----	0,456	0,01441	40,84	5,40%
Q01667	Chlorophyll a-b binding protein 6, chloroplastic OS=Arabidopsis thaliana GN=LHCA1 PE=1 SV=1	5	---	----	-0,22	0,01421	40,28	5,40%
Q9S9P1;Q9SKZ3	40S ribosomal protein S12-1 OS=Arabidopsis thaliana GN=RPS12A PE=2 SV=1	3	---	----	0,35	0,01461	41,41	5,50%
O65719;P22953	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	4	---	----	0,25	0,01441	40,84	5,50%
Q8LDU4	Red chlorophyll catabolite reductase, chloroplastic OS=Arabidopsis thaliana GN=RCCR PE=1 SV=2	8	---	----	-0,209	0,01461	41,41	5,50%
Q9FFH6	Fasciclin-like arabinogalactan protein 13 OS=Arabidopsis thaliana GN=FLA13 PE=1 SV=1	4	---	----	-0,311	0,01461	41,41	5,50%
Q9FG71	ER membrane protein complex subunit 8/9 homolog OS=Arabidopsis thaliana GN=EMB2731 PE=2 SV=1	2	---	----	0,684	0,01481	41,98	5,60%
P42643;P46077;Q01525;	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	---	----	0,453	0,01521	43,11	5,60%
P42804	Glutamyl-tRNA reductase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMA1 PE=1 SV=2	3	---	----	0,414	0,01501	42,54	5,60%
Q8L606	Putative uncharacterized protein At3g53560 OS=Arabidopsis thaliana GN=At3g53560 PE=2 SV=1	4	---	----	0,408	0,01501	42,54	5,60%
Q9FIH8	Insulinase (Peptidase family M16) family protein OS=Arabidopsis thaliana GN=At5g42390 PE=2 SV=1	5	---	----	0,357	0,01481	41,98	5,60%
P54121	Protein AIG2 OS=Arabidopsis thaliana GN=AIG2 PE=2 SV=1	1	---	----	0,541	0,01521	43,11	5,70%
O49160	Eukaryotic translation initiation factor 3 subunit C OS=Arabidopsis thaliana GN=TIF3C1 PE=1 SV=2	4	---	----	0,298	0,01521	43,11	5,70%
Q9SN86	Malate dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=At3g47520 PE=1 SV=1	11	---	----	-0,165	0,01541	43,68	5,70%
Q9SIN5	Protein COLD-REGULATED 15B, chloroplastic OS=Arabidopsis thaliana GN=COR15B PE=1 SV=1	7	---	----	-0,225	0,01521	43,11	5,70%
Q07488	Blue copper protein OS=Arabidopsis thaliana GN=BCB PE=1 SV=2	1	---	----	-0,554	0,01521	43,11	5,70%
Q9SJH7	Citrate synthase 3, peroxisomal OS=Arabidopsis thaliana GN=CSY3 PE=2 SV=1	2	---	----	-0,582	0,01521	43,11	5,70%
Q9SP02	Peptidyl-prolyl cis-trans isomerase CYP20-1 OS=Arabidopsis thaliana GN=CYP20-1 PE=1 SV=1	3	---	----	0,516	0,01582	44,84	5,80%
P55826	Protoporphyrinogen oxidase 1, chloroplastic OS=Arabidopsis thaliana GN=PPOX1 PE=1 SV=1	12	---	----	0,186	0,01601	45,38	5,90%

Q9SCY3	Photosynthetic NDH subunit of lumenal location 4, chloroplastic OS=Arabidopsis thaliana GN=PNSL4 PE=1 SV=1	2	---	----	-0,356	0,01581	44,81	5,90%
F4IWK4	Sucrase/ferredoxin-like protein OS=Arabidopsis thaliana GN=At3g27570 PE=4 SV=1	2	---	----	0,701	0,01641	46,51	6,00%
Q9LHH3	FKBP-type peptidyl-prolyl cis-trans isomerase, putative OS=Arabidopsis thaliana GN=At3g12345 PE=1 SV=1	4	---	----	-0,26	0,01621	45,95	6,00%
Q9LMU2	At1g17860/F2H15_8 OS=Arabidopsis thaliana GN=F2H15.9 PE=2 SV=1	2	---	----	-0,384	0,01641	46,51	6,00%
Q9M439	Branched-chain-amino-acid aminotransferase 2, chloroplastic OS=Arabidopsis thaliana GN=BCAT2 PE=1 SV=1	1	---	----	-0,928	0,01621	45,95	6,00%
P34789	40S ribosomal protein S28-2 OS=Arabidopsis thaliana GN=RPS28C PE=3 SV=1	1	---	----	0,452	0,01681	47,65	6,10%
Q9SIZ2	Eukaryotic translation initiation factor 2 subunit 1 OS=Arabidopsis thaliana GN=At2g40290 PE=2 SV=2	5	---	----	0,363	0,01661	47,08	6,10%
Q9LZG7	Glutathione S-transferase U27 OS=Arabidopsis thaliana GN=GSTU27 PE=2 SV=1	4	---	----	0,327	0,01681	47,65	6,10%
Q9C5Z1	Eukaryotic translation initiation factor 3 subunit B OS=Arabidopsis thaliana GN=TIF3B1 PE=1 SV=1	7	---	----	0,253	0,01661	47,08	6,10%
Q9XFT3-2	Isoform 2 of Oxygen-evolving enhancer protein 3-1, chloroplastic OS=Arabidopsis thaliana GN=PSBQ1	10	---	----	-0,102	0,01661	47,08	6,10%
O49006	Pectinesterase/pectinesterase inhibitor 3 OS=Arabidopsis thaliana GN=PME3 PE=2 SV=2	11	---	----	-0,139	0,01661	47,08	6,10%
P27323	Heat shock protein 90-1 OS=Arabidopsis thaliana GN=HSP90-1 PE=1 SV=3	10	---	----	-0,227	0,01661	47,08	6,10%
Q9SD07	Protein STRICTOSIDINE SYNTHASE-LIKE 4 OS=Arabidopsis thaliana GN=SSL4 PE=1 SV=1	3	---	----	-0,512	0,01681	47,65	6,10%
Q39222;Q9FJH0	Ras-related protein RABA1b OS=Arabidopsis thaliana GN=RABA1B PE=2 SV=1	2	---	----	0,378	0,01721	48,78	6,20%
O22769	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Arabidopsis thaliana GN=At4g02580 PE=2 SV=3	4	---	----	0,309	0,01721	48,78	6,20%
F4J5S1	Clustered mitochondria protein OS=Arabidopsis thaliana GN=FMT PE=2 SV=1	7	---	----	0,291	0,01701	48,21	6,20%
P59232;Q9SHE7	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=1 SV=2	2	---	----	0,136	0,01701	48,21	6,20%
Q9LDY5	Peptidyl-prolyl cis-trans isomerase FKBP17-2, chloroplastic OS=Arabidopsis thaliana GN=FKBP17-2 PE=1 SV=1	5	---	----	-0,292	0,01701	48,21	6,20%
P60129	Photosystem II reaction center protein L OS=Arabidopsis thaliana GN=psbL PE=3 SV=1	1	---	----	0,511	0,01761	49,91	6,30%
O81149;Q42134	Proteasome subunit alpha type-5-A OS=Arabidopsis thaliana GN=PAE1 PE=1 SV=1	6	---	----	0,222	0,01741	49,35	6,30%
P46286;Q42064	60S ribosomal protein L8-1 OS=Arabidopsis thaliana GN=RPL8A PE=1 SV=2	4	---	----	0,211	0,01761	49,91	6,30%
P31166-2	Isoform 2 of Adenine phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=APT1	6	---	----	0,24	0,01781	50,48	6,40%
P28186;Q9FJF1;Q9FPJ4;Q	Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	1	---	----	0,379	0,01821	51,61	6,50%
P29402;Q38798	Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1	3	---	----	0,367	0,01821	51,61	6,50%
F4K329	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g42765 PE=4 SV=1	3	---	----	-0,359	0,01801	51,05	6,50%
P61837;Q06611;Q39196	Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1	3	---	----	-0,426	0,01821	51,61	6,50%
O80634	Photosynthetic NDH subunit of lumenal location 1, chloroplastic OS=Arabidopsis thaliana GN=PNSL1 PE=1 SV=2	5	---	----	-0,336	0,01881	53,32	6,70%
P34802	Heterodimeric geranylgeranyl pyrophosphate synthase large subunit 1, chloroplastic OS=Arabidopsis thaliana GN=GGP	3	---	----	0,429	0,01921	54,45	6,80%
O24653	Guanosine nucleotide diphosphate dissociation inhibitor 2 OS=Arabidopsis thaliana GN=GDI2 PE=2 SV=1	4	---	----	0,307	0,01901	53,88	6,80%
Q39089	Protein PALE CRESS, chloroplastic OS=Arabidopsis thaliana GN=PAC PE=2 SV=1	2	---	----	0,481	0,01941	55,02	6,90%
O80774	AT2G34250 protein OS=Arabidopsis thaliana GN=At2g34250 PE=2 SV=1	6	---	----	0,324	0,01941	55,02	6,90%
Q9ZVF3	MLP-like protein 328 OS=Arabidopsis thaliana GN=MLP328 PE=2 SV=1	4	---	----	0,295	0,01941	55,02	6,90%
Q8GXR9	Alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=NDC1 PE	10	---	----	-0,228	0,01961	55,58	6,90%
Q8VZF1	Acetate/butyrate--CoA ligase AAE7, peroxisomal OS=Arabidopsis thaliana GN=AAE7 PE=1 SV=1	7	---	----	-0,238	0,01961	55,58	6,90%
F4J6T7	Putative alpha-xylosidase 2 OS=Arabidopsis thaliana GN=XYL2 PE=5 SV=1	1	---	----	-0,4	0,01961	55,58	6,90%
P82869	Peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic OS=Arabidopsis thaliana GN=CYP37 PE=1 SV=3	8	---	----	-0,232	0,01981	56,15	7,00%
Q42029	Oxygen-evolving enhancer protein 2-1, chloroplastic OS=Arabidopsis thaliana GN=PSBP1 PE=1 SV=2	12	---	----	0,087	0,02022	57,31	7,10%
Q9SAB3	Polyadenylate-binding protein RBP45B OS=Arabidopsis thaliana GN=RBP45B PE=1 SV=1	3	---	----	0,354	0,02061	58,42	7,20%
P93832;Q9FMT1;Q9SA14	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1	3	---	----	0,328	0,02061	58,42	7,20%
P60040	60S ribosomal protein L7-2 OS=Arabidopsis thaliana GN=RPL7B PE=2 SV=1	4	---	----	0,279	0,02061	58,42	7,20%
Q8RWN9	Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial OS=Ara	10	---	----	0,175	0,02041	57,85	7,20%
P50318;Q9LD57	Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=2 SV=3	9	---	----	-0,103	0,02042	57,88	7,20%
P46644	Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1	3	---	----	-0,352	0,02061	58,42	7,20%
Q8H0W1	Chloroplast processing peptidase OS=Arabidopsis thaliana GN=PLSP1 PE=2 SV=2	2	---	----	-0,577	0,02061	58,42	7,20%
Q9FGH3	Cinnamoyl-CoA reductase-like protein OS=Arabidopsis thaliana GN=At5g58490 PE=2 SV=1	3	---	----	0,408	0,02081	58,98	7,30%
Q42529	Tryptophan synthase alpha chain, chloroplastic OS=Arabidopsis thaliana GN=TSA1 PE=1 SV=1	4	---	----	0,34	0,02101	59,55	7,30%
O82179	Glycine cleavage system H protein 2, mitochondrial OS=Arabidopsis thaliana GN=GDH2 PE=2 SV=1	2	---	----	0,481	0,02121	60,12	7,40%
P34893	10 kDa chaperonin OS=Arabidopsis thaliana GN=CPN10 PE=3 SV=1	5	---	----	0,246	0,02141	60,68	7,40%
Q9C6M1	GDT1-like protein 4 OS=Arabidopsis thaliana GN=At1g25520 PE=2 SV=1	1	---	----	0,902	0,02161	61,25	7,50%
Q9LEV3	CBS domain-containing protein CBSX3, mitochondrial OS=Arabidopsis thaliana GN=CBSX3 PE=1 SV=1	7	---	----	-0,232	0,02161	61,25	7,50%
Q96528	Catalase-1 OS=Arabidopsis thaliana GN=CAT1 PE=2 SV=3	5	---	----	-0,253	0,02162	61,28	7,50%
Q9FWS4	50S ribosomal protein L31, chloroplastic OS=Arabidopsis thaliana GN=RPL31 PE=2 SV=1	5	---	----	-0,208	0,02201	62,39	7,60%
Q8LPJ4	ABC transporter E family member 2 OS=Arabidopsis thaliana GN=ABCE2 PE=2 SV=1	5	---	----	0,322	0,02221	62,95	7,70%
Q93WJ8	Probable monodehydroascorbate reductase, cytoplasmic isoform 4 OS=Arabidopsis thaliana GN=At5g03630 PE=2 SV=1	14	---	----	0,155	0,02221	62,95	7,70%
Q93V74	AT4g34180/F28A23_60 OS=Arabidopsis thaliana GN=At4g34180 PE=2 SV=1	6	---	----	-0,21	0,02221	62,95	7,70%

Q9SGU7	At1g64680 OS=Arabidopsis thaliana GN=At1g64680 PE=2 SV=1	4	---	----	-0,354	0,02241	63,52	7,70%
P59223	40S ribosomal protein S13-1 OS=Arabidopsis thaliana GN=RPS13A PE=2 SV=1	1	---	----	0,516	0,02281	64,65	7,80%
F4JZY1	COP1-interactive protein 1 OS=Arabidopsis thaliana GN=CIP1 PE=4 SV=1	12	---	----	0,219	0,02261	64,09	7,80%
Q9M1X3	AT3g63160/F16M2_10 OS=Arabidopsis thaliana GN=F16M2_10 PE=1 SV=1	1	KSDSDDATVPPPSG	none	-0,332	0,02281	64,65	7,80%
O49506	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 OS=Arabidopsis thaliana GN=GLO5 PE=1 SV=1	1	---	----	-0,333	0,02281	64,65	7,80%
P61837;Q06611	Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1	2	---	----	-0,358	0,02261	64,09	7,80%
Q96327	ERBB-3 BINDING PROTEIN 1 OS=Arabidopsis thaliana GN=EBP1 PE=2 SV=1	8	---	----	0,265	0,02321	65,79	7,90%
Q9LPR4	2-isopropylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=IPMS1 PE=1 SV=2	11	---	----	0,211	0,02301	65,22	7,90%
P19456;P20649	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	9	---	----	0,18	0,02321	65,79	7,90%
O48676	UDP-glycosyltransferase 74B1 OS=Arabidopsis thaliana GN=UGT74B1 PE=1 SV=1	5	---	----	0,272	0,02362	66,95	8,00%
P51414	60S ribosomal protein L26-1 OS=Arabidopsis thaliana GN=RPL26A PE=2 SV=2	7	---	----	0,182	0,02341	66,35	8,00%
Q9T076	Early nodulin-like protein 2 OS=Arabidopsis thaliana GN=At4g27520 PE=1 SV=1	8	---	----	-0,163	0,02361	66,92	8,00%
Q9LXU4	Putative uncharacterized protein At5g12950/T24H18_120 OS=Arabidopsis thaliana GN=T24H18_120 PE=2 SV=1	12	---	----	-0,198	0,02361	66,92	8,00%
Q94B52	Translation initiation factor IF-3 OS=Arabidopsis thaliana GN=T10C21.40 PE=2 SV=1	3	---	----	-0,414	0,02341	66,35	8,00%
Q9FE06	Protein EXORDIUM-like 2 OS=Arabidopsis thaliana GN=EXL2 PE=2 SV=1	3	---	----	-0,435	0,02361	66,92	8,00%
P42643;P42644;P42645;P	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	---	----	0,552	0,02401	68,05	8,10%
Q8L8Y0	40S ribosomal protein S2-1 OS=Arabidopsis thaliana GN=RPS2A PE=2 SV=2	2	---	----	0,518	0,02421	68,62	8,10%
O23144	Proton pump-interactor 1 OS=Arabidopsis thaliana GN=PPI1 PE=1 SV=2	2	---	----	0,495	0,02401	68,05	8,10%
Q9FWA3;Q9SH69	6-phosphogluconate dehydrogenase, decarboxylating 3 OS=Arabidopsis thaliana GN=At3g02360 PE=2 SV=1	1	---	----	0,465	0,02381	67,49	8,10%
Q9LZ06	Glutathione S-transferase L3 OS=Arabidopsis thaliana GN=GSTL3 PE=2 SV=1	9	---	----	0,176	0,02421	68,62	8,10%
Q9MA15	Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic OS=Arabidopsis thaliana GN=At1g796	12	---	----	-0,18	0,02421	68,62	8,10%
Q94A68	Uncharacterized oxidoreductase At1g06690, chloroplastic OS=Arabidopsis thaliana GN=At1g06690 PE=2 SV=1	9	---	----	-0,231	0,02401	68,05	8,10%
Q9C6E4	Protein EXORDIUM-like 1 OS=Arabidopsis thaliana GN=EXL1 PE=2 SV=1	2	---	----	-0,495	0,02421	68,62	8,10%
Q43316	Porphobilinogen deaminase, chloroplastic OS=Arabidopsis thaliana GN=HEMC PE=1 SV=1	12	---	----	0,142	0,02441	69,19	8,20%
Q9M5K2;Q9M5K3	Dihydrolipoyl dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=LPD2 PE=1 SV=1	7	---	----	-0,162	0,02461	69,75	8,20%
Q0WPR4	Serine carboxypeptidase-like 34 OS=Arabidopsis thaliana GN=SCPL34 PE=2 SV=2	7	---	----	-0,226	0,02442	69,22	8,20%
F4JYC1	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g35180 PE=1 SV=1	1	---	----	1,091	0,02501	70,89	8,30%
Q8VZ74	GTP-binding protein Era OS=Arabidopsis thaliana GN=K1F13.13 PE=2 SV=1	1	---	----	0,805	0,02521	71,46	8,40%
Q9SL96	Expressed protein OS=Arabidopsis thaliana GN=At2g25670 PE=2 SV=1	1	---	----	0,499	0,02521	71,46	8,40%
Q9C9K3;Q9SYP2	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2 OS=Arabidopsis thaliana GN=PFP-ALPHA2	5	---	----	0,338	0,02521	71,46	8,40%
Q8W4H8	Inactive GDSL esterase/lipase-like protein 23 OS=Arabidopsis thaliana GN=GLL23 PE=1 SV=1	3	---	----	-0,493	0,02561	72,59	8,50%
Q84K46	At1g27330 OS=Arabidopsis thaliana GN=At1g27330 PE=2 SV=1	1	---	----	0,5	0,02601	73,72	8,60%
Q9LW20	Probable inactive shikimate kinase like 1, chloroplastic OS=Arabidopsis thaliana GN=SKL1 PE=2 SV=1	3	---	----	0,395	0,02581	73,16	8,60%
Q5XF33	Magnesium-chelatase subunit ChlI-2, chloroplastic OS=Arabidopsis thaliana GN=CHLI2 PE=1 SV=1	3	---	----	0,376	0,02601	73,72	8,60%
Q94BT9	Copper transport protein ATX1 OS=Arabidopsis thaliana GN=ATX1 PE=1 SV=1	2	---	----	0,251	0,02621	74,29	8,60%
P93033;Q9FI53	Fumarate hydratase 1, mitochondrial OS=Arabidopsis thaliana GN=FUM1 PE=2 SV=2	5	---	----	0,2	0,02601	73,72	8,60%
Q9FPJ4	Ras-related protein RABD2b OS=Arabidopsis thaliana GN=RABD2B PE=2 SV=1	8	---	----	0,198	0,02582	73,18	8,60%
O23006	LysM domain-containing GPI-anchored protein 2 OS=Arabidopsis thaliana GN=LYM2 PE=1 SV=1	2	---	----	-0,487	0,02601	73,72	8,60%
Q56WN1	Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2	3	---	----	0,435	0,02641	74,86	8,70%
Q38929;Q42553	Isopentenyl-diphosphate Delta-isomerase I, chloroplastic OS=Arabidopsis thaliana GN=IPP1 PE=2 SV=3	3	---	----	0,255	0,02641	74,86	8,70%
O81742	Beta-adaptin-like protein C OS=Arabidopsis thaliana GN=BETAC-AD PE=1 SV=2	8	---	----	0,232	0,02641	74,86	8,70%
Q38885	Preprotein translocase subunit SCY1, chloroplastic OS=Arabidopsis thaliana GN=SCY1 PE=1 SV=2	5	---	----	-0,35	0,02661	75,42	8,70%
A8MPR5	AAA-type ATPase family protein OS=Arabidopsis thaliana GN=EMB2083 PE=4 SV=1	2	---	----	-0,852	0,02661	75,42	8,70%
Q9LFG2	Diaminopimelate epimerase, chloroplastic OS=Arabidopsis thaliana GN=DAPF PE=1 SV=1	7	---	----	0,224	0,02701	76,56	8,80%
Q9SF16	T-complex protein 1 subunit eta OS=Arabidopsis thaliana GN=CCT7 PE=1 SV=1	12	---	----	0,204	0,02722	77,15	8,90%
Q9SEU6	Thioredoxin M4, chloroplastic OS=Arabidopsis thaliana GN=At3g15360 PE=2 SV=2	4	---	----	-0,171	0,02722	77,15	8,90%
Q9FLQ4	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1, mitochondrial	4	---	----	0,361	0,02761	78,26	9,00%
O64530	Thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial OS=Arabidopsis thaliana GN=STR1 PE=1 SV=1	5	---	----	0,212	0,02781	78,83	9,00%
F4JTP5	ACT-like protein tyrosine kinase family protein OS=Arabidopsis thaliana GN=At4g38470 PE=1 SV=1	1	---	----	-0,491	0,02781	78,83	9,00%
B9DGT7	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	1	---	----	0,489	0,02801	79,39	9,10%
Q9LXQ2	At3g44100 OS=Arabidopsis thaliana GN=F26G5_50 PE=2 SV=1	2	---	----	-0,297	0,02801	79,39	9,10%
Q9LXV3	Dicarboxylate transporter 1, chloroplastic OS=Arabidopsis thaliana GN=DIT1 PE=1 SV=1	2	---	----	-0,299	0,02781	78,83	9,10%
Q8RXX5	50S ribosomal protein L19-2, chloroplastic OS=Arabidopsis thaliana GN=At5g47190 PE=2 SV=1	2	---	----	-0,301	0,02821	79,96	9,10%
P37107	Signal recognition particle 54 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=FFC PE=1 SV=1	13	---	----	-0,181	0,02842	80,55	9,20%
Q9FRL3	Sugar transporter ERD6-like 6 OS=Arabidopsis thaliana GN=At1g75220 PE=1 SV=1	1	---	----	-0,471	0,02841	80,53	9,20%

Q84W56	Putative uncharacterized protein At5g63420 OS=Arabidopsis thaliana GN=emb2746 PE=1 SV=1	12	---	----	-0,174	0,02882	81,69	9,30%
O04130;O49485;Q9LT69	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2	1	---	----	0,455	0,02922	82,82	9,40%
Q9FLT9	AT5g24650/K18P6_19 OS=Arabidopsis thaliana GN=At5g24650 PE=2 SV=1	3	---	----	0,401	0,02941	83,36	9,40%
Q9MAP3	50S ribosomal protein L11, chloroplastic OS=Arabidopsis thaliana GN=RPL11 PE=2 SV=1	6	---	----	-0,172	0,02901	82,23	9,40%
Q93XZ7	At5g42570 OS=Arabidopsis thaliana GN=K16E1.4 PE=1 SV=1	2	---	----	0,422	0,02941	83,36	9,50%
Q9M8D3	Probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At1g7	8	---	----	0,289	0,02961	83,93	9,50%
B9DGT7;B9DHQ0;P29511	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	4	---	----	0,207	0,02981	84,49	9,50%
Q93VR4	MLP-like protein 423 OS=Arabidopsis thaliana GN=MLP423 PE=2 SV=1	8	---	----	0,205	0,02941	83,36	9,50%
F4JFN3;Q9STX5	HEAT SHOCK PROTEIN 89.1 OS=Arabidopsis thaliana GN=Hsp89.1 PE=3 SV=1	1	---	----	0,377	0,03001	85,06	9,60%
Q39142	Light-harvesting chlorophyll protein complex II subunit B1 OS=Arabidopsis thaliana GN=Lhb1B1 PE=1 SV=1	4	---	----	0,118	0,03022	85,66	9,60%
P49107	Photosystem I reaction center subunit N, chloroplastic OS=Arabidopsis thaliana GN=PSAN PE=1 SV=2	6	---	----	-0,163	0,03002	85,09	9,60%
Q9FMF7	Dicarboxylate transporter 2.1, chloroplastic OS=Arabidopsis thaliana GN=DIT2-1 PE=1 SV=1	4	---	----	-0,227	0,03021	85,63	9,60%
O04496	Aspartyl protease-like protein OS=Arabidopsis thaliana GN=F21M12.13 PE=2 SV=1	5	---	----	-0,217	0,03041	86,19	9,70%
rev_F4ICB6	reversed Cyclin-dependent kinase-like protein OS=Arabidopsis thaliana GN=IBS1 PE=4 SV=1	1	---	----	0,434	0,03101	87,90	9,80%
Q9CAF5	ABC transporter I family member 6, chloroplastic OS=Arabidopsis thaliana GN=ABCI6 PE=1 SV=1	3	---	----	0,364	0,03101	87,90	9,80%
Q9LMS7	T10F20.8 protein OS=Arabidopsis thaliana GN=T10F20.8 PE=4 SV=1	8	---	----	0,234	0,03082	87,36	9,80%
Q9M0Z3	K(+) efflux antiporter 3, chloroplastic OS=Arabidopsis thaliana GN=KEA3 PE=2 SV=2	3	---	----	-0,428	0,03081	87,33	9,80%
O64490	F20D22.6 protein OS=Arabidopsis thaliana GN=F20D22.6 PE=2 SV=1	4	---	----	0,279	0,03141	89,03	9,90%
F4IAX1	Putative copper amine oxidase OS=Arabidopsis thaliana GN=At1g31710 PE=3 SV=1	2	---	----	-0,537	0,03141	89,03	9,90%
Q4V3D1	At1g48620 OS=Arabidopsis thaliana GN=HON5 PE=1 SV=1	1	---	----	-0,753	0,03141	89,03	9,90%
Q9C827;Q9CAA0	Coatomer subunit beta'-2 OS=Arabidopsis thaliana GN=At1g52360 PE=2 SV=1	4	---	----	0,267	0,03181	90,16	10,00%
Q93VA8	Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g76010 PE=2 SV=1	5	---	----	0,242	0,03161	89,60	10,00%
Q9M156	UDP-glycosyltransferase 72B1 OS=Arabidopsis thaliana GN=UGT72B1 PE=1 SV=1	2	---	----	0,402	0,03222	91,32	10,10%
Q94BY3	Translocon-associated protein subunit beta OS=Arabidopsis thaliana GN=At5g14030 PE=2 SV=1	2	---	----	0,354	0,03221	91,30	10,10%
Q42262	40S ribosomal protein S3a-2 OS=Arabidopsis thaliana GN=RPS3AB PE=2 SV=3	5	---	----	0,239	0,03241	91,86	10,20%
Q8LB10	ATP-dependent Clp protease proteolytic subunit-related protein 4, chloroplastic OS=Arabidopsis thaliana GN=CLPR4 PE	5	---	----	0,198	0,03261	92,43	10,20%
Q8VZR8	Putative proline-rich protein OS=Arabidopsis thaliana GN=At4g28300 PE=1 SV=1	1	---	----	-1,002	0,03261	92,43	10,20%
P59224	40S ribosomal protein S13-2 OS=Arabidopsis thaliana GN=RPS13B PE=2 SV=1	1	---	----	0,7	0,03301	93,56	10,30%
P35131	Ubiquitin-conjugating enzyme E2 8 OS=Arabidopsis thaliana GN=UBC8 PE=1 SV=1	1	---	----	0,392	0,03281	93,00	10,30%
F4K1U5	Transport protein particle (TRAPP) component OS=Arabidopsis thaliana GN=At5g54750 PE=4 SV=1	3	---	----	0,368	0,03301	93,56	10,30%
Q8VYW6	Gamma-glutamyltranspeptidase 1 OS=Arabidopsis thaliana GN=GGT1 PE=2 SV=1	4	---	----	0,385	0,03341	94,70	10,40%
Q9SIE3	At2g22230/T26C19.11 OS=Arabidopsis thaliana GN=At2g22230 PE=2 SV=2	2	---	----	-0,316	0,03321	94,13	10,40%
Q93Z16	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Arabidopsis thaliana GN=RPN2 PE=2 SV=	10	---	----	0,213	0,03361	95,26	10,50%
P59232;Q39256;Q9SHE7	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=1 SV=2	3	---	----	0,208	0,03382	95,86	10,50%
Q8H0U5	Protein TIC 62, chloroplastic OS=Arabidopsis thaliana GN=TIC62 PE=1 SV=1	13	---	----	-0,147	0,03401	96,40	10,50%
Q8GWA1	Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial OS=Arabidopsis thaliana GN=NDA1 PE=2 S	4	---	----	-0,251	0,03401	96,40	10,50%
B9DGT7;P11139;P29511	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	1	---	----	0,571	0,03401	96,40	10,60%
Q9SRT9	UDP-arabinopyranose mutase 1 OS=Arabidopsis thaliana GN=RGP1 PE=1 SV=1	4	---	----	0,301	0,03441	97,53	10,60%
Q9ZT91	Elongation factor Tu, mitochondrial OS=Arabidopsis thaliana GN=TUFA PE=1 SV=1	10	---	----	0,163	0,03421	96,97	10,60%
Q94AD1	Putative DNA-binding protein At1g48610 OS=Arabidopsis thaliana GN=At1g48610 PE=1 SV=1	2	---	----	-0,477	0,03401	96,40	10,60%
P56779	Cytochrome b559 subunit alpha OS=Arabidopsis thaliana GN=psbE PE=1 SV=4	4	---	----	-0,144	0,03482	98,69	10,70%
Q94K71	Haloacid dehalogenase-like hydrolase domain-containing protein At3g48420 OS=Arabidopsis thaliana GN=At3g48420 P	7	---	----	-0,172	0,03461	98,10	10,70%
C0Z361	Chaperonin 60 subunit beta 3, chloroplastic OS=Arabidopsis thaliana GN=CPN60B3 PE=1 SV=1	6	---	----	0,272	0,03521	99,80	10,80%
P56778	Photosystem II CP43 reaction center protein OS=Arabidopsis thaliana GN=psbC PE=1 SV=3	14	---	----	0,077	0,03522	99,83	10,80%
P92964	Serine/arginine-rich splicing factor RS31 OS=Arabidopsis thaliana GN=RS31 PE=1 SV=2	1	ARSPEYDR	Phospho S3	0,772	0,03581	101,50	10,90%
Q9FE18	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Arabidopsis thaliana GN=T1K7.8 PE=2 SV=1	1	---	----	0,692	0,03581	101,50	10,90%
O22263	Protein disulfide-isomerase like 2-1 OS=Arabidopsis thaliana GN=PDIL2-1 PE=2 SV=1	1	---	----	0,623	0,03541	100,37	10,90%
Q8LC83	40S ribosomal protein S24-2 OS=Arabidopsis thaliana GN=RPS24B PE=2 SV=2	2	---	----	0,357	0,03541	100,37	10,90%
Q9SZ30	Imidazole glycerol phosphate synthase hisHF, chloroplastic OS=Arabidopsis thaliana GN=HISN4 PE=2 SV=1	16	---	----	-0,182	0,03562	100,96	10,90%
P54904	Pyrroline-5-carboxylate reductase OS=Arabidopsis thaliana GN=PROC1 PE=2 SV=1	1	---	----	-1,241	0,03541	100,37	10,90%
P54150	Peptide methionine sulfoxide reductase A4, chloroplastic OS=Arabidopsis thaliana GN=MSR4 PE=1 SV=2	5	---	----	0,237	0,03601	102,07	11,00%
O04331	Prohibitin-3, mitochondrial OS=Arabidopsis thaliana GN=PHB3 PE=1 SV=1	9	---	----	0,185	0,03581	101,50	11,00%
Q8GUN7	Adenylosuccinate lyase OS=Arabidopsis thaliana GN=At1g36280 PE=2 SV=1	2	---	----	0,461	0,03661	103,77	11,10%
Q9SA78	Coatomer subunit epsilon-1 OS=Arabidopsis thaliana GN=At1g30630 PE=2 SV=1	4	---	----	0,255	0,03641	103,20	11,10%
P42699	Plastocyanin major isoform, chloroplastic OS=Arabidopsis thaliana GN=DRT112 PE=1 SV=2	1	---	----	0,201	0,03661	103,77	11,10%

Q9ZVA4	Curculin-like (Mannose-binding) lectin family protein OS=Arabidopsis thaliana GN=F9K20.10 PE=2 SV=1	10	---	----	0,184	0,03661	103,77	11,10%
Q39172;Q39173	NADP-dependent alkenal double bond reductase P1 OS=Arabidopsis thaliana GN=P1 PE=1 SV=1	1	---	----	0,482	0,03701	104,90	11,20%
Q680A5	Ribose-phosphate pyrophosphokinase 4 OS=Arabidopsis thaliana GN=PRS4 PE=1 SV=2	5	---	----	0,25	0,03701	104,90	11,20%
Q9XFS9	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Arabidopsis thaliana GN=DXR PE=2 SV=2	11	---	----	0,151	0,03702	104,93	11,20%
P24102;Q9LHB9	Peroxidase 22 OS=Arabidopsis thaliana GN=PER22 PE=1 SV=2	1	---	----	-0,4	0,03701	104,90	11,20%
Q9SQR3	Probable strigolactone esterase D14 homolog OS=Arabidopsis thaliana GN=D14 PE=1 SV=1	2	---	----	-0,467	0,03721	105,47	11,20%
Q9SU26	AT4g12600/T1P17_190 OS=Arabidopsis thaliana GN=At4g12600 PE=2 SV=1	1	---	----	0,688	0,03761	106,60	11,30%
Q9SYL9	50S ribosomal protein L13, chloroplastic OS=Arabidopsis thaliana GN=RPL13 PE=2 SV=1	3	---	----	0,252	0,03761	106,60	11,30%
Q8RW93	Putative lipid-binding protein At4g00165 OS=Arabidopsis thaliana GN=At4g00165 PE=2 SV=1	3	---	----	-0,287	0,03741	106,04	11,30%
O23095	60S acidic ribosomal protein P1-2 OS=Arabidopsis thaliana GN=RPP1B PE=1 SV=2	2	---	----	0,448	0,03821	108,30	11,50%
Q96520	Peroxidase 12 OS=Arabidopsis thaliana GN=PER12 PE=1 SV=1	8	---	----	-0,161	0,03841	108,87	11,50%
Q8W4S4;Q9SJT7	V-type proton ATPase subunit a3 OS=Arabidopsis thaliana GN=VHA-a3 PE=1 SV=1	6	---	----	-0,201	0,03841	108,87	11,50%
O80944	Aldo-keto reductase family 4 member C8 OS=Arabidopsis thaliana GN=AKR4C8 PE=1 SV=2	9	---	----	0,16	0,03861	109,44	11,60%
Q9CA67	Geranylgeranyl diphosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=CHLP PE=1 SV=1	11	---	----	0,135	0,03881	110,00	11,60%
Q9LPK9	F24J8.11 protein OS=Arabidopsis thaliana GN=F24J8.11 PE=2 SV=1	3	---	----	-0,229	0,03881	110,00	11,60%
Q9LSB4	TSA1-like protein OS=Arabidopsis thaliana GN=NAI2 PE=1 SV=1	2	---	----	0,545	0,03921	111,14	11,70%
Q9FNP8;Q9SGA6	40S ribosomal protein S19-3 OS=Arabidopsis thaliana GN=RPS19C PE=2 SV=1	2	---	----	0,291	0,03941	111,70	11,80%
Q9LD55	Eukaryotic translation initiation factor 3 subunit A OS=Arabidopsis thaliana GN=TIF3A1 PE=1 SV=1	11	---	----	0,178	0,03941	111,70	11,80%
Q9SMT7	Oxalate--CoA ligase OS=Arabidopsis thaliana GN=AAE3 PE=1 SV=1	10	---	----	-0,17	0,03981	112,84	11,90%
Q9LUM0	1-phosphatidylinositol-3-phosphate 5-kinase FAB1B OS=Arabidopsis thaliana GN=FAB1B PE=2 SV=1	1	---	----	-0,479	0,03981	112,84	11,90%
Q9ZRW8	Glutathione S-transferase U19 OS=Arabidopsis thaliana GN=GSTU19 PE=2 SV=1	7	---	----	0,139	0,04041	114,54	12,00%
Q9SD66	Putative uncharacterized protein At3g47070 OS=Arabidopsis thaliana GN=F13I12.120 PE=1 SV=1	7	---	----	-0,126	0,04041	114,54	12,00%
Q94AZ4	Probable calcium-binding protein CML13 OS=Arabidopsis thaliana GN=CML13 PE=2 SV=1	8	---	----	0,17	0,04061	115,11	12,10%
O80860;Q8W585	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic OS=Arabidopsis thaliana GN=FTSH2 PE=1 SV=1	17	---	----	-0,103	0,04101	116,24	12,10%
P42737-2	Isoform 2 of Beta carbonic anhydrase 2, chloroplastic OS=Arabidopsis thaliana GN=BCA2	10	---	----	-0,114	0,04081	115,67	12,10%
Q9LUS7	Rapid alkalinization factor 23 OS=Arabidopsis thaliana GN=RALF23 PE=1 SV=1	3	---	----	-0,318	0,04081	115,67	12,10%
F4JBU0	Phosphoglycerate mutase family protein OS=Arabidopsis thaliana GN=At3g60440 PE=4 SV=1	2	---	----	0,389	0,04142	117,40	12,20%
F4IYK3	Armadillo/beta-catenin-like repeat-containing protein OS=Arabidopsis thaliana GN=At3g08943 PE=4 SV=1	8	---	----	0,222	0,04141	117,37	12,20%
Q9LMQ2	Chlorophyll A-B binding protein OS=Arabidopsis thaliana GN=F7H2.16 PE=1 SV=1	12	---	----	-0,101	0,04122	116,83	12,20%
O81208	High-light-induced protein, chloroplastic OS=Arabidopsis thaliana GN=HLIP PE=1 SV=1	3	---	----	-0,253	0,04141	117,37	12,20%
Q9LTR2	Protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic OS=Arabidopsis thaliana GN=TGD2 PE=2 SV=1	7	---	----	-0,255	0,04122	116,83	12,20%
Q9FFE6	Probable acyl-activating enzyme 5, peroxisomal OS=Arabidopsis thaliana GN=AAE5 PE=2 SV=1	3	---	----	-0,328	0,04161	117,94	12,20%
O65639	Cold shock protein 1 OS=Arabidopsis thaliana GN=CSP1 PE=1 SV=1	1	---	----	0,645	0,04201	119,07	12,30%
Q9SCX8	Purple acid phosphatase 17 OS=Arabidopsis thaliana GN=PAP17 PE=2 SV=1	1	---	----	0,539	0,04221	119,64	12,40%
Q93Y08	ABC transporter-like OS=Arabidopsis thaliana GN=MXK3.17 PE=2 SV=1	4	---	----	0,335	0,04221	119,64	12,40%
Q9FFN4	Beta-galactosidase 6 OS=Arabidopsis thaliana GN=BGAL6 PE=2 SV=1	10	---	----	-0,199	0,04241	120,21	12,40%
Q39033	Phosphoinositide phospholipase C 2 OS=Arabidopsis thaliana GN=PLC2 PE=1 SV=1	3	---	----	-0,29	0,04221	119,64	12,40%
Q9LHI0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Arabidopsis thaliana GN=At3g12260 PE=2 SV=1	3	---	----	0,305	0,04261	120,77	12,50%
Q9FMG0	2-nitropropane dioxygenase-like protein OS=Arabidopsis thaliana GN=At5g64250 PE=1 SV=1	5	---	----	-0,28	0,04281	121,34	12,50%
Q9SRX2	60S ribosomal protein L19-1 OS=Arabidopsis thaliana GN=RPL19A PE=2 SV=1	3	---	----	0,286	0,04321	122,48	12,60%
Q9SJV2	Putative NADPH dependent mannose 6-phosphate reductase OS=Arabidopsis thaliana GN=At2g21250 PE=2 SV=1	7	---	----	0,224	0,04341	123,04	12,60%
Q07473;Q9XF88	Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1	3	---	----	-0,198	0,04341	123,04	12,60%
Q9M1X3	AT3g63160/F16M2_10 OS=Arabidopsis thaliana GN=F16M2_10 PE=1 SV=1	2	---	----	-0,269	0,04342	123,07	12,60%
Q9M1R2	Class II aaRS and biotin synthetases superfamily protein OS=Arabidopsis thaliana GN=T17J13.80 PE=2 SV=1	9	---	----	0,189	0,04361	123,61	12,70%
Q41963	Aquaporin TIP1-2 OS=Arabidopsis thaliana GN=TIP1-2 PE=1 SV=2	1	---	----	-0,259	0,04401	124,74	12,80%
Q9S841	Oxygen-evolving enhancer protein 1-2, chloroplastic OS=Arabidopsis thaliana GN=PSBO2 PE=1 SV=1	9	---	----	-0,104	0,04441	125,88	12,90%
Q9FQ25	Protein TONNEAU 1a OS=Arabidopsis thaliana GN=TON1A PE=1 SV=1	1	---	----	-0,649	0,04461	126,44	12,90%
P49690	60S ribosomal protein L23 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=3	4	---	----	0,188	0,04501	127,58	13,00%
rev_B9DGU7	reversed Thiamine pyrophosphokinase 1 OS=Arabidopsis thaliana GN=TPK1 PE=2 SV=1	1	---	----	-0,8	0,04541	128,71	13,10%
Q9FE58	60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1	2	---	----	0,344	0,04581	129,84	13,20%
O22287	Mannose-1-phosphate guanylyltransferase 1 OS=Arabidopsis thaliana GN=CYT1 PE=1 SV=1	4	---	----	0,272	0,04581	129,84	13,20%
Q9LHH7	Bifunctional protein FolD 2 OS=Arabidopsis thaliana GN=FOLD2 PE=2 SV=1	8	---	----	0,207	0,04561	129,28	13,20%
Q9FYC2	Pheophorbide a oxygenase, chloroplastic OS=Arabidopsis thaliana GN=PAO PE=1 SV=1	4	---	----	-0,275	0,04601	130,41	13,20%
Q9ZU97	Protein VAC14 homolog OS=Arabidopsis thaliana GN=VAC14 PE=1 SV=2	1	---	----	-0,663	0,04601	130,41	13,20%
F4HQH8	RNA-binding (RRM/RBD/RNP motifs) family protein OS=Arabidopsis thaliana GN=At1g01080 PE=4 SV=1	7	---	----	-0,225	0,04621	130,98	13,30%

Q39231	Sucrose transport protein SUC2 OS=Arabidopsis thaliana GN=SUC2 PE=1 SV=2	1	---	----	0,821	0,04761	134,95	13,60%
P42794	60S ribosomal protein L11-2 OS=Arabidopsis thaliana GN=RPL11B PE=2 SV=2	6	---	----	0,151	0,04741	134,38	13,60%
Q42605	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 OS=Arabidopsis thaliana GN=UGE1 PE=1 SV=2	6	---	----	-0,193	0,04761	134,95	13,60%
Q8H166	Thiol protease aleurain OS=Arabidopsis thaliana GN=ALEU PE=1 SV=2	4	---	----	0,36	0,04781	135,51	13,70%
P16180	30S ribosomal protein S17, chloroplastic OS=Arabidopsis thaliana GN=RPS17 PE=1 SV=1	4	---	----	0,248	0,04801	136,08	13,70%
O23403	PsbP domain-containing protein 1, chloroplastic OS=Arabidopsis thaliana GN=PPD1 PE=1 SV=1	1	---	----	0,791	0,04841	137,21	13,80%
Q9LZK5	DnaJ protein ERDJ3B OS=Arabidopsis thaliana GN=ERDJ3B PE=1 SV=1	1	---	----	0,64	0,04861	137,78	13,80%
Q9SXJ7	Chaperone protein ClpC2, chloroplastic OS=Arabidopsis thaliana GN=CLPC2 PE=2 SV=1	3	---	----	0,447	0,04862	137,81	13,80%
P56767	Photosystem I P700 chlorophyll a apoprotein A2 OS=Arabidopsis thaliana GN=psaB PE=3 SV=1	13	---	----	0,099	0,04921	139,48	13,90%
O23406	UDP-glycosyltransferase 75D1 OS=Arabidopsis thaliana GN=UGT75D1 PE=2 SV=2	10	---	----	-0,192	0,04881	138,35	13,90%
Q9ZSR7	Triose phosphate/phosphate translocator TPT, chloroplastic OS=Arabidopsis thaliana GN=TPT PE=2 SV=1	4	---	----	-0,203	0,04921	139,48	13,90%
Q8RY62	At2g04690/F28I8.27 OS=Arabidopsis thaliana GN=At2g04690 PE=2 SV=1	2	---	----	-0,33	0,04901	138,91	13,90%
F4JSP1	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At4g31530 PE=4 SV=1	3	---	----	-0,366	0,04861	137,78	13,90%
Q9FLL8	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g41110 PE=4 SV=1	1	---	----	-0,751	0,04901	138,91	13,90%
O82399;Q9ZP05	Probable malate dehydrogenase, glyoxysomal OS=Arabidopsis thaliana GN=At2g22780 PE=2 SV=1	1	---	----	-0,305	0,04941	140,05	14,00%
O23290	60S ribosomal protein L36a OS=Arabidopsis thaliana GN=RPL36AA PE=2 SV=3	2	---	----	0,348	0,05001	141,75	14,10%
Q9FVC8	4-hydroxy-tetrahydrodipicolinate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=DHDPS2 PE=1 SV=2	4	---	----	0,319	0,05041	142,88	14,20%
Q9MAH3	Protein DJ-1 homolog B OS=Arabidopsis thaliana GN=DJ1B PE=1 SV=1	4	---	----	0,313	0,05062	143,48	14,30%
Q39242	Thioredoxin reductase 2 OS=Arabidopsis thaliana GN=NTR2 PE=2 SV=2	6	---	----	0,219	0,05061	143,45	14,30%
O80526	ATP-citrate synthase alpha chain protein 3 OS=Arabidopsis thaliana GN=ACLA-3 PE=2 SV=1	5	---	----	-0,277	0,05122	145,18	14,40%
Q0WPT7	Uncharacterized methyltransferase At2g41040, chloroplastic OS=Arabidopsis thaliana GN=At2g41040 PE=2 SV=1	2	---	----	-0,375	0,05121	145,15	14,40%
Q94CD8	Glucan endo-1,3-beta-glucosidase 4 OS=Arabidopsis thaliana GN=At3g13560 PE=1 SV=1	1	---	----	0,587	0,05181	146,85	14,50%
Q9SU83	Alkaline-phosphatase-like protein OS=Arabidopsis thaliana GN=T16L4.190 PE=2 SV=1	2	---	----	0,57	0,05181	146,85	14,50%
P37271	Phytoene synthase, chloroplastic OS=Arabidopsis thaliana GN=PSY1 PE=2 SV=2	3	---	----	0,411	0,05181	146,85	14,50%
Q39043	Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	2	---	----	0,385	0,05201	147,42	14,50%
P94078	Alpha-mannosidase OS=Arabidopsis thaliana GN=At3g26720 PE=2 SV=1	5	---	----	-0,237	0,05161	146,28	14,50%
O22229	NADPH-dependent thioredoxin reductase 3 OS=Arabidopsis thaliana GN=NTRC PE=1 SV=2	5	---	----	-0,261	0,05201	147,42	14,50%
Q9SMW7	Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=btf3 PE=1 SV=1	6	---	----	0,253	0,05261	149,12	14,60%
Q9M8M7	Acetylornithine aminotransferase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=WIN1 PE=1 SV=1	10	---	----	0,169	0,05201	147,42	14,60%
Q9LHA8	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1	7	---	----	-0,137	0,05221	147,98	14,60%
F4ISP4	Protein ovule abortion 4 OS=Arabidopsis thaliana GN=OVA4 PE=3 SV=1	2	---	----	-0,347	0,05221	147,98	14,60%
P47924	Bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic OS=Arabidopsis thaliana GN=RIBA1 PE=1 SV=2	4	---	----	0,283	0,05302	150,28	14,70%
Q8L6Y1	Ubiquitin carboxyl-terminal hydrolase 14 OS=Arabidopsis thaliana GN=UBP14 PE=1 SV=1	1	---	----	0,851	0,05381	152,52	14,90%
Q9FMN0	Putative uncharacterized protein At5g42890 OS=Arabidopsis thaliana GN=SCP2 PE=2 SV=1	3	---	----	0,28	0,05361	151,95	14,90%
F4HQD4	Heat shock 70 kDa protein 15 OS=Arabidopsis thaliana GN=HSP70-15 PE=1 SV=1	5	---	----	0,205	0,05381	152,52	14,90%
Q42290	Probable mitochondrial-processing peptidase subunit beta OS=Arabidopsis thaliana GN=At3g02090 PE=2 SV=2	18	---	----	0,128	0,05362	151,98	14,90%
P24636	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	2	---	----	0,294	0,05441	154,22	15,10%
Q84VQ4	NAD(P)H-quinone oxidoreductase subunit U, chloroplastic OS=Arabidopsis thaliana GN=ndhU PE=1 SV=1	4	---	----	-0,281	0,05481	155,35	15,20%
Q6NQG3	At1g16790 OS=Arabidopsis thaliana GN=At1g16790 PE=2 SV=1	2	---	----	-0,469	0,05521	156,49	15,20%
Q8H1Y0	Pyruvate dehydrogenase E1 component subunit alpha-2, mitochondrial OS=Arabidopsis thaliana GN=IAR4 PE=1 SV=2	6	---	----	0,219	0,05521	156,49	15,30%
Q42546	SAL1 phosphatase OS=Arabidopsis thaliana GN=SAL1 PE=1 SV=1	8	---	----	0,19	0,05561	157,62	15,30%
rev_F4JRP0	reversed Protein STICHEL-like 3 OS=Arabidopsis thaliana GN=At4g18820 PE=3 SV=1	1	---	----	-0,606	0,05561	157,62	15,30%
O23249	Cyclin-dependent kinases regulatory subunit 1 OS=Arabidopsis thaliana GN=CKS1 PE=1 SV=1	1	---	----	0,608	0,05601	158,76	15,40%
Q9SPE6	Alpha-soluble NSF attachment protein 2 OS=Arabidopsis thaliana GN=ASNAP2 PE=1 SV=1	5	---	----	0,229	0,05621	159,32	15,40%
Q94F20	At5g25460 OS=Arabidopsis thaliana GN=At5g25460 PE=2 SV=1	7	---	----	0,173	0,05601	158,76	15,40%
Q9SJ12	Probable ATP synthase 24 kDa subunit, mitochondrial OS=Arabidopsis thaliana GN=At2g21870 PE=1 SV=1	7	---	----	0,166	0,05641	159,89	15,40%
Q8VZH2	Aminopeptidase M1 OS=Arabidopsis thaliana GN=APM1 PE=1 SV=1	22	---	----	-0,114	0,05581	158,19	15,40%
Q8H1Q1	Thylakoid lumenal protein At1g12250, chloroplastic OS=Arabidopsis thaliana GN=At1g12250 PE=1 SV=1	9	---	----	-0,171	0,05621	159,32	15,40%
Q9LNE6	UDP-glycosyltransferase 89C1 OS=Arabidopsis thaliana GN=UGT89C1 PE=2 SV=1	2	---	----	0,577	0,05661	160,46	15,50%
Q9FI47	Putative uncharacterized protein At5g51010 OS=Arabidopsis thaliana GN=At5g51010 PE=2 SV=1	1	---	----	-0,389	0,05681	161,02	15,50%
Q9SK50	Protein TIC 55, chloroplastic OS=Arabidopsis thaliana GN=TIC55 PE=2 SV=1	10	---	----	-0,155	0,05701	161,59	15,60%
P59231;Q8VZB9	60S ribosomal protein L10a-3 OS=Arabidopsis thaliana GN=RPL10AC PE=1 SV=1	1	---	----	0,409	0,05761	163,29	15,70%
Q9M2U2	Very-long-chain enoyl-CoA reductase OS=Arabidopsis thaliana GN=ECR PE=1 SV=1	4	---	----	0,338	0,05781	163,86	15,70%
Q9LK57	Pentatricopeptide repeat-containing protein At3g13160, mitochondrial OS=Arabidopsis thaliana GN=At3g13160 PE=2 S	1	---	----	0,591	0,05861	166,13	15,80%
Q9SK74	Zinc finger CCCH domain-containing protein 21 OS=Arabidopsis thaliana GN=At2g20280 PE=3 SV=1	3	---	----	0,347	0,05781	163,86	15,80%

O82290	Probable inactive shikimate kinase like 2, chloroplastic OS=Arabidopsis thaliana GN=SKL2 PE=2 SV=2	3	---	----	0,321	0,05841	165,56	15,80%
P93033	Fumarate hydratase 1, mitochondrial OS=Arabidopsis thaliana GN=FUM1 PE=2 SV=2	5	---	----	0,286	0,05842	165,59	15,80%
Q9LUV2	Probable protein Pop3 OS=Arabidopsis thaliana GN=At3g17210 PE=1 SV=1	6	---	----	0,163	0,05821	164,99	15,80%
Q9S9N6	Photosynthetic NDH subunit of subcomplex B 1, chloroplastic OS=Arabidopsis thaliana GN=PNSB1 PE=2 SV=1	9	---	----	-0,161	0,05842	165,59	15,80%
Q9LYR5	Peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic OS=Arabidopsis thaliana GN=FKBP19 PE=1 SV=1	5	---	----	-0,225	0,05801	164,42	15,80%
Q9FFR3;Q9SH69	6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV	3	---	----	-0,292	0,05841	165,56	15,80%
Q9LQK7	Protein ABCI7, chloroplastic OS=Arabidopsis thaliana GN=ABCI7 PE=1 SV=1	3	---	----	0,275	0,05902	167,29	15,90%
Q42586	Uridine 5'-monophosphate synthase OS=Arabidopsis thaliana GN=PYRE-F PE=2 SV=2	6	---	----	0,239	0,05841	165,56	15,90%
Q96291	2-Cys peroxiredoxin BAS1, chloroplastic OS=Arabidopsis thaliana GN=BAS1 PE=1 SV=2	4	---	----	-0,145	0,05901	167,26	15,90%
P35614;Q39097	Eukaryotic peptide chain release factor subunit 1-3 OS=Arabidopsis thaliana GN=ERF1-3 PE=1 SV=1	1	---	----	0,408	0,05941	168,39	16,00%
Q9FMN4	Thioredoxin-like protein Clot OS=Arabidopsis thaliana GN=At5g42850 PE=2 SV=1	2	---	----	0,385	0,05941	168,39	16,00%
Q41975	Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2	1	---	----	-0,36	0,05962	168,99	16,00%
B3H5S2;P10796;P10797	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=At5g38410 PE=3 SV=1	2	---	----	-0,082	0,05981	169,53	16,10%
Q9T029	40S ribosomal protein S25-4 OS=Arabidopsis thaliana GN=RPS25E PE=2 SV=1	1	---	----	0,587	0,06061	171,79	16,20%
O65378	1-aminocyclopropane-1-carboxylate oxidase 3 OS=Arabidopsis thaliana GN=At1g12010 PE=2 SV=1	1	---	----	0,423	0,06081	172,36	16,20%
Q9C500	WPP domain-containing protein 2 OS=Arabidopsis thaliana GN=WPP2 PE=1 SV=1	3	---	----	0,23	0,06081	172,36	16,20%
Q9SCY0	Phosphoglucomutase, chloroplastic OS=Arabidopsis thaliana GN=PGMP PE=1 SV=2	16	---	----	-0,109	0,06082	172,39	16,20%
Q9FY50	50S ribosomal protein L10, chloroplastic OS=Arabidopsis thaliana GN=RPL10 PE=2 SV=1	8	---	----	-0,168	0,06041	171,23	16,20%
Q9FIJ7	Adenylate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At5g47840 PE=1 SV=1	8	---	----	-0,174	0,06101	172,93	16,20%
Q944A7	Probable serine/threonine-protein kinase At4g35230 OS=Arabidopsis thaliana GN=At4g35230 PE=1 SV=1	3	---	----	-0,334	0,06081	172,36	16,20%
O23406;Q9LR44	UDP-glycosyltransferase 75D1 OS=Arabidopsis thaliana GN=UGT75D1 PE=2 SV=2	1	---	----	-0,381	0,06061	171,79	16,20%
Q9C829	Nuclear pore complex protein NUP50A OS=Arabidopsis thaliana GN=NUP50A PE=1 SV=1	1	---	----	-0,638	0,06041	171,23	16,20%
Q8H104	Asx tRNA synthetase (AspRS/AsnRS) class II core domain-contating protein OS=Arabidopsis thaliana GN=At4g26870 PE=	1	---	----	-0,663	0,06021	170,66	16,20%
Q9LX88	40S ribosomal protein S15a-4 OS=Arabidopsis thaliana GN=RPS15AD PE=2 SV=3	1	---	----	0,592	0,06141	174,06	16,30%
Q9FJN8	Ras-related protein RABA4a OS=Arabidopsis thaliana GN=RABA4A PE=1 SV=1	1	---	----	0,41	0,06141	174,06	16,30%
P31167;P40941	ADP,ATP carrier protein 1, mitochondrial OS=Arabidopsis thaliana GN=AAC1 PE=1 SV=2	7	---	----	0,127	0,06121	173,49	16,30%
Q9LYF0	At5g11810 OS=Arabidopsis thaliana GN=T22P22_200 PE=2 SV=1	1	---	----	-0,455	0,06161	174,63	16,30%
Q9LHG9	Nascent polypeptide-associated complex subunit alpha-like protein 1 OS=Arabidopsis thaliana GN=At3g12390 PE=1 SV=	5	---	----	0,207	0,06181	175,20	16,40%
Q8VZB5	Putative uncharacterized protein At5g14260 OS=Arabidopsis thaliana GN=F18O22_50 PE=2 SV=1	9	---	----	-0,169	0,06261	177,46	16,60%
O23365	Cytochrome P450 97B3, chloroplastic OS=Arabidopsis thaliana GN=CYP97B3 PE=2 SV=2	5	---	----	-0,258	0,06301	178,60	16,60%
O48717	At2g26500 OS=Arabidopsis thaliana GN=At2g26500 PE=2 SV=1	1	---	----	-0,283	0,06281	178,03	16,60%
Q944G9	Probable fructose-bisphosphate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=FBA2 PE=1 SV=2	12	---	----	-0,092	0,06382	180,89	16,70%
P56798	30S ribosomal protein S3, chloroplastic OS=Arabidopsis thaliana GN=rps3 PE=3 SV=1	9	---	----	-0,154	0,06361	180,30	16,70%
Q27GI3	Nucleobase-ascorbate transporter 6 OS=Arabidopsis thaliana GN=NAT6 PE=2 SV=2	2	---	----	-0,304	0,06362	180,33	16,70%
Q1G3L2	Polyketide cyclase / dehydrase and lipid transport protein OS=Arabidopsis thaliana GN=At4g01883 PE=2 SV=1	3	---	----	-0,322	0,06321	179,16	16,70%
F4J8X6	Nuclear transport factor 2 and RNA recognition motif domain-containing protein OS=Arabidopsis thaliana GN=At3g251	1	---	----	-1,06	0,06321	179,16	16,70%
P29514	Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1	1	---	----	0,411	0,06421	182,00	16,80%
Q9SGR6	AT1G76160 protein OS=Arabidopsis thaliana GN=sks5 PE=2 SV=1	6	---	----	0,196	0,06361	180,30	16,80%
Q41931	1-aminocyclopropane-1-carboxylate oxidase 2 OS=Arabidopsis thaliana GN=ACO2 PE=2 SV=2	7	---	----	0,162	0,06421	182,00	16,80%
O23553	Beta-amylase 3, chloroplastic OS=Arabidopsis thaliana GN=BAM3 PE=1 SV=3	10	---	----	0,16	0,06381	180,86	16,80%
P46248	Aspartate aminotransferase, chloroplastic OS=Arabidopsis thaliana GN=ASP5 PE=1 SV=2	19	---	----	0,089	0,06421	182,00	16,80%
O64903	Nucleoside diphosphate kinase II, chloroplastic OS=Arabidopsis thaliana GN=NDPK2 PE=1 SV=2	6	---	----	-0,186	0,06441	182,56	16,80%
Q9ZVJ4	Peptidyl-prolyl cis-trans isomerase CYP22 OS=Arabidopsis thaliana GN=CYP22 PE=1 SV=1	1	---	----	-0,522	0,06401	181,43	16,80%
Q9ZUG4	Methylthioribose-1-phosphate isomerase OS=Arabidopsis thaliana GN=At2g05830 PE=1 SV=2	5	---	----	0,24	0,06501	184,27	16,90%
Q9SF40	60S ribosomal protein L4-1 OS=Arabidopsis thaliana GN=RPL4A PE=2 SV=1	4	---	----	0,194	0,06461	183,13	16,90%
Q944G9;Q9SJU4	Probable fructose-bisphosphate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=FBA2 PE=1 SV=2	5	---	----	-0,09	0,06462	183,16	16,90%
Q9ZUX0	At2g27680/F15K20.22 OS=Arabidopsis thaliana GN=At2g27680 PE=2 SV=1	6	---	----	-0,187	0,06522	184,86	16,90%
Q9M1X2	Fatty-acid-binding protein 1 OS=Arabidopsis thaliana GN=FAP1 PE=1 SV=1	4	---	----	-0,328	0,06481	183,70	16,90%
Q9MAT3	F13M7.16 protein OS=Arabidopsis thaliana GN=F13M7.16 PE=2 SV=1	2	---	----	0,564	0,06541	185,40	17,00%
O64948	Lon protease homolog 2, peroxisomal OS=Arabidopsis thaliana GN=LON2 PE=2 SV=1	1	---	----	-0,916	0,06521	184,83	17,00%
Q9FPS3	Ubiquitin carboxyl-terminal hydrolase 24 OS=Arabidopsis thaliana GN=UBP24 PE=1 SV=1	1	---	----	-1,707	0,06541	185,40	17,00%
P57106;P93819	Malate dehydrogenase, cytoplasmic 2 OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1	5	---	----	0,139	0,06601	187,10	17,10%
P56753	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic OS=Arabidopsis thaliana GN=ndhH PE=1 SV=1	10	---	----	-0,155	0,06601	187,10	17,10%
P56801	30S ribosomal protein S8, chloroplastic OS=Arabidopsis thaliana GN=rps8 PE=3 SV=1	5	---	----	-0,172	0,06621	187,67	17,10%
Q94K52	Putative uncharacterized protein At1g02475 OS=Arabidopsis thaliana GN=At1g02475 PE=2 SV=1	3	---	----	-0,285	0,06602	187,13	17,10%

rev_Q9SJ62	reversed At2g35880/F11F19.21 OS=Arabidopsis thaliana GN=At2g35880 PE=2 SV=2	1	---	----	0,624	0,06681	189,37	17,20%
Q9M339	40S ribosomal protein S3-2 OS=Arabidopsis thaliana GN=RPS3B PE=1 SV=1	3	---	----	0,34	0,06721	190,50	17,30%
F4IAX0	Putative copper amine oxidase OS=Arabidopsis thaliana GN=At1g31690 PE=3 SV=1	2	---	----	-0,539	0,06721	190,50	17,30%
Q5GM68	Phosphoenolpyruvate carboxylase 2 OS=Arabidopsis thaliana GN=PPC2 PE=1 SV=2	25	---	----	0,092	0,06741	191,07	17,40%
O64818	Uncharacterized protein At2g23090 OS=Arabidopsis thaliana GN=At2g23090 PE=1 SV=1	1	---	----	0,624	0,06861	194,47	17,50%
O04905;Q8VY84	UMP-CMP kinase 3 OS=Arabidopsis thaliana GN=UMK3 PE=1 SV=1	1	---	----	0,489	0,06842	193,93	17,50%
Q9XF88	Chlorophyll a-b binding protein CP29.2, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.2 PE=1 SV=1	7	---	----	-0,14	0,06821	193,34	17,50%
P92963	Ras-related protein RABB1c OS=Arabidopsis thaliana GN=RABB1C PE=1 SV=1	4	---	----	-0,258	0,06802	192,80	17,50%
Q8VXY0	Expressed protein OS=Arabidopsis thaliana GN=At2g36145 PE=2 SV=1	4	---	----	-0,269	0,06841	193,90	17,50%
Q9LPN5	At3g10640 OS=Arabidopsis thaliana GN=F18K10.26 PE=2 SV=1	1	---	----	0,749	0,06861	194,47	17,60%
P48006;Q84WM9;Q9SCX	Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2	1	---	----	0,372	0,06861	194,47	17,60%
Q9AV97	2-dehydro-3-deoxyphosphooctonate aldolase 1 OS=Arabidopsis thaliana GN=KDSA1 PE=1 SV=2	2	---	----	0,339	0,06901	195,60	17,60%
Q9LFW1	UDP-arabinopyranose mutase 2 OS=Arabidopsis thaliana GN=RGP2 PE=1 SV=1	6	---	----	0,215	0,06841	193,90	17,60%
Q9SZB2	Protein TIC 22, chloroplastic OS=Arabidopsis thaliana GN=TIC22 PE=1 SV=1	6	---	----	-0,22	0,06921	196,17	17,70%
Q9SA56	Photosystem I reaction center subunit II-2, chloroplastic OS=Arabidopsis thaliana GN=PSAD2 PE=1 SV=1	1	---	----	-0,262	0,06941	196,74	17,70%
P22197	Fructose-bisphosphate aldolase, cytoplasmic isozyme OS=Arabidopsis thaliana GN=At4g26520 PE=2 SV=2	1	---	----	-0,512	0,06961	197,30	17,70%
Q39099	Xyloglucan endotransglucosylase/hydrolase protein 4 OS=Arabidopsis thaliana GN=XTH4 PE=1 SV=1	4	---	----	0,231	0,07021	199,00	17,80%
Q9SDS7	V-type proton ATPase subunit C OS=Arabidopsis thaliana GN=VHA-C PE=1 SV=1	13	---	----	-0,125	0,06981	197,87	17,80%
Q9FL44	Proline-rich family protein OS=Arabidopsis thaliana GN=At5g07020 PE=2 SV=1	3	---	----	-0,183	0,07001	198,44	17,80%
Q9FW48	Leucine-rich repeat-containing protein OS=Arabidopsis thaliana GN=T1E4.2 PE=4 SV=1	4	---	----	-0,202	0,07002	198,47	17,80%
O48832	Probable senescence related protein OS=Arabidopsis thaliana GN=ERD7 PE=1 SV=1	1	---	----	1,016	0,07061	200,14	17,90%
Q8LBI1	60S ribosomal protein L5-1 OS=Arabidopsis thaliana GN=ATL5 PE=2 SV=2	1	---	----	0,291	0,07081	200,71	17,90%
Q9C909	Glycine-rich RNA-binding protein 5, mitochondrial OS=Arabidopsis thaliana GN=RBG5 PE=2 SV=1	2	---	----	0,279	0,07061	200,14	17,90%
Q93ZG7	DEAD-box ATP-dependent RNA helicase 38 OS=Arabidopsis thaliana GN=RH38 PE=1 SV=2	4	---	----	0,274	0,07042	199,60	17,90%
Q9FNC9	Mitochondrial import receptor subunit TOM9-2 OS=Arabidopsis thaliana GN=TOM9-2 PE=1 SV=3	3	---	----	0,244	0,07061	200,14	17,90%
Q9SUT5	Protein SGT1 homolog B OS=Arabidopsis thaliana GN=SGT1B PE=1 SV=1	4	---	----	0,241	0,07122	201,87	17,90%
O65902	Cyclase-associated protein 1 OS=Arabidopsis thaliana GN=CAP1 PE=2 SV=1	5	---	----	0,233	0,07141	202,41	17,90%
P19456;P20431;P20649;C	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	5	---	----	0,183	0,07101	201,27	17,90%
Q9T0H1	At4g13500 OS=Arabidopsis thaliana GN=T6G15.50 PE=2 SV=1	3	---	----	-0,248	0,07121	201,84	17,90%
Q9FK25	Flavone 3'-O-methyltransferase 1 OS=Arabidopsis thaliana GN=OMT1 PE=1 SV=1	6	---	----	0,202	0,07161	202,97	18,00%
P56805	30S ribosomal protein S15, chloroplastic OS=Arabidopsis thaliana GN=rps15 PE=3 SV=1	4	---	----	-0,211	0,07161	202,97	18,00%
Q9C554	Expansin-A1 OS=Arabidopsis thaliana GN=EXPA1 PE=2 SV=1	2	---	----	-0,391	0,07141	202,41	18,00%
Q9SZW7	GDSL esterase/lipase At4g30140 OS=Arabidopsis thaliana GN=At4g30140 PE=2 SV=1	2	---	----	-0,397	0,07121	201,84	18,00%
Q9SU93	Putative uncharacterized protein AT4g29520 OS=Arabidopsis thaliana GN=T16L4.30 PE=4 SV=1	1	---	----	0,628	0,07241	205,24	18,10%
O22914	Calvin cycle protein CP12-1, chloroplastic OS=Arabidopsis thaliana GN=CP12-1 PE=1 SV=1	2	---	----	0,241	0,07241	205,24	18,10%
Q9FLT0	100 kDa coactivator-like protein OS=Arabidopsis thaliana GN=Tudor2 PE=2 SV=1	9	---	----	0,209	0,07301	206,94	18,20%
Q9XF89	Chlorophyll a-b binding protein CP26, chloroplastic OS=Arabidopsis thaliana GN=LHCB5 PE=1 SV=1	17	---	----	-0,057	0,07281	206,37	18,20%
O80565	Outer envelope pore protein 37, chloroplastic OS=Arabidopsis thaliana GN=OEP37 PE=2 SV=2	2	---	----	-0,29	0,07301	206,94	18,20%
P51418	60S ribosomal protein L18a-2 OS=Arabidopsis thaliana GN=RPL18AB PE=2 SV=2	2	---	----	0,234	0,07341	208,07	18,30%
P14671	Tryptophan synthase beta chain 1, chloroplastic OS=Arabidopsis thaliana GN=TSB1 PE=2 SV=1	7	---	----	0,19	0,07342	208,10	18,30%
rev_Q9SL03	reversed Callose synthase 2 OS=Arabidopsis thaliana GN=CALS2 PE=2 SV=3	1	---	----	-0,556	0,07341	208,07	18,30%
Q9FF98	AT5g23820/MRO11_14 OS=Arabidopsis thaliana GN=UQI3 PE=2 SV=1	3	---	----	-0,187	0,07401	209,78	18,40%
Q8RWU7	Plant UBX domain-containing protein 4 OS=Arabidopsis thaliana GN=PUX4 PE=1 SV=1	1	---	----	-0,532	0,07401	209,78	18,40%
O65396	Aminomethyltransferase, mitochondrial OS=Arabidopsis thaliana GN=GDCST PE=2 SV=1	15	---	----	0,083	0,07461	211,48	18,50%
P82538	PsbP-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=PPL1 PE=1 SV=1	7	---	----	-0,152	0,07521	213,18	18,60%
Q9SUY2	AT3g52230/F4F15_340 OS=Arabidopsis thaliana GN=F4F15.340 PE=2 SV=1	4	---	----	-0,24	0,07502	212,64	18,60%
Q7Y1Z8	Malonyl-CoA decarboxylase OS=Arabidopsis thaliana GN=At4g04320 PE=2 SV=1	2	---	----	-0,519	0,07481	212,04	18,60%
rev_Q0WM93	reversed AAA-type ATPase family protein OS=Arabidopsis thaliana GN=At4g02480 PE=2 SV=1	1	---	----	0,43	0,07561	214,31	18,70%
Q940G0	Transmembrane 9 superfamily member 1 OS=Arabidopsis thaliana GN=TMN1 PE=1 SV=1	2	---	----	0,406	0,07541	213,74	18,70%
O24412	26S proteasome non-ATPase regulatory subunit 7 homolog A OS=Arabidopsis thaliana GN=RPN8A PE=1 SV=1	5	---	----	0,27	0,07601	215,44	18,80%
F4J3M2	Plastid transcriptionally active 3 OS=Arabidopsis thaliana GN=PTAC3 PE=4 SV=1	2	---	----	0,538	0,07661	217,14	18,90%
P25856;P25857;Q9LPW0	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3	3	---	----	-0,104	0,07641	216,58	18,90%
Q43127;Q8LCE1	Glutamine synthetase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLN2 PE=1 SV=1	2	---	----	0,267	0,07721	218,85	19,00%
Q29Q34	Alcohol dehydrogenase-like protein OS=Arabidopsis thaliana GN=At5g19440 PE=2 SV=1	4	---	----	0,24	0,07782	220,57	19,20%
Q680K2	Haloacid dehalogenase-like hydrolase domain-containing protein At4g39970 OS=Arabidopsis thaliana GN=At4g39970 P	5	---	----	-0,225	0,07842	222,27	19,20%

Q8GZ51	At5g62720 OS=Arabidopsis thaliana GN=At5g62720 PE=2 SV=1	2	---	----	-0,347	0,07821	221,68	19,20%
F4JB05	Ribosomal protein S5/Elongation factor G/III/V family protein OS=Arabidopsis thaliana GN=At3g12915 PE=4 SV=1	2	---	----	0,5	0,07901	223,95	19,30%
Q9LIN3	Glycine-rich RNA-binding protein RZ1A OS=Arabidopsis thaliana GN=RZ1A PE=1 SV=1	2	---	----	0,404	0,07861	222,81	19,30%
O80574;Q8LB01	4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic OS=Arabidopsis thaliana GN=DAPB1 PE=2 SV=2	2	---	----	-0,345	0,07881	223,38	19,30%
Q9FFW8	Tryptophan synthase beta chain OS=Arabidopsis thaliana GN=TSBtype2 PE=2 SV=1	2	---	----	-0,373	0,07881	223,38	19,30%
Q9SKY8	Heat shock 70 kDa protein 8 OS=Arabidopsis thaliana GN=HSP70-8 PE=1 SV=1	1	---	----	-0,537	0,07841	222,25	19,30%
F4JD67	Proline-rich family protein OS=Arabidopsis thaliana GN=At3g06870 PE=4 SV=1	1	---	----	-0,566	0,07841	222,25	19,30%
Q9ZNT1	NADH--cytochrome b5 reductase 1 OS=Arabidopsis thaliana GN=CBR1 PE=1 SV=1	2	---	----	0,416	0,07921	224,51	19,40%
Q2HIK4	At1g29990 OS=Arabidopsis thaliana GN=PFD6 PE=2 SV=1	2	---	----	0,276	0,07941	225,08	19,40%
O82487	Phosphoenolpyruvate carboxylase family protein OS=Arabidopsis thaliana GN=T12H20.10 PE=1 SV=1	3	---	----	-0,315	0,07961	225,65	19,40%
Q9SYX1	AT4g17600/dl4835w OS=Arabidopsis thaliana GN=Lil3:1 PE=2 SV=1	5	---	----	0,192	0,07981	226,21	19,50%
O49403	Heat stress transcription factor A-4a OS=Arabidopsis thaliana GN=HSFA4A PE=2 SV=1	1	---	----	0,567	0,08041	227,92	19,60%
Q39102	ATP-dependent zinc metalloprotease FTSH 1, chloroplastic OS=Arabidopsis thaliana GN=FTSH1 PE=1 SV=2	5	---	----	-0,228	0,08082	229,08	19,60%
P92941	Chloride channel protein CLC-a OS=Arabidopsis thaliana GN=CLC-A PE=1 SV=2	1	---	----	-0,381	0,08061	228,48	19,60%
Q8VZK2	Translation machinery-associated protein 22 OS=Arabidopsis thaliana GN=At5g11900 PE=2 SV=1	2	---	----	0,404	0,08141	230,75	19,70%
Q9FHX5	Glucan endo-1,3-beta-glucosidase 10 OS=Arabidopsis thaliana GN=At5g42100 PE=1 SV=1	3	---	----	0,271	0,08121	230,18	19,70%
Q43725	Cysteine synthase, mitochondrial OS=Arabidopsis thaliana GN=OASC PE=1 SV=3	6	---	----	0,209	0,08142	230,78	19,70%
Q9S7H1	Photosystem I reaction center subunit II-1, chloroplastic OS=Arabidopsis thaliana GN=psaD1 PE=1 SV=1	1	---	----	-0,264	0,08102	229,64	19,70%
Q9LI74	Protein CHUP1, chloroplastic OS=Arabidopsis thaliana GN=CHUP1 PE=1 SV=1	1	SKDDSSVQSSPSR	Phospho S10	-1,387	0,08141	230,75	19,70%
O23240	D-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=D2HGDH PE=1 SV=3	3	---	----	-0,429	0,08182	231,91	19,80%
Q9LF41	Probable ubiquitin conjugation factor E4 OS=Arabidopsis thaliana GN=PUB1 PE=2 SV=1	1	---	----	0,852	0,08281	234,72	19,90%
Q9FMD5	Protein TIC 40, chloroplastic OS=Arabidopsis thaliana GN=TIC40 PE=1 SV=1	8	---	----	0,147	0,08241	233,58	19,90%
Q949Q5	Photosystem I subunit O OS=Arabidopsis thaliana GN=PSAO PE=1 SV=1	2	---	----	-0,188	0,08261	234,15	19,90%
C0LGG8	Probable LRR receptor-like serine/threonine-protein kinase At1g53430 OS=Arabidopsis thaliana GN=At1g53430 PE=1 S	4	---	----	-0,29	0,08221	233,02	19,90%
Q9LRP1	Novel plant SNARE 13 OS=Arabidopsis thaliana GN=NPSN13 PE=1 SV=1	1	---	----	-0,519	0,08242	233,61	19,90%
Q9ZUF6	Putative subtilisin serine protease OS=Arabidopsis thaliana GN=At2g05920 PE=2 SV=1	2	---	----	0,425	0,08381	237,55	20,10%
Q39129	Thiosulfate sulfurtransferase 16, chloroplastic OS=Arabidopsis thaliana GN=STR16 PE=1 SV=2	2	---	----	0,322	0,08341	236,42	20,10%
O23627	Glycine--tRNA ligase 1, mitochondrial OS=Arabidopsis thaliana GN=GLYRS-1 PE=2 SV=1	20	---	----	0,097	0,08341	236,42	20,10%
P56761	Photosystem II D2 protein OS=Arabidopsis thaliana GN=psbD PE=1 SV=3	10	---	----	0,079	0,08362	237,01	20,10%
Q94C48	Putative uncharacterized protein At4g32330 OS=Arabidopsis thaliana GN=At4g32330 PE=1 SV=1	1	---	----	0,544	0,08421	238,69	20,20%
O48661;Q9ZUB3	Spermidine synthase 2 OS=Arabidopsis thaliana GN=SPDSYN2 PE=1 SV=2	2	---	----	0,257	0,08421	238,69	20,20%
Q08112;Q9FY64	40S ribosomal protein S15-1 OS=Arabidopsis thaliana GN=RPS15A PE=2 SV=1	3	---	----	0,191	0,08421	238,69	20,20%
F4KAK0	Tautomerase/MIF superfamily protein OS=Arabidopsis thaliana GN=At5g57170 PE=4 SV=1	1	---	----	-0,32	0,08501	240,95	20,30%
Q66GJ1	At4g12320 OS=Arabidopsis thaliana GN=CYP706A6 PE=2 SV=1	1	---	----	0,611	0,08621	244,36	20,50%
Q9SUT9	Reticulon-like protein B2 OS=Arabidopsis thaliana GN=RTNLB2 PE=1 SV=1	1	---	----	0,462	0,08641	244,92	20,50%
Q9FFP6;Q9FNN1	Pyruvate kinase OS=Arabidopsis thaliana GN=At5g63680 PE=3 SV=1	2	---	----	0,342	0,08641	244,92	20,50%
Q9LST0	AT5g60160/f15l12_20 OS=Arabidopsis thaliana GN=At5g60160 PE=2 SV=1	4	---	----	0,321	0,08601	243,79	20,50%
O04603	50S ribosomal protein L5, chloroplastic OS=Arabidopsis thaliana GN=RPL5 PE=2 SV=1	11	---	----	-0,109	0,08621	244,36	20,50%
Q9SZ53	Probable protein phosphatase 2C 60 OS=Arabidopsis thaliana GN=At4g31860 PE=2 SV=1	1	---	----	-0,372	0,08561	242,65	20,50%
Q93Z72	AT5g16970/F2K13_120 OS=Arabidopsis thaliana GN=At5g17000 PE=2 SV=1	3	---	----	0,371	0,08621	244,36	20,60%
Q9STG6	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Arabidopsis thaliana GN=DUT PE=1 SV=1	2	---	----	0,335	0,08681	246,06	20,60%
Q0WP12	Thiocyanate methyltransferase 1 OS=Arabidopsis thaliana GN=HOL1 PE=1 SV=1	8	---	----	0,157	0,08621	244,36	20,60%
Q9SIK2	40S ribosomal protein S25-2 OS=Arabidopsis thaliana GN=RPS25B PE=2 SV=1	1	---	----	0,52	0,08741	247,76	20,70%
Q9S9N1	Heat shock 70 kDa protein 5 OS=Arabidopsis thaliana GN=HSP70-5 PE=2 SV=1	1	---	----	0,388	0,08781	248,89	20,70%
Q2V2S7	NAD(P)H-quinone oxidoreductase subunit M, chloroplastic OS=Arabidopsis thaliana GN=ndhM PE=2 SV=1	3	---	----	0,241	0,08762	248,35	20,70%
P42825;Q94AW8	Chaperone protein dnaJ 2 OS=Arabidopsis thaliana GN=ATJ2 PE=1 SV=2	5	---	----	0,182	0,08721	247,19	20,70%
Q8H7F6	Bifunctional monothiol glutaredoxin-S16, chloroplastic OS=Arabidopsis thaliana GN=GRXS16 PE=1 SV=2	8	---	----	0,174	0,08802	249,49	20,70%
P56777	Photosystem II CP47 reaction center protein OS=Arabidopsis thaliana GN=psbB PE=1 SV=1	15	---	----	0,059	0,08781	248,89	20,70%
O80796	Membrane-associated protein VIPP1, chloroplastic OS=Arabidopsis thaliana GN=VIPP1 PE=1 SV=1	12	---	----	-0,107	0,08721	247,19	20,70%
Q8L866	Copper amine oxidase family protein OS=Arabidopsis thaliana GN=At2g42490 PE=2 SV=1	2	---	----	-0,331	0,08761	248,32	20,70%
Q9C9Z2	Putative uncharacterized protein At3g08640 OS=Arabidopsis thaliana GN=F17O14.11 PE=2 SV=1	2	---	----	0,38	0,08821	250,02	20,80%
Q9T0P4;Q9ZNZ7	Ferredoxin-dependent glutamate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=GLU2 PE=1 SV=2	6	---	----	-0,144	0,08802	249,49	20,80%
Q9CAK8	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=ISPF PE=1 SV=1	4	---	----	-0,223	0,08861	251,16	20,80%
Q9FHY8	At5g41950 OS=Arabidopsis thaliana GN=At5g41950 PE=1 SV=1	2	---	----	0,405	0,08882	251,75	20,90%
Q96255;Q9SHP0	Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1	5	---	----	0,202	0,08921	252,86	20,90%

Q944G6	AT4g03150/F4C21_7 OS=Arabidopsis thaliana GN=At4g03150 PE=2 SV=1	1	---	----	0,532	0,08941	253,43	21,00%
Q08112	40S ribosomal protein S15-1 OS=Arabidopsis thaliana GN=RPS15A PE=2 SV=1	1	---	----	0,312	0,08961	253,99	21,00%
Q8RWG1	Uncharacterized aarF domain-containing protein kinase At4g31390, chloroplastic OS=Arabidopsis thaliana GN=At4g31	12	---	----	-0,16	0,08961	253,99	21,00%
B3LFA4;F4IPY2	At5g38830 OS=Arabidopsis thaliana GN=At5g38830 PE=2 SV=1	1	---	----	-0,373	0,08941	253,43	21,00%
O22446	Histone deacetylase 19 OS=Arabidopsis thaliana GN=HDA19 PE=1 SV=2	1	---	----	1,144	0,09021	255,69	21,10%
O48588	Molybdenum cofactor sulfurase family protein OS=Arabidopsis thaliana GN=T19K24.17 PE=2 SV=1	2	---	----	0,38	0,09021	255,69	21,10%
Q05728	Phosphoribosylformylglycinamidine cyclo-ligase, chloroplastic OS=Arabidopsis thaliana GN=PUR5 PE=1 SV=2	4	---	----	-0,28	0,09042	256,29	21,10%
Q9T0A4	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic OS=Arabidopsis thaliana GN=ndhS PE=1 SV=1	8	---	----	-0,153	0,09101	257,96	21,20%
P23686;Q9LUT2	S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2	1	---	----	0,539	0,09121	258,53	21,30%
O64888	Ribose-phosphate pyrophosphokinase 5, chloroplastic OS=Arabidopsis thaliana GN=PRS5 PE=2 SV=2	1	---	----	-0,578	0,09141	259,09	21,30%
O49460	Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1	4	---	----	0,234	0,09221	261,36	21,40%
P42760;P46422	Glutathione S-transferase F6 OS=Arabidopsis thaliana GN=GSTF6 PE=2 SV=2	1	---	----	0,376	0,09281	263,06	21,50%
Q8RY94	Adenylosuccinate lyase OS=Arabidopsis thaliana GN=At4g18440 PE=2 SV=1	5	---	----	0,176	0,09221	261,36	21,50%
Q9C7M2	Putative uncharacterized protein F14C21.55 OS=Arabidopsis thaliana GN=F14C21.55 PE=1 SV=1	1	---	----	-0,473	0,09241	261,93	21,50%
Q9SUI6	Photosystem I reaction center subunit VI-2, chloroplastic OS=Arabidopsis thaliana GN=PSAH2 PE=2 SV=1	2	---	----	-0,311	0,09341	264,76	21,60%
Q8LPQ6	ABC transporter B family member 28 OS=Arabidopsis thaliana GN=ABCB28 PE=2 SV=1	6	---	----	-0,229	0,09341	264,76	21,70%
Q6ICZ8	Nascent polypeptide-associated complex subunit alpha-like protein 3 OS=Arabidopsis thaliana GN=At5g13850 PE=1 SV	1	---	----	0,369	0,09401	266,46	21,80%
Q0WRJ7	Peptidyl-prolyl cis-trans isomerase FKBP20-2, chloroplastic OS=Arabidopsis thaliana GN=FKBP20-2 PE=1 SV=1	2	---	----	-0,36	0,09421	267,03	21,80%
O04619	Mitochondrial adenine nucleotide transporter ADNT1 OS=Arabidopsis thaliana GN=ADNT1 PE=2 SV=1	1	---	----	0,512	0,09461	268,16	21,90%
Q9SA34	Inosine-5'-monophosphate dehydrogenase 2 OS=Arabidopsis thaliana GN=At1g16350 PE=1 SV=1	5	---	----	0,199	0,09561	271,00	21,90%
Q9LVM2	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic OS=Arabidopsis thaliana GN=ndhN PE=2 SV=1	5	---	----	-0,204	0,09522	269,89	21,90%
Q9LVA4	Invertase/pectin methylesterase inhibitor family protein / DC 1.2-like protein OS=Arabidopsis thaliana GN=MMI9.18 PE	1	---	----	-0,372	0,09461	268,16	21,90%
Q39218	Serine acetyltransferase 3, mitochondrial OS=Arabidopsis thaliana GN=SAT3 PE=1 SV=3	1	---	----	0,607	0,09561	271,00	22,00%
Q9ZRE2	Ras-related protein RABD1 OS=Arabidopsis thaliana GN=RABD1 PE=1 SV=1	2	---	----	0,554	0,09541	270,43	22,00%
Q9LXM8	60S acidic ribosomal protein P2-4 OS=Arabidopsis thaliana GN=RPP2D PE=2 SV=1	1	---	----	0,391	0,09602	272,16	22,00%
Q9M3D2;Q9SF53	60S ribosomal protein L35-3 OS=Arabidopsis thaliana GN=RPL35C PE=2 SV=1	1	---	----	0,296	0,09561	271,00	22,00%
Q9SZA3	Eukaryotic translation initiation factor 3 subunit K OS=Arabidopsis thaliana GN=TIF3K1 PE=2 SV=1	3	---	----	0,296	0,09581	271,57	22,00%
Q8GYL5;Q9SIK2;Q9T029	40S ribosomal protein S25-3 OS=Arabidopsis thaliana GN=RPS25D PE=3 SV=2	2	---	----	0,265	0,09521	269,86	22,00%
O80585	Methylenetetrahydrofolate reductase 2 OS=Arabidopsis thaliana GN=MTHFR2 PE=1 SV=2	9	---	----	0,178	0,09561	271,00	22,00%
O80439	30S ribosomal protein S31, chloroplastic OS=Arabidopsis thaliana GN=RPS31 PE=1 SV=1	3	---	----	0,162	0,09522	269,89	22,00%
F4IT21	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g43945 PE=4 SV=1	3	---	----	-0,243	0,09661	273,83	22,10%
P24101;Q9SMU8	Peroxidase 33 OS=Arabidopsis thaliana GN=PER33 PE=1 SV=1	1	---	----	-0,278	0,09682	274,43	22,10%
P83755	Photosystem II protein D1 OS=Arabidopsis thaliana GN=psbA PE=1 SV=2	7	---	----	0,075	0,09701	274,97	22,20%
Q9STW6	Heat shock 70 kDa protein 6, chloroplastic OS=Arabidopsis thaliana GN=HSP70-6 PE=1 SV=1	12	---	----	-0,091	0,09741	276,10	22,20%
Q9C522	ATP-citrate synthase beta chain protein 1 OS=Arabidopsis thaliana GN=ACLB-1 PE=2 SV=1	12	---	----	0,155	0,09781	277,23	22,30%
Q8LFC0	Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial OS=Arabidopsis thaliana GN=IDH1 PE=2 SV=2	3	---	----	0,259	0,09841	278,93	22,40%
Q9M9W1	60S ribosomal protein L22-2 OS=Arabidopsis thaliana GN=RPL22B PE=2 SV=1	2	---	----	0,254	0,09842	278,96	22,40%
Q94A94	Diaminopimelate decarboxylase 2, chloroplastic OS=Arabidopsis thaliana GN=LYSA2 PE=2 SV=1	3	---	----	0,239	0,09802	277,83	22,40%
Q9SK39	Probable steroid-binding protein 3 OS=Arabidopsis thaliana GN=MP3 PE=1 SV=1	4	---	----	0,187	0,09882	280,10	22,40%
Q38798	Calnexin homolog 2 OS=Arabidopsis thaliana GN=At5g07340 PE=2 SV=2	2	---	----	-0,447	0,09841	278,93	22,40%
F4I2A0	Prolyl oligopeptidase OS=Arabidopsis thaliana GN=At1g76140 PE=4 SV=1	5	---	----	0,243	0,09881	280,07	22,50%
Q9FEC1	At1g34000/F12G12_210 OS=Arabidopsis thaliana GN=T15K4.5 PE=2 SV=1	2	---	----	-0,298	0,09901	280,64	22,50%
Q9SLJ2	At1g54410 OS=Arabidopsis thaliana GN=F20D21.23 PE=2 SV=1	1	---	----	0,347	0,09981	282,90	22,60%
Q8LD03	40S ribosomal protein S7-3 OS=Arabidopsis thaliana GN=RPS7C PE=1 SV=2	5	---	----	0,225	0,10082	285,77	22,80%
P54609	Cell division control protein 48 homolog A OS=Arabidopsis thaliana GN=CDC48A PE=1 SV=1	5	---	----	0,25	0,10101	286,30	22,90%
Q9SZ11	Glycerophosphodiester phosphodiesterase GDPDL3 OS=Arabidopsis thaliana GN=GDPDL3 PE=1 SV=3	7	---	----	-0,164	0,10141	287,44	22,90%
Q9SR67	AT3g10020/T22K18_16 OS=Arabidopsis thaliana GN=T22K18.16 PE=2 SV=1	2	---	----	-0,317	0,10142	287,47	22,90%
F4HRY1	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g73650 PE=4 SV=1	1	---	----	-0,537	0,10102	286,33	22,90%
Q9SR62	Putative uncharacterized protein At3g09970 OS=Arabidopsis thaliana GN=T22K18.22 PE=2 SV=1	1	---	----	0,526	0,10219	289,65	23,00%
P48491;Q9SKP6	Triosephosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=CTIMC PE=1 SV=2	1	---	----	0,251	0,10241	290,27	23,00%
Q9SPK5	Formate--tetrahydrofolate ligase OS=Arabidopsis thaliana GN=THFS PE=2 SV=1	12	---	----	0,114	0,10201	289,14	23,00%
Q9XQC7	GrpE protein homolog OS=Arabidopsis thaliana GN=grpE PE=2 SV=1	12	---	----	-0,112	0,10221	289,71	23,00%
Q39172	NADP-dependent alkenal double bond reductase P1 OS=Arabidopsis thaliana GN=P1 PE=1 SV=1	5	---	----	-0,199	0,10241	290,27	23,00%
Q8S8R9	At2g34585 OS=Arabidopsis thaliana GN=At2g34580 PE=1 SV=1	1	---	----	-0,465	0,10261	290,84	23,00%
O82299	Putative chloroplast RNA binding protein OS=Arabidopsis thaliana GN=At2g35410 PE=1 SV=1	7	---	----	-0,145	0,10241	290,27	23,10%

Q96251	ATP synthase subunit O, mitochondrial OS=Arabidopsis thaliana GN=At5g13450 PE=1 SV=2	7	---	----	-0,161	0,10321	292,54	23,10%
Q8RXX5;Q8W463	50S ribosomal protein L19-2, chloroplastic OS=Arabidopsis thaliana GN=At5g47190 PE=2 SV=1	2	---	----	-0,217	0,10301	291,97	23,10%
F4II29	Cytoplasmic tRNA export protein OS=Arabidopsis thaliana GN=At2g40730 PE=1 SV=1	1	---	----	0,545	0,10361	293,67	23,20%
Q8GWE0	Pentatricopeptide repeat-containing protein At4g16390, chloroplastic OS=Arabidopsis thaliana GN=P67 PE=1 SV=3	2	---	----	0,33	0,10361	293,67	23,20%
O03042	Ribulose bisphosphate carboxylase large chain OS=Arabidopsis thaliana GN=rbcL PE=1 SV=1	32	---	----	-0,031	0,10341	293,11	23,20%
Q9SMX3	Mitochondrial outer membrane protein porin 3 OS=Arabidopsis thaliana GN=VDAC3 PE=1 SV=3	9	---	----	0,112	0,10409	295,04	23,30%
P23321	Oxygen-evolving enhancer protein 1-1, chloroplastic OS=Arabidopsis thaliana GN=PSBO1 PE=1 SV=2	10	---	----	0,076	0,10421	295,37	23,30%
Q56XG6	DEAD-box ATP-dependent RNA helicase 15 OS=Arabidopsis thaliana GN=RH15 PE=1 SV=3	5	---	----	0,212	0,10541	298,78	23,50%
O23593;Q9LVT8	AT4g17520/dl4795w OS=Arabidopsis thaliana GN=dl4795w PE=1 SV=1	2	---	----	0,229	0,10562	299,37	23,60%
Q8H107;Q9FLQ4	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	4	---	----	0,174	0,10641	301,61	23,60%
P42732	30S ribosomal protein S13, chloroplastic OS=Arabidopsis thaliana GN=RPS13 PE=2 SV=1	8	---	----	-0,139	0,10621	301,04	23,60%
O65572	Carotenoid 9,10(9',10')-cleavage dioxygenase 1 OS=Arabidopsis thaliana GN=CCD1 PE=1 SV=2	8	---	----	-0,177	0,10622	301,07	23,60%
O49506;Q9LRR9	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 OS=Arabidopsis thaliana GN=GLO5 PE=1 SV=1	1	---	----	-0,18	0,10609	300,70	23,60%
Q9M277	AT3g61870/F21F14_40 OS=Arabidopsis thaliana GN=F21F14.40 PE=2 SV=1	3	---	----	-0,208	0,10662	302,21	23,60%
P49200	40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2	1	---	----	0,349	0,10641	301,61	23,70%
Q8W4E2	V-type proton ATPase subunit B3 OS=Arabidopsis thaliana GN=VHA-B3 PE=2 SV=1	2	---	----	-0,179	0,10661	302,18	23,70%
Q9SW33	Thylakoid lumenal 17.9 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At4g24930 PE=1 SV=1	5	---	----	-0,192	0,10722	303,91	23,70%
Q94JX9	Nascent polypeptide-associated complex subunit alpha-like protein 2 OS=Arabidopsis thaliana GN=At3g49470 PE=2 SV=	4	---	----	-0,162	0,10721	303,88	23,80%
F4J036	Post-illumination chlorophyll fluorescence increase protein OS=Arabidopsis thaliana GN=PIFI PE=4 SV=1	3	---	----	0,312	0,10809	306,37	23,90%
Q9SL42	Peptidyl-prolyl cis-trans isomerase Pin1 OS=Arabidopsis thaliana GN=PIN1 PE=1 SV=1	5	---	----	0,189	0,10782	305,61	23,90%
Q68KI4	Sodium/hydrogen exchanger 1 OS=Arabidopsis thaliana GN=NHX1 PE=1 SV=2	1	---	----	-0,568	0,10822	306,74	23,90%
Q9M7Z1	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=A	5	---	----	-0,211	0,10901	308,98	24,00%
Q9FJF1	Putative GTP-binding protein ara-3 OS=Arabidopsis thaliana GN=At5g59840 PE=2 SV=1	1	---	----	-0,612	0,10861	307,85	24,00%
P46310	Omega-3 fatty acid desaturase, chloroplastic OS=Arabidopsis thaliana GN=FAD7 PE=2 SV=1	1	---	----	0,344	0,10921	309,55	24,10%
Q944B0	Peptidyl-prolyl cis-trans isomerase FKBP16-1, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-1 PE=2 SV=1	2	---	----	-0,281	0,10961	310,68	24,10%
P93050	Probable LRR receptor-like serine/threonine-protein kinase RKF3 OS=Arabidopsis thaliana GN=RKF3 PE=2 SV=1	1	---	----	0,72	0,11001	311,81	24,20%
Q8VZ95	Vesicle-associated protein 1-1 OS=Arabidopsis thaliana GN=PVA11 PE=1 SV=1	2	---	----	0,352	0,10982	311,28	24,20%
Q9M5J8	Polygalacturonase inhibitor 2 OS=Arabidopsis thaliana GN=PGIP2 PE=2 SV=2	2	---	----	-0,27	0,11041	312,95	24,20%
P28186	Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	1	---	----	-0,412	0,11009	312,04	24,20%
Q8L7B5	Chaperonin CPN60-like 1, mitochondrial OS=Arabidopsis thaliana GN=At2g33210 PE=2 SV=1	6	---	----	0,186	0,11081	314,08	24,30%
P54887;P54888	Delta-1-pyrroline-5-carboxylate synthase A OS=Arabidopsis thaliana GN=P5CSA PE=1 SV=1	8	---	----	-0,155	0,11082	314,11	24,30%
Q9M2U7	AT3g54400/T12E18_90 OS=Arabidopsis thaliana GN=T12E18_90 PE=2 SV=1	7	---	----	-0,145	0,11202	317,51	24,50%
P45434	Translocon-associated protein subunit alpha OS=Arabidopsis thaliana GN=At2g21160 PE=2 SV=3	1	---	----	0,384	0,11221	318,05	24,60%
Q9LJE4	Chaperonin 60 subunit beta 2, chloroplastic OS=Arabidopsis thaliana GN=CPN60B2 PE=1 SV=1	5	---	----	0,154	0,11281	319,75	24,70%
O49686	Abscisic acid receptor PYR1 OS=Arabidopsis thaliana GN=PYR1 PE=1 SV=1	2	---	----	0,449	0,11409	323,38	24,80%
Q8H107	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	3	---	----	0,293	0,11381	322,58	24,80%
Q9LHA8;Q9S9N1	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1	1	---	----	0,275	0,11361	322,02	24,80%
Q9FFR3	6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV	6	---	----	0,183	0,11341	321,45	24,80%
Q9SLI4	At1g54500/F20D21_31 OS=Arabidopsis thaliana GN=F20D21.31 PE=2 SV=1	5	---	----	-0,224	0,11341	321,45	24,80%
P10795	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1A PE=1 SV=2	1	EHGNSPGYYDGR	none	0,114	0,11441	324,29	24,90%
Q38922	Ras-related protein RABB1b OS=Arabidopsis thaliana GN=RABB1B PE=2 SV=1	2	---	----	-0,295	0,11409	323,38	24,90%
F4JT30	Putative triglyceride lipase OS=Arabidopsis thaliana GN=At4g13550 PE=4 SV=1	1	---	----	-0,509	0,11501	325,99	25,00%
Q9SRI1	Protein transport protein SEC13 homolog A OS=Arabidopsis thaliana GN=SEC13A PE=1 SV=1	5	---	----	0,221	0,11581	328,25	25,10%
Q9SIU0	NAD-dependent malic enzyme 1, mitochondrial OS=Arabidopsis thaliana GN=NAD-ME1 PE=1 SV=1	6	---	----	0,201	0,11602	328,85	25,10%
Q8W4E2;Q9SZN1	V-type proton ATPase subunit B3 OS=Arabidopsis thaliana GN=VHA-B3 PE=2 SV=1	21	---	----	-0,078	0,11581	328,25	25,10%
Q84WT8	Cysteine proteinase inhibitor 4 OS=Arabidopsis thaliana GN=CYS4 PE=3 SV=2	3	---	----	-0,231	0,11609	329,05	25,10%
Q9C5F3	Putative uncharacterized protein At4g28025 OS=Arabidopsis thaliana GN=At4g28025 PE=2 SV=1	1	---	----	-0,496	0,11561	327,69	25,10%
Q8L7N0	T-complex protein 1 subunit zeta 2 OS=Arabidopsis thaliana GN=CCT6B PE=1 SV=1	8	---	----	0,155	0,11662	330,55	25,20%
Q5GM68;Q9MAH0	Phosphoenolpyruvate carboxylase 2 OS=Arabidopsis thaliana GN=PPC2 PE=1 SV=2	10	---	----	0,14	0,11662	330,55	25,20%
F4KHG6	Carboxyl-terminal-processing peptidase 1, chloroplastic OS=Arabidopsis thaliana GN=CTPA1 PE=1 SV=1	1	---	----	-0,514	0,11662	330,55	25,20%
Q94AU7;Q9C6B3	Gamma carbonic anhydrase 3, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA3 PE=1 SV=1	1	---	----	0,504	0,11721	332,22	25,30%
P42644;P42645;Q96300	14-3-3-like protein GF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2	1	---	----	0,373	0,11741	332,79	25,30%
F4JMJ1	Heat shock 70 kDa protein 17 OS=Arabidopsis thaliana GN=HSP70-17 PE=2 SV=1	5	---	----	0,232	0,11721	332,22	25,30%
Q96529	Adenylosuccinate synthetase, chloroplastic OS=Arabidopsis thaliana GN=PURA PE=1 SV=1	10	---	----	0,144	0,11742	332,82	25,30%
P45724	Phenylalanine ammonia-lyase 2 OS=Arabidopsis thaliana GN=PAL2 PE=1 SV=2	1	---	----	0,496	0,11841	335,62	25,40%

Q9FJA6;Q9SIP7	40S ribosomal protein S3-3 OS=Arabidopsis thaliana GN=RPS3C PE=1 SV=1	1	---	----	0,302	0,11809	334,71	25,40%
Q9SJ66	Probable sucrose-phosphatase 2 OS=Arabidopsis thaliana GN=SPP2 PE=2 SV=2	7	---	----	0,173	0,11809	334,71	25,40%
Q9ZQE5	Pentatricopeptide repeat-containing protein At2g15690 OS=Arabidopsis thaliana GN=PCMP-H66 PE=2 SV=2	1	---	----	-0,508	0,11801	334,49	25,40%
Q8H1F4	Coatomer subunit zeta-3 OS=Arabidopsis thaliana GN=At4g08520 PE=2 SV=1	4	---	----	0,26	0,11882	336,79	25,50%
Q94BT2	Auxin-induced in root cultures protein 12 OS=Arabidopsis thaliana GN=AIR12 PE=1 SV=3	4	---	----	-0,155	0,11901	337,32	25,50%
Q682S0	Root phototropism protein 2 OS=Arabidopsis thaliana GN=RPT2 PE=1 SV=2	6	---	----	-0,197	0,11921	337,89	25,50%
Q9SVM8	Glycine-rich RNA-binding protein 2, mitochondrial OS=Arabidopsis thaliana GN=RBG2 PE=1 SV=1	4	---	----	0,211	0,11981	339,59	25,60%
Q9C5R8	2-Cys peroxiredoxin BAS1-like, chloroplastic OS=Arabidopsis thaliana GN=At5g06290 PE=2 SV=3	3	---	----	-0,198	0,12009	340,38	25,70%
Q8S2T0	Protein GRIP OS=Arabidopsis thaliana GN=GRIP PE=1 SV=2	1	---	----	0,469	0,12081	342,43	25,80%
Q9SK22	40S ribosomal protein S16-1 OS=Arabidopsis thaliana GN=RPS16A PE=2 SV=1	1	---	----	0,397	0,12101	342,99	25,80%
Q9C9P4	3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic OS=Arabidopsis thaliana GN=KAS2 PE=1 SV=1	5	---	----	-0,205	0,12061	341,86	25,80%
Q94C78	Putative uncharacterized protein At3g51140 OS=Arabidopsis thaliana GN=At3g51140 PE=2 SV=1	1	---	----	0,559	0,12121	343,56	25,90%
O65787	Cytochrome P450 71B6 OS=Arabidopsis thaliana GN=CYP71B6 PE=2 SV=1	1	---	----	0,471	0,12209	346,05	26,00%
O49377	Vesicle-associated membrane protein 711 OS=Arabidopsis thaliana GN=VAMP711 PE=1 SV=2	3	---	----	-0,335	0,12241	346,96	26,00%
P24101;Q9LHB9	Peroxidase 33 OS=Arabidopsis thaliana GN=PER33 PE=1 SV=1	1	---	----	-0,356	0,12209	346,05	26,00%
F4IDS7	Zinc ion binding protein OS=Arabidopsis thaliana GN=At1g12470 PE=4 SV=1	1	---	----	-0,481	0,12181	345,26	26,00%
Q9ZPH2	Monothiol glutaredoxin-S17 OS=Arabidopsis thaliana GN=GRXS17 PE=1 SV=1	4	---	----	0,286	0,12261	347,53	26,10%
O48773	Protein disulfide-isomerase 2-3 OS=Arabidopsis thaliana GN=PDIL2-3 PE=2 SV=1	4	---	----	0,234	0,12409	351,72	26,20%
Q9SAK4	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=ALDH5F1 PE=1 SV=2	13	---	----	-0,124	0,12361	350,36	26,20%
Q9FMD7	Probable inactive receptor kinase At5g16590 OS=Arabidopsis thaliana GN=At5g16590 PE=1 SV=1	2	---	----	-0,333	0,12361	350,36	26,20%
Q96514	Cytochrome P450 71B7 OS=Arabidopsis thaliana GN=CYP71B7 PE=1 SV=1	3	---	----	0,298	0,12461	353,20	26,30%
O82514;Q9FK35	Adenylate kinase 4 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=2	1	---	----	0,279	0,12409	351,72	26,30%
Q96255	Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1	3	---	----	0,234	0,12442	352,66	26,30%
Q9C8D8	Eukaryotic translation initiation factor 3 subunit J OS=Arabidopsis thaliana GN=F15E12.10 PE=2 SV=1	3	---	----	0,233	0,12409	351,72	26,30%
P51818	Heat shock protein 90-3 OS=Arabidopsis thaliana GN=HSP90-3 PE=1 SV=2	3	---	----	0,212	0,12482	353,79	26,30%
Q9FNE2	Glutaredoxin-C2 OS=Arabidopsis thaliana GN=GRXC2 PE=2 SV=1	5	---	----	0,144	0,12461	353,20	26,30%
P56773	Cytochrome b6 OS=Arabidopsis thaliana GN=petB PE=1 SV=1	6	---	----	-0,117	0,12481	353,76	26,30%
Q9FJP3	50S ribosomal protein L29, chloroplastic OS=Arabidopsis thaliana GN=RPL29 PE=1 SV=1	4	---	----	-0,134	0,12501	354,33	26,30%
Q9SJ03	Expressed protein OS=Arabidopsis thaliana GN=At2g21960 PE=2 SV=2	6	---	----	-0,174	0,12409	351,72	26,30%
Q9C5A9	ATP synthase subunit beta-3, mitochondrial OS=Arabidopsis thaliana GN=At5g08680 PE=2 SV=1	21	---	----	0,069	0,12542	355,49	26,40%
Q9SYP2	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 1 OS=Arabidopsis thaliana GN=PFP-ALPHA1	5	---	----	0,211	0,12619	357,67	26,50%
Q0WLB5	Clathrin heavy chain 2 OS=Arabidopsis thaliana GN=CHC2 PE=1 SV=1	7	---	----	0,186	0,12661	358,87	26,50%
O80860	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic OS=Arabidopsis thaliana GN=FTSH2 PE=1 SV=1	13	---	----	-0,094	0,12662	358,89	26,50%
Q9FUZ2	Peptide deformylase 1B, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=PDF1B PE=1 SV=2	6	---	----	-0,162	0,12609	357,39	26,50%
Q9SU40	Monocopper oxidase-like protein SKU5 OS=Arabidopsis thaliana GN=SKU5 PE=1 SV=1	8	---	----	-0,167	0,12581	356,60	26,50%
Q39221	SEC12-like protein 2 OS=Arabidopsis thaliana GN=STL2P PE=1 SV=4	3	---	----	-0,322	0,12609	357,39	26,50%
Q8GW61	Sugar transport protein 14 OS=Arabidopsis thaliana GN=STP14 PE=2 SV=2	1	---	----	-0,611	0,12609	357,39	26,50%
Q9LIS3	UDP-glucuronate 4-epimerase 6 OS=Arabidopsis thaliana GN=GAE6 PE=1 SV=1	1	---	----	1,25	0,12781	362,27	26,60%
rev_F4IFD0	reversed Aminotransferase-like, plant mobile domain family protein OS=Arabidopsis thaliana GN=At2g04865 PE=1 SV=	1	---	----	0,53	0,12741	361,13	26,60%
P29515;Q56YW9	Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	1	---	----	0,225	0,12721	360,57	26,60%
Q9C827	Coatomer subunit beta'-2 OS=Arabidopsis thaliana GN=At1g52360 PE=2 SV=1	5	---	----	0,225	0,12762	361,73	26,60%
P36210	50S ribosomal protein L12-1, chloroplastic OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=1	10	---	----	-0,094	0,12819	363,34	26,60%
Q9FJA6	40S ribosomal protein S3-3 OS=Arabidopsis thaliana GN=RPS3C PE=1 SV=1	1	---	----	0,346	0,12801	362,83	26,70%
O48529	Rhodanese-like domain-containing protein 9, chloroplastic OS=Arabidopsis thaliana GN=STR9 PE=2 SV=1	5	---	----	-0,166	0,12761	361,70	26,70%
Q9LS94	Ras-related protein RABG3f OS=Arabidopsis thaliana GN=RABG3F PE=2 SV=1	2	---	----	-0,206	0,12809	363,06	26,70%
O23157	AT4g37300/C7A10_60 OS=Arabidopsis thaliana GN=C7A10.60 PE=1 SV=1	5	---	----	-0,208	0,12781	362,27	26,70%
A1A6M1	At4g13670 OS=Arabidopsis thaliana GN=PTAC5 PE=2 SV=1	3	---	----	-0,271	0,12819	363,34	26,70%
Q9ZQ94	UDP-glycosyltransferase 73C5 OS=Arabidopsis thaliana GN=UGT73C5 PE=2 SV=1	1	---	----	-0,337	0,12861	364,53	26,70%
Q9LYN2	Ferritin-3, chloroplastic OS=Arabidopsis thaliana GN=FER3 PE=2 SV=1	2	---	----	0,385	0,12982	367,96	26,90%
Q9LF97	CBS domain-containing protein CBSCBSPB3 OS=Arabidopsis thaliana GN=CBSCBSPB3 PE=1 SV=1	5	---	----	0,258	0,13009	368,72	27,00%
Q9SV68	Putative quinone-oxidoreductase homolog, chloroplastic OS=Arabidopsis thaliana GN=At4g13010 PE=2 SV=1	6	---	----	-0,165	0,13021	369,07	27,00%
Q29Q44	At2g04360 OS=Arabidopsis thaliana GN=At2g04360 PE=2 SV=1	1	---	----	-0,485	0,13041	369,64	27,00%
F4HS68	Tetratricopeptide repeat-containing protein OS=Arabidopsis thaliana GN=EMB2753 PE=4 SV=1	12	---	----	0,146	0,13122	371,93	27,10%
Q67YI9	Clathrin interactor EPSIN 2 OS=Arabidopsis thaliana GN=EPSIN2 PE=1 SV=1	1	SRSVDNYGSR	Phospho S1	0,923	0,13209	374,39	27,20%
O49203	Nucleoside diphosphate kinase III, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=NDPK3 PE=1 SV=1	5	---	----	0,144	0,13162	373,07	27,20%

Q9FKX3	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g66090 PE=2 SV=1	5	---	----	-0,163	0,13161	373,04	27,20%
Q9FJ82	Putative 4-hydroxy-tetrahydrodipicolinate reductase 3, chloroplastic OS=Arabidopsis thaliana GN=DAPB3 PE=2 SV=1	2	---	----	-0,432	0,13209	374,39	27,20%
Q8LAK5	At4g30330 OS=Arabidopsis thaliana GN=At4g30330 PE=2 SV=1	1	---	----	-0,563	0,13209	374,39	27,20%
Q8LPL3	Ascorbate oxidase-like protein OS=Arabidopsis thaliana GN=At5g21100 PE=2 SV=1	1	---	----	-0,745	0,13209	374,39	27,20%
Q0WWW9	D-xylose-proton symporter-like 3, chloroplastic OS=Arabidopsis thaliana GN=At5g59250 PE=2 SV=2	2	---	----	-0,289	0,13202	374,20	27,30%
Q9SIV6	Expressed protein OS=Arabidopsis thaliana GN=At2g16460 PE=2 SV=2	1	---	----	0,598	0,13362	378,73	27,50%
Q9S7H1;Q9SA56	Photosystem I reaction center subunit II-1, chloroplastic OS=Arabidopsis thaliana GN=psaD1 PE=1 SV=1	7	---	----	-0,068	0,13381	379,27	27,50%
Q8VZ23	NAD(P)-linked oxidoreductase superfamily protein OS=Arabidopsis thaliana GN=At1g04420 PE=2 SV=1	11	---	----	-0,127	0,13381	379,27	27,50%
Q9LI77	Glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GATA PE=2	7	---	----	-0,15	0,13419	380,34	27,50%
Q6NPM8	Bifunctional phosphatase IMPL2, chloroplastic OS=Arabidopsis thaliana GN=HISN7 PE=1 SV=1	2	---	----	-0,375	0,13401	379,84	27,50%
Q9SFU6;Q9SJM0	Callose synthase 9 OS=Arabidopsis thaliana GN=CALS9 PE=2 SV=2	1	---	----	-0,608	0,13421	380,41	27,50%
F4IV84	RPM1-interacting protein 4-like protein OS=Arabidopsis thaliana GN=At2g04410 PE=1 SV=1	1	SDSPGKDEPGYNK	Phospho S3	-0,701	0,13461	381,54	27,60%
Q9SAB1	Heat shock 70 kDa protein 16 OS=Arabidopsis thaliana GN=HSP70-16 PE=2 SV=1	2	---	----	0,364	0,13621	386,08	27,70%
Q9FX94	Probable carboxylesterase 5 OS=Arabidopsis thaliana GN=CXE5 PE=2 SV=1	2	---	----	0,327	0,13561	384,38	27,70%
Q39230	Serine--tRNA ligase OS=Arabidopsis thaliana GN=At5g27470 PE=2 SV=1	9	---	----	0,148	0,13601	385,51	27,70%
O65390	Aspartic proteinase A1 OS=Arabidopsis thaliana GN=APA1 PE=1 SV=1	10	---	----	0,132	0,13609	385,73	27,70%
P42731	Polyadenylate-binding protein 2 OS=Arabidopsis thaliana GN=PAB2 PE=1 SV=1	12	---	----	0,127	0,13602	385,54	27,70%
Q9S9N9	Cinnamoyl-CoA reductase 1 OS=Arabidopsis thaliana GN=CCR1 PE=1 SV=1	1	---	----	0,48	0,13561	384,38	27,80%
P60039;Q9LHP1	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	3	---	----	0,248	0,13601	385,51	27,80%
Q9SN96	AT3g46430/F18L15_150 OS=Arabidopsis thaliana GN=F18L15.150 PE=2 SV=1	2	---	----	0,212	0,13581	384,94	27,80%
P10896-2	Isoform Short of Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RC	1	---	----	-0,292	0,13601	385,51	27,80%
Q8LBP6	At5g08410 OS=Arabidopsis thaliana GN=FTRA2 PE=2 SV=1	3	---	----	-0,211	0,13809	391,40	28,00%
Q9C5J8	Outer envelope protein 80, chloroplastic OS=Arabidopsis thaliana GN=OEP80 PE=2 SV=1	4	---	----	-0,242	0,13809	391,40	28,00%
P42759	Dehydrin ERD10 OS=Arabidopsis thaliana GN=ERD10 PE=1 SV=1	1	---	----	0,351	0,13809	391,40	28,10%
Q9SGT7	At1g56110/T6H22_9 OS=Arabidopsis thaliana GN=T6H22.10 PE=2 SV=1	2	---	----	0,227	0,13801	391,18	28,10%
Q9SR73	40S ribosomal protein S28-1 OS=Arabidopsis thaliana GN=RPS28A PE=3 SV=1	1	---	----	0,218	0,13881	393,45	28,10%
Q9LFJ8	UDP-glycosyltransferase 78D2 OS=Arabidopsis thaliana GN=UGT78D2 PE=2 SV=1	3	---	----	0,35	0,13942	395,17	28,20%
Q9SA87	FAD-binding Berberine family protein OS=Arabidopsis thaliana GN=T5I8.17 PE=2 SV=1	1	---	----	-0,454	0,13921	394,58	28,20%
Q9LXC6	Gb|AAD14519.1 OS=Arabidopsis thaliana GN=F17I14_190 PE=1 SV=1	1	---	----	0,481	0,14009	397,07	28,30%
P61843	Photosystem I assembly protein Ycf3 OS=Arabidopsis thaliana GN=ycf3 PE=3 SV=1	2	---	----	0,24	0,14001	396,85	28,30%
Q9XI55	F9L1.8 protein OS=Arabidopsis thaliana GN=F9L1.8 PE=2 SV=1	9	---	----	0,127	0,13981	396,28	28,30%
Q93ZM6	AT5g63620/MBK5_9 OS=Arabidopsis thaliana GN=At5g63620 PE=2 SV=1	2	---	----	-0,297	0,14009	397,07	28,30%
Q9SYW8	Lhca2 protein OS=Arabidopsis thaliana GN=Lhca2 PE=2 SV=1	7	---	----	-0,092	0,14062	398,58	28,40%
Q9SHJ6	Peroxisomal and mitochondrial division factor 2 OS=Arabidopsis thaliana GN=PMD2 PE=1 SV=1	4	---	----	0,218	0,14161	401,38	28,50%
O04630	Threonine--tRNA ligase, mitochondrial OS=Arabidopsis thaliana GN=THRRS PE=2 SV=3	11	---	----	0,117	0,14219	403,02	28,50%
Q9FLX7	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial OS=Arabidopsis thaliana G	5	---	----	0,163	0,14302	405,38	28,60%
P56797	30S ribosomal protein S2, chloroplastic OS=Arabidopsis thaliana GN=rps2 PE=3 SV=1	10	---	----	-0,125	0,14219	403,02	28,60%
P61841	30S ribosomal protein S7, chloroplastic OS=Arabidopsis thaliana GN=rps7-A PE=1 SV=1	6	---	----	-0,137	0,14209	402,73	28,60%
Q9SKZ1	Transcription factor Pur-alpha 1 OS=Arabidopsis thaliana GN=PURA1 PE=1 SV=2	4	---	----	-0,193	0,14209	402,73	28,60%
Q9FJD0	Vacuolar protein sorting-associated protein 26A OS=Arabidopsis thaliana GN=VPS26A PE=2 SV=1	2	---	----	-0,289	0,14209	402,73	28,60%
Q9M263	Germin-like protein subfamily 2 member 4 OS=Arabidopsis thaliana GN=GLP10 PE=2 SV=1	1	---	----	-0,346	0,14261	404,22	28,60%
Q6NL24	At4g16210 OS=Arabidopsis thaliana GN=ECHIA PE=2 SV=1	2	---	----	-0,404	0,14209	402,73	28,60%
O04951;P48578;Q07098	Serine/threonine-protein phosphatase PP2A-5 catalytic subunit OS=Arabidopsis thaliana GN=PP2A5 PE=1 SV=1	1	---	----	0,674	0,14321	405,92	28,70%
P20431	ATPase 3, plasma membrane-type OS=Arabidopsis thaliana GN=AHA3 PE=1 SV=2	3	---	----	0,354	0,14421	408,75	28,70%
Q8H126	Putative uncharacterized protein At5g13030 OS=Arabidopsis thaliana GN=At5g13030 PE=2 SV=1	7	---	----	0,19	0,14461	409,88	28,70%
Q9CA90	Glyoxylate/hydroxypyruvate reductase A HPR2 OS=Arabidopsis thaliana GN=HPR2 PE=1 SV=1	5	---	----	0,168	0,14409	408,40	28,70%
P27202	Photosystem II 10 kDa polypeptide, chloroplastic OS=Arabidopsis thaliana GN=PSBR PE=1 SV=1	5	---	----	0,123	0,14382	407,65	28,70%
P29197	Chaperonin CPN60, mitochondrial OS=Arabidopsis thaliana GN=CPN60 PE=2 SV=2	13	---	----	0,114	0,14419	408,69	28,70%
P10795	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1A PE=1 SV=2	3	---	----	-0,079	0,14419	408,69	28,70%
Q9FH02	ATP-dependent zinc metalloprotease FTSH 5, chloroplastic OS=Arabidopsis thaliana GN=FTSH5 PE=1 SV=1	7	---	----	-0,103	0,14441	409,32	28,70%
Q1EBV7	Sodium/pyruvate cotransporter BASS2, chloroplastic OS=Arabidopsis thaliana GN=BASS2 PE=2 SV=1	1	---	----	-0,276	0,14421	408,75	28,70%
Q949X9	Multicopper oxidase LPR2 OS=Arabidopsis thaliana GN=LPR2 PE=2 SV=1	1	---	----	-0,472	0,14301	405,35	28,70%
Q93Z08	Glucan endo-1,3-beta-glucosidase 6 OS=Arabidopsis thaliana GN=At5g58090 PE=1 SV=2	1	---	----	-0,488	0,14382	407,65	28,70%
Q940Z5	Phenolic glucoside malonyltransferase 1 OS=Arabidopsis thaliana GN=PMAT1 PE=1 SV=1	1	---	----	-0,614	0,14401	408,18	28,70%
Q9S834	ATP-dependent Clp protease proteolytic subunit 5, chloroplastic OS=Arabidopsis thaliana GN=CLPP5 PE=1 SV=1	4	---	----	0,155	0,14501	411,02	28,80%

Q93ZN9	LL-diaminopimelate aminotransferase, chloroplastic OS=Arabidopsis thaliana GN=DAP PE=1 SV=1	12	---	----	0,103	0,14381	407,62	28,80%
Q9ZWA8	Fasciclin-like arabinogalactan protein 9 OS=Arabidopsis thaliana GN=FLA9 PE=1 SV=1	4	---	----	-0,154	0,14501	411,02	28,80%
Q42406	Peptidyl-prolyl cis-trans isomerase CYP18-4 OS=Arabidopsis thaliana GN=CYP18-4 PE=1 SV=1	5	---	----	0,135	0,14621	414,42	28,90%
P46309	Glutamate--cysteine ligase, chloroplastic OS=Arabidopsis thaliana GN=GSH1 PE=1 SV=2	8	---	----	0,121	0,14621	414,42	29,00%
Q9LSV0	Glyoxylate/succinic semialdehyde reductase 1 OS=Arabidopsis thaliana GN=GLYR1 PE=1 SV=1	10	---	----	0,115	0,14619	414,35	29,00%
F4K1D3	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=At5g35680 PE=3 SV=1	3	---	----	0,211	0,14809	419,74	29,20%
Q944I4	D-glycerate 3-kinase, chloroplastic OS=Arabidopsis thaliana GN=GLYK PE=1 SV=2	13	---	----	-0,098	0,14809	419,74	29,20%
Q9AST9	At1g73110/F3N23_39 OS=Arabidopsis thaliana GN=At1g73110 PE=2 SV=1	7	---	----	-0,158	0,14841	420,66	29,20%
Q8L7S9	Thioredoxin Y2, chloroplastic OS=Arabidopsis thaliana GN=At1g43560 PE=2 SV=1	3	---	----	-0,199	0,14781	418,96	29,20%
Q9C5W3	NAD kinase 2, chloroplastic OS=Arabidopsis thaliana GN=NADK2 PE=1 SV=1	1	---	----	-0,864	0,14809	419,74	29,20%
Q9C787	Putative uncharacterized protein At1g69510 OS=Arabidopsis thaliana GN=F10D13_16 PE=1 SV=1	1	---	----	0,541	0,14809	419,74	29,30%
Q9LVH6	Aldose 1-epimerase OS=Arabidopsis thaliana GN=At3g17940 PE=3 SV=1	2	---	----	0,375	0,14881	421,79	29,30%
Q8LPR9	Protein TIC110, chloroplastic OS=Arabidopsis thaliana GN=TIC110 PE=1 SV=1	26	---	----	0,075	0,14922	422,95	29,30%
Q9CAP8	Long chain acyl-CoA synthetase 9, chloroplastic OS=Arabidopsis thaliana GN=LACS9 PE=2 SV=1	9	---	----	-0,131	0,14809	419,74	29,30%
Q42593	L-ascorbate peroxidase T, chloroplastic OS=Arabidopsis thaliana GN=APXT PE=2 SV=2	8	---	----	-0,134	0,14901	422,36	29,30%
O22609	Protease Do-like 1, chloroplastic OS=Arabidopsis thaliana GN=DEGP1 PE=1 SV=2	9	---	----	-0,142	0,14941	423,49	29,30%
Q9LVH5	Outer envelope protein 64, chloroplastic OS=Arabidopsis thaliana GN=OEP64 PE=1 SV=1	3	---	----	0,308	0,15042	426,35	29,40%
P42799;Q42522	Glutamate-1-semialdehyde 2,1-aminomutase 1, chloroplastic OS=Arabidopsis thaliana GN=GSA1 PE=2 SV=1	6	---	----	0,12	0,15041	426,32	29,40%
P23321;Q9S841	Oxygen-evolving enhancer protein 1-1, chloroplastic OS=Arabidopsis thaliana GN=PSBO1 PE=1 SV=2	11	---	----	0,057	0,14981	424,62	29,40%
Q93Z70	Probable N-acetyl-gamma-glutamyl-phosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=At2g19940 PE=1	11	---	----	-0,127	0,14982	424,65	29,40%
Q9FT97	Alpha-galactosidase 1 OS=Arabidopsis thaliana GN=AGAL1 PE=2 SV=1	3	---	----	-0,22	0,15018	425,69	29,40%
Q9FXT6	Peroxisomal membrane protein PEX14 OS=Arabidopsis thaliana GN=PEX14 PE=1 SV=2	2	---	----	-0,29	0,15008	425,41	29,40%
Q9ZVQ4	Glutathione S-transferase Z2 OS=Arabidopsis thaliana GN=GSTZ2 PE=3 SV=1	1	---	----	-0,327	0,15018	425,69	29,40%
Q9FGT8	Outer membrane lipoprotein-like OS=Arabidopsis thaliana GN=K21L19.6 PE=2 SV=1	6	---	----	-0,121	0,15121	428,59	29,50%
Q06611	Aquaporin PIP1-2 OS=Arabidopsis thaliana GN=PIP1-2 PE=1 SV=1	4	---	----	-0,146	0,15161	429,73	29,60%
Q8L968	Inosine triphosphate pyrophosphatase OS=Arabidopsis thaliana GN=At4g13720 PE=2 SV=1	2	---	----	-0,285	0,15208	431,08	29,60%
F4I354	Double-stranded DNA-binding-like protein OS=Arabidopsis thaliana GN=At1g29850 PE=1 SV=1	1	---	----	0,478	0,15208	431,08	29,70%
Q9LS47	Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like protein OS=Arabidopsis thaliana GN=At3g18430	1	---	----	0,644	0,15408	436,74	30,00%
Q9SJ68	At2g35820 OS=Arabidopsis thaliana GN=At2g35820 PE=2 SV=2	2	---	----	0,309	0,15408	436,74	30,00%
Q93ZC2	AT5g36230/T30G6_9 OS=Arabidopsis thaliana GN=At5g36230 PE=2 SV=1	3	---	----	0,205	0,15408	436,74	30,00%
Q9FLF0	40S ribosomal protein S9-2 OS=Arabidopsis thaliana GN=RPS9C PE=2 SV=1	1	---	----	-0,422	0,15408	436,74	30,00%
Q9FZK4	F17L21.10 OS=Arabidopsis thaliana GN=NTF2A PE=2 SV=1	1	---	----	0,32	0,15601	442,20	30,20%
P05466	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic OS=Arabidopsis thaliana GN=At2g45300 PE=2 SV=3	5	---	----	0,202	0,15561	441,06	30,20%
Q9ZU52	Probable fructose-bisphosphate aldolase 3, chloroplastic OS=Arabidopsis thaliana GN=FBA3 PE=1 SV=1	8	---	----	0,145	0,15521	439,93	30,20%
Q8LAS8	S-formylglutathione hydrolase OS=Arabidopsis thaliana GN=SFGH PE=1 SV=2	6	---	----	0,138	0,15541	440,50	30,20%
Q8VY57;Q93Y31	ADP-RIBOSYLATION FACTOR-like protein OS=Arabidopsis thaliana GN=ARLA1C PE=2 SV=1	3	---	----	-0,218	0,15642	443,36	30,30%
P48641	Glutathione reductase, cytosolic OS=Arabidopsis thaliana GN=At3g24170 PE=2 SV=1	8	---	----	0,14	0,15682	444,49	30,40%
Q8LB47	GrpE protein homolog OS=Arabidopsis thaliana GN=AR192 PE=2 SV=1	1	---	----	0,228	0,15818	448,36	30,50%
Q8L9C4	Very-long-chain 3-oxoacyl-CoA reductase 1 OS=Arabidopsis thaliana GN=KCR1 PE=1 SV=1	5	---	----	0,204	0,15801	447,87	30,50%
O48661	Spermidine synthase 2 OS=Arabidopsis thaliana GN=SPDSYN2 PE=1 SV=2	4	---	----	0,199	0,15808	448,08	30,50%
F4HWQ8	Cell wall / vacuolar inhibitor of fructosidase 1 OS=Arabidopsis thaliana GN=C/VIF1 PE=1 SV=1	2	---	----	-0,286	0,15808	448,08	30,50%
Q8LFL5	At1g49975 OS=Arabidopsis thaliana GN=At1g49975 PE=2 SV=1	2	---	----	-0,325	0,15781	447,30	30,50%
Q9LZH9	60S ribosomal protein L7a-2 OS=Arabidopsis thaliana GN=RPL7AB PE=1 SV=1	2	---	----	0,184	0,15801	447,87	30,60%
Q9CAT7	Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=T18K17.10 PE=2 SV=1	4	---	----	0,246	0,15942	451,86	30,70%
F4IBH5	LETM1-like protein OS=Arabidopsis thaliana GN=At1g65540 PE=4 SV=1	2	---	----	0,364	0,16008	453,75	30,80%
Q8L742	Amine oxidase OS=Arabidopsis thaliana GN=At4g12290 PE=2 SV=1	3	---	----	0,305	0,16081	455,80	30,80%
Q9LJE5	AT3g13460/MRP15_10 OS=Arabidopsis thaliana GN=ECT2 PE=2 SV=1	3	---	----	0,258	0,16018	454,03	30,80%
Q9FFH6;Q9ZWA8	Fasciclin-like arabinogalactan protein 13 OS=Arabidopsis thaliana GN=FLA13 PE=1 SV=1	1	---	----	0,208	0,16062	455,26	30,80%
Q9C8P0	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic OS=Ara	6	---	----	-0,156	0,16008	453,75	30,80%
Q9XIR0	At1g64850/F13O11_15 OS=Arabidopsis thaliana GN=F13O11.15 PE=2 SV=1	1	---	----	-0,432	0,16008	453,75	30,80%
Q948K8;Q9XI98	Ras-related protein RABG3a OS=Arabidopsis thaliana GN=RABG3A PE=2 SV=1	1	---	----	-0,457	0,16008	453,75	30,80%
Q9LV09	Protein BOBBER 1 OS=Arabidopsis thaliana GN=BOB1 PE=1 SV=1	1	---	----	0,703	0,16161	458,07	30,90%
Q93V56	Soluble inorganic pyrophosphatase 1 OS=Arabidopsis thaliana GN=PPA1 PE=1 SV=1	2	---	----	0,436	0,16208	459,42	30,90%
Q9C5C5	Thioredoxin-like 4, chloroplastic OS=Arabidopsis thaliana GN=At1g07700 PE=2 SV=1	1	---	----	0,427	0,16218	459,70	30,90%
Q84MC2	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8 OS=Arabidopsis thaliana GN=LOG8 PE=1 SV=1	2	---	----	0,354	0,16208	459,42	30,90%

Q94KE3	Pyruvate kinase OS=Arabidopsis thaliana GN=At3g52990 PE=2 SV=1	3	---	----	0,227	0,16161	458,07	30,90%
Q9T034	Probable phenylalanine--tRNA ligase alpha subunit OS=Arabidopsis thaliana GN=At4g39280 PE=2 SV=3	4	---	----	0,213	0,16218	459,70	30,90%
F4JFN3;Q9SIF2	HEAT SHOCK PROTEIN 89.1 OS=Arabidopsis thaliana GN=Hsp89.1 PE=3 SV=1	3	---	----	0,197	0,16101	456,37	30,90%
Q9ZU25	Probable mitochondrial-processing peptidase subunit alpha-1 OS=Arabidopsis thaliana GN=At1g51980 PE=2 SV=1	18	---	----	0,091	0,16221	459,77	30,90%
P31414	Pyrophosphate-energized vacuolar membrane proton pump 1 OS=Arabidopsis thaliana GN=AVP1 PE=1 SV=1	14	---	----	-0,083	0,16121	456,94	30,90%
Q9ASS6	Photosynthetic NDH subunit of lumenal location 5, chloroplastic OS=Arabidopsis thaliana GN=PNSL5 PE=1 SV=1	3	---	----	-0,142	0,16261	460,90	30,90%
Q8L5Z1	GDSL esterase/lipase At1g33811 OS=Arabidopsis thaliana GN=At1g33811 PE=2 SV=1	2	---	----	-0,326	0,16208	459,42	30,90%
Q9ZVT6	BSD domain-containing protein OS=Arabidopsis thaliana GN=F15K9.5 PE=1 SV=1	1	---	----	0,438	0,16342	463,20	31,00%
Q9M0N1	Plant UBX domain-containing protein 10 OS=Arabidopsis thaliana GN=PUX10 PE=2 SV=1	1	---	----	0,31	0,16208	459,42	31,00%
Q9ZV24	Outer envelope pore protein 16-1, chloroplastic OS=Arabidopsis thaliana GN=OEP161 PE=1 SV=1	5	---	----	0,104	0,16341	463,17	31,00%
Q8LAP6	Probable plastid-lipid-associated protein 12, chloroplastic OS=Arabidopsis thaliana GN=PAP12 PE=2 SV=1	13	---	----	-0,114	0,16208	459,42	31,00%
Q9M0A5	Gamma-glutamyl peptidase 3 OS=Arabidopsis thaliana GN=At4g30550 PE=4 SV=1	1	---	----	-0,566	0,16341	463,17	31,00%
F4J9A0	Nodulin/glutamine synthase-like protein OS=Arabidopsis thaliana GN=At3g53180 PE=1 SV=1	4	---	----	-0,251	0,16408	465,09	31,10%
P93834;Q42525;Q9FZG4	Hexokinase-2 OS=Arabidopsis thaliana GN=HXK2 PE=1 SV=1	1	---	----	0,349	0,16608	470,75	31,30%
Q9SUQ9	AT4g23680/F9D16_150 OS=Arabidopsis thaliana GN=F9D16.150 PE=2 SV=1	3	---	----	0,213	0,16521	468,27	31,30%
O48737	Thioredoxin M1, chloroplastic OS=Arabidopsis thaliana GN=At1g03680 PE=2 SV=1	5	---	----	-0,095	0,16501	467,71	31,30%
Q500U9	At1g03030 OS=Arabidopsis thaliana GN=At1g03030 PE=2 SV=1	1	---	----	-0,444	0,16541	468,84	31,30%
Q8L8V4	At3g07640 OS=Arabidopsis thaliana GN=At3g07640 PE=2 SV=1	1	---	----	-0,669	0,16522	468,30	31,30%
Q9C681	Probable histone H2A.1 OS=Arabidopsis thaliana GN=At1g51060 PE=1 SV=1	1	---	----	0,304	0,16601	470,54	31,40%
O23264	Selenium-binding protein 1 OS=Arabidopsis thaliana GN=SBP1 PE=1 SV=1	8	---	----	-0,124	0,16608	470,75	31,40%
O49482	Cinnamyl alcohol dehydrogenase 5 OS=Arabidopsis thaliana GN=CAD5 PE=1 SV=1	2	---	----	0,246	0,16742	474,54	31,50%
P55737	Heat shock protein 90-2 OS=Arabidopsis thaliana GN=HSP90-2 PE=1 SV=1	2	---	----	0,182	0,16818	476,71	31,50%
Q01525	14-3-3-like protein GF14 omega OS=Arabidopsis thaliana GN=GRF2 PE=2 SV=2	7	---	----	0,131	0,16721	473,94	31,50%
Q940I2	Putative uncharacterized protein MED24.18 OS=Arabidopsis thaliana GN=MED24.18 PE=2 SV=1	5	---	----	-0,135	0,16741	474,51	31,50%
O48593	Asparagine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=SYNO PE=2 SV=3	3	---	----	-0,235	0,16761	475,08	31,50%
Q39222	Ras-related protein RABA1b OS=Arabidopsis thaliana GN=RABA1B PE=2 SV=1	2	---	----	0,343	0,16801	476,21	31,60%
P34790;Q9SKQ0	Peptidyl-prolyl cis-trans isomerase CYP18-3 OS=Arabidopsis thaliana GN=CYP18-3 PE=1 SV=1	3	---	----	0,115	0,16808	476,42	31,60%
Q9FNH6	Harpin-induced protein-like OS=Arabidopsis thaliana GN=NHL3 PE=2 SV=1	2	---	----	-0,217	0,16808	476,42	31,60%
Q8L5Z7	Sorting nexin 2A OS=Arabidopsis thaliana GN=SNX2A PE=1 SV=1	1	---	----	-0,891	0,16808	476,42	31,60%
F4JLM5	Isoleucyl-tRNA synthetase OS=Arabidopsis thaliana GN=At4g10320 PE=3 SV=1	8	---	----	0,174	0,16921	479,61	31,70%
Q8VZP1	(DL)-glycerol-3-phosphatase 2 OS=Arabidopsis thaliana GN=GPP2 PE=1 SV=1	2	---	----	0,495	0,17008	482,09	31,80%
P42798;Q9LX88	40S ribosomal protein S15a-1 OS=Arabidopsis thaliana GN=RPS15AA PE=2 SV=2	1	---	----	0,319	0,16981	481,31	31,80%
Q9FLB7	At5g05370 OS=Arabidopsis thaliana GN=At5g05370 PE=2 SV=1	1	---	----	-0,288	0,17008	482,09	31,80%
Q9MB58	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase OS=Arabidopsis thaliana GN=FKFBP PE=1 SV=1	1	SLSASSFLIDTK	Phospho S3	-1,182	0,16961	480,75	31,80%
P29511	Tubulin alpha-6 chain OS=Arabidopsis thaliana GN=TUBA6 PE=1 SV=1	1	---	----	0,313	0,17162	486,44	32,00%
Q9SJQ0	Pyruvate kinase OS=Arabidopsis thaliana GN=At2g36580 PE=2 SV=2	2	---	----	0,241	0,17161	486,41	32,00%
Q95748	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 OS=Arabidopsis thaliana GN=NAD9 PE=2 SV=2	9	---	----	0,136	0,17162	486,44	32,00%
D7SFH9;Q7Y208	Glycerophosphodiester phosphodiesterase protein kinase domain-containing GDPDL2 OS=Arabidopsis thaliana GN=GD	2	---	----	-0,207	0,17181	486,98	32,00%
Q93Z51	Probable inactive nicotinamidase At3g16190 OS=Arabidopsis thaliana GN=At3g16190 PE=2 SV=1	2	---	----	-0,347	0,17181	486,98	32,00%
F4KDA6	Protein LOW PSII ACCUMULATION 2, chloroplastic OS=Arabidopsis thaliana GN=LPA2 PE=1 SV=1	1	---	----	-0,426	0,17221	488,11	32,00%
F4I5H7	Putative anthranilate phosphoribosyltransferase OS=Arabidopsis thaliana GN=At1g70570 PE=4 SV=1	1	---	----	-1,124	0,17101	484,71	32,00%
Q9XI11	F8K7.9 OS=Arabidopsis thaliana GN=F8K7.9 PE=2 SV=1	9	---	----	-0,15	0,17242	488,71	32,10%
O65355	Gamma-glutamyl hydrolase 2 OS=Arabidopsis thaliana GN=GGH2 PE=1 SV=2	1	---	----	0,469	0,17361	492,08	32,20%
Q9SV91	At4g10300 OS=Arabidopsis thaliana GN=F24G24.100 PE=2 SV=1	1	---	----	0,31	0,17418	493,71	32,20%
Q9FGS4	Quinolinate synthase, chloroplastic OS=Arabidopsis thaliana GN=QS PE=1 SV=1	1	---	----	0,274	0,17408	493,43	32,20%
O48844	26S proteasome non-ATPase regulatory subunit 1 homolog A OS=Arabidopsis thaliana GN=RPN2A PE=1 SV=1	6	---	----	0,16	0,17361	492,08	32,20%
Q9C8P0;Q9SQI8	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic OS=Arak	2	---	----	-0,168	0,17422	493,81	32,20%
F4K4G6	RING/FYVE/PHD zinc finger-containing protein OS=Arabidopsis thaliana GN=At5g36670 PE=4 SV=1	1	---	----	-0,423	0,17361	492,08	32,20%
Q9ZR12	GRR1-like protein 1 OS=Arabidopsis thaliana GN=GRH1 PE=1 SV=1	1	---	----	-0,431	0,17341	491,52	32,20%
Q00218;Q9SK84	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=DHS2 PE=2 SV=2	1	---	----	0,238	0,17401	493,22	32,30%
O65449	At4g22010 OS=Arabidopsis thaliana GN=sks4 PE=2 SV=1	6	---	----	-0,196	0,17481	495,48	32,30%
Q56ZZ7	Plastidic glucose transporter 4 OS=Arabidopsis thaliana GN=At5g16150 PE=1 SV=2	2	---	----	-0,28	0,17408	493,43	32,30%
Q9C9K3	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2 OS=Arabidopsis thaliana GN=PFP-ALPHA2	2	---	----	0,327	0,17621	499,45	32,40%
O04314	PYK10-binding protein 1 OS=Arabidopsis thaliana GN=PBP1 PE=1 SV=1	6	---	----	0,145	0,17618	499,38	32,40%
P41376;P41377;Q94A52	Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	2	---	----	0,193	0,17618	499,38	32,50%

P42798	40S ribosomal protein S15a-1 OS=Arabidopsis thaliana GN=RPS15AA PE=2 SV=2	2	---	----	0,181	0,17701	501,72	32,50%
Q04836	31 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP31A PE=1 SV=1	7	---	----	-0,078	0,17681	501,15	32,50%
Q9LV33	Beta-glucosidase 44 OS=Arabidopsis thaliana GN=BGLU44 PE=2 SV=1	15	---	----	-0,097	0,17608	499,10	32,50%
Q94K59	Phosphorylase family protein OS=Arabidopsis thaliana GN=At4g24350 PE=2 SV=1	3	---	----	-0,283	0,17608	499,10	32,50%
Q8VY01	Serine carboxypeptidase-like 46 OS=Arabidopsis thaliana GN=SCPL46 PE=2 SV=1	2	---	----	-0,342	0,17661	500,59	32,50%
Q8GXB1	UPF0548 protein At2g17695 OS=Arabidopsis thaliana GN=At2g17695 PE=2 SV=1	1	---	----	-0,4	0,17608	499,10	32,50%
Q9LPG6;Q9SYM5	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-red	2	---	----	0,34	0,17842	505,72	32,70%
Q949S6	NAD(P)-linked oxidoreductase-like protein OS=Arabidopsis thaliana GN=At1g14345 PE=2 SV=1	2	---	----	-0,256	0,17861	506,26	32,70%
Q9SMZ4	Alpha-aminoadipic semialdehyde synthase OS=Arabidopsis thaliana GN=LKR/SDH PE=1 SV=1	3	---	----	-0,291	0,17808	504,76	32,70%
O04848	Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1	1	---	----	-0,356	0,17818	505,05	32,70%
Q9LK61	30S ribosomal protein S10, chloroplastic OS=Arabidopsis thaliana GN=RPS10 PE=2 SV=1	2	---	----	-0,172	0,17942	508,55	32,80%
Q9SZ83	Uncharacterized oxidoreductase At4g09670 OS=Arabidopsis thaliana GN=At4g09670 PE=1 SV=1	6	---	----	-0,144	0,18008	510,43	32,90%
Q9FL69	Probable ADP-ribosylation factor GTPase-activating protein AGD5 OS=Arabidopsis thaliana GN=AGD5 PE=1 SV=1	1	ARSPPRVEQER	Phospho S3	-0,404	0,18008	510,43	32,90%
O04848;O81826;Q94F49;	Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1	1	---	----	-0,515	0,17941	508,52	32,90%
Q42418;Q42449	Profilin-2 OS=Arabidopsis thaliana GN=PRO2 PE=2 SV=1	1	---	----	0,222	0,18061	511,92	33,00%
F4JL11;Q96321	Importin subunit alpha-2 OS=Arabidopsis thaliana GN=IMPA2 PE=1 SV=1	1	---	----	0,303	0,18221	516,46	33,10%
Q9LQ55	Dynamin-2B OS=Arabidopsis thaliana GN=DRP2B PE=1 SV=2	2	---	----	0,274	0,18181	515,33	33,10%
Q9M3C6	Putative calcium homeostasis regulator OS=Arabidopsis thaliana GN=T26I12.130 PE=2 SV=1	5	---	----	0,166	0,18201	515,89	33,10%
O64517	Metacaspase-4 OS=Arabidopsis thaliana GN=AMC4 PE=1 SV=1	8	---	----	0,14	0,18201	515,89	33,10%
O65660	AT4g39730/T19P19_120 OS=Arabidopsis thaliana GN=At4g39730 PE=2 SV=1	3	---	----	-0,164	0,18182	515,35	33,10%
F4ITW1	5'-nucleotidase / magnesium ion binding protein OS=Arabidopsis thaliana GN=At2g38680 PE=4 SV=1	1	---	----	1,106	0,18181	515,33	33,20%
O23016	Probable voltage-gated potassium channel subunit beta OS=Arabidopsis thaliana GN=KAB1 PE=1 SV=1	11	---	----	0,119	0,18261	517,59	33,20%
F4IKM1	Tropinone reductase homolog At2g29340 OS=Arabidopsis thaliana GN=At2g29340 PE=2 SV=1	5	---	----	-0,237	0,18181	515,33	33,20%
Q8VYN6	ATP-dependent 6-phosphofructokinase 5, chloroplastic OS=Arabidopsis thaliana GN=PFK5 PE=1 SV=1	1	---	----	-0,491	0,18261	517,59	33,20%
Q8LPF1	Pentatricopeptide repeat-containing protein At5g15980, mitochondrial OS=Arabidopsis thaliana GN=At5g15980 PE=2 S	1	---	----	0,419	0,18422	522,16	33,40%
F4JM22	Uncharacterized protein OS=Arabidopsis thaliana GN=At4g28740 PE=4 SV=1	2	---	----	-0,279	0,18408	521,77	33,40%
Q08298	Dehydration-responsive protein RD22 OS=Arabidopsis thaliana GN=RD22 PE=2 SV=1	3	---	----	-0,164	0,18462	523,29	33,50%
Q9STT3	Aldose 1-epimerase OS=Arabidopsis thaliana GN=T23J7.130 PE=2 SV=1	2	---	----	-0,268	0,18501	524,40	33,50%
P55034	26S proteasome non-ATPase regulatory subunit 4 homolog OS=Arabidopsis thaliana GN=RPN10 PE=1 SV=1	4	---	----	0,202	0,18581	526,66	33,60%
O82514	Adenylate kinase 4 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=2	7	---	----	0,115	0,18602	527,26	33,60%
Q94B35	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=ISPH PE=2 SV=1	11	---	----	0,11	0,18608	527,44	33,60%
Q8GYZ3	Putative uncharacterized protein At1g19130/F14D16_18 OS=Arabidopsis thaliana GN=At1g19130 PE=2 SV=1	2	---	----	0,398	0,18681	529,50	33,70%
Q8W4M5	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 1 OS=Arabidopsis thaliana GN=PFP-BETA1 P	3	---	----	0,248	0,18642	528,39	33,70%
Q9M7X9	Thioredoxin-like protein CITRX, chloroplastic OS=Arabidopsis thaliana GN=CITRX PE=1 SV=1	4	---	----	0,21	0,18661	528,93	33,70%
Q8RWI0	Putative uncharacterized protein At1g54520 OS=Arabidopsis thaliana GN=At1g54520 PE=1 SV=1	4	---	----	-0,217	0,18701	530,06	33,70%
Q96283;Q9FIF9	Ras-related protein RABA2c OS=Arabidopsis thaliana GN=RABA2C PE=2 SV=4	1	---	----	0,443	0,18808	533,11	33,80%
P51413	60S ribosomal protein L17-2 OS=Arabidopsis thaliana GN=RPL17B PE=2 SV=2	1	---	----	0,437	0,18781	532,33	33,80%
Q94JT5	AT4g35220/F23E12_220 OS=Arabidopsis thaliana GN=At4g35220 PE=2 SV=1	1	---	----	0,423	0,18808	533,11	33,80%
P32961;P46010	Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	1	---	----	0,286	0,18808	533,11	33,80%
Q84W89;Q8LA13	DEAD-box ATP-dependent RNA helicase 37 OS=Arabidopsis thaliana GN=RH37 PE=2 SV=2	3	---	----	-0,273	0,18808	533,11	33,80%
Q9S9K7	Probable histone H2AXb OS=Arabidopsis thaliana GN=At1g54690 PE=1 SV=1	1	---	----	-0,282	0,18761	531,76	33,80%
F4I7I0	Alanine aminotransferase 1, mitochondrial OS=Arabidopsis thaliana GN=ALAAT1 PE=1 SV=1	13	---	----	-0,097	0,18941	536,87	34,00%
Q8LDU1	AT3G03890 protein OS=Arabidopsis thaliana GN=At3g03890 PE=2 SV=1	1	---	----	-0,407	0,18941	536,87	34,00%
F4K2D7	LETM1-like protein OS=Arabidopsis thaliana GN=At5g06220 PE=4 SV=1	1	---	----	1,092	0,19018	539,06	34,10%
Q9SFU0	Protein transport protein Sec24-like At3g07100 OS=Arabidopsis thaliana GN=At3g07100 PE=2 SV=2	2	---	----	0,309	0,19008	538,77	34,10%
Q9SMN1	Gamma carbonic anhydrase-like 2, mitochondrial OS=Arabidopsis thaliana GN=GAMMACAL2 PE=1 SV=1	3	---	----	0,233	0,19042	539,73	34,10%
Q8LCL3	60S ribosomal protein L27-2 OS=Arabidopsis thaliana GN=RPL27B PE=2 SV=2	3	---	----	0,216	0,19002	538,60	34,10%
P30184;Q944P7	Leucine aminopeptidase 1 OS=Arabidopsis thaliana GN=PM25 PE=1 SV=1	6	---	----	0,102	0,19061	540,27	34,10%
Q8VZ57	Putative hydrolase OS=Arabidopsis thaliana GN=At1g52510 PE=2 SV=1	10	---	----	-0,107	0,19081	540,83	34,10%
Q8GYL5;Q9T029	40S ribosomal protein S25-3 OS=Arabidopsis thaliana GN=RPS25D PE=3 SV=2	1	---	----	0,17	0,19202	544,26	34,30%
Q6NPL0	At4g09040 OS=Arabidopsis thaliana GN=At4g09040 PE=2 SV=1	4	---	----	-0,181	0,19208	544,44	34,30%
O23708	Proteasome subunit alpha type-2-A OS=Arabidopsis thaliana GN=PAB1 PE=1 SV=1	8	---	----	0,128	0,19382	549,37	34,60%
Q9ZPI5	Peroxisomal fatty acid beta-oxidation multifunctional protein MFP2 OS=Arabidopsis thaliana GN=MFP2 PE=1 SV=1	11	---	----	-0,117	0,19441	551,04	34,60%
Q8VZC3	Delta-1-pyrroline-5-carboxylate dehydrogenase 12A1, mitochondrial OS=Arabidopsis thaliana GN=ALDH12A1 PE=2 SV=	3	---	----	-0,207	0,19408	550,11	34,60%
F4JKZ9	Uncharacterized protein OS=Arabidopsis thaliana GN=At4g16060 PE=4 SV=1	3	---	----	-0,244	0,19408	550,11	34,60%

O82533	Cell division protein FtsZ homolog 2-1, chloroplastic OS=Arabidopsis thaliana GN=FTSZ2-1 PE=1 SV=2	6	---	----	0,177	0,19522	553,33	34,70%
Q9LRJ9	Cysteine-rich repeat secretory protein 38 OS=Arabidopsis thaliana GN=CRRSP38 PE=2 SV=1	4	---	----	-0,227	0,19482	552,20	34,70%
Q8RWY5	Putative uncharacterized protein At3g10040 OS=Arabidopsis thaliana GN=At3g10040 PE=2 SV=2	1	---	----	0,388	0,19618	556,06	34,80%
P46077	14-3-3-like protein GF14 phi OS=Arabidopsis thaliana GN=GRF4 PE=1 SV=2	7	---	----	0,117	0,19582	555,04	34,80%
P0DH95	Calmodulin-1 OS=Arabidopsis thaliana GN=CAM1 PE=2 SV=1	4	---	----	0,116	0,19581	555,01	34,80%
O65271	Bifunctional protein FolD 4, chloroplastic OS=Arabidopsis thaliana GN=FOLD4 PE=2 SV=1	3	---	----	-0,208	0,19608	555,78	34,80%
Q9LEX1	At3g61050 OS=Arabidopsis thaliana GN=T27I15_140 PE=1 SV=1	2	---	----	-0,269	0,19608	555,78	34,80%
Q9SRN0	At3g11660 OS=Arabidopsis thaliana GN=T19F11.6 PE=2 SV=1	1	---	----	-0,427	0,19681	557,84	34,80%
Q9FMA3	Peroxisome biogenesis protein 5 OS=Arabidopsis thaliana GN=PEX5 PE=1 SV=1	1	---	----	-0,478	0,19608	555,78	34,80%
Q94BT0	Sucrose-phosphate synthase 1 OS=Arabidopsis thaliana GN=SPS1 PE=1 SV=1	5	---	----	0,173	0,19741	559,54	34,90%
O22886	Uroporphyrinogen decarboxylase 2, chloroplastic OS=Arabidopsis thaliana GN=HEME2 PE=2 SV=1	11	---	----	-0,113	0,19701	558,41	34,90%
Q9FGZ9	Ubiquitin-like protein 5 OS=Arabidopsis thaliana GN=UBL5 PE=3 SV=1	1	---	----	0,384	0,19802	561,27	35,00%
O23207	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 2 OS=Arabidopsis thaliana GN=At4g36750 PE=1 SV=1	1	---	----	-0,401	0,19841	562,38	35,00%
F4J8C7	Phosphoglycerate mutase-like protein OS=Arabidopsis thaliana GN=At3g01310 PE=1 SV=1	3	---	----	0,253	0,19882	563,54	35,10%
Q39173	NADP-dependent alkenal double bond reductase P2 OS=Arabidopsis thaliana GN=P2 PE=2 SV=2	4	---	----	0,213	0,19941	565,21	35,10%
Q94CJ5	At5g12470 OS=Arabidopsis thaliana GN=At5g12470 PE=2 SV=1	5	---	----	-0,129	0,19901	564,08	35,10%
Q9SRD9	Putative uncharacterized protein F28O16.11 OS=Arabidopsis thaliana GN=F28O16.11 PE=4 SV=1	1	---	----	0,432	0,20008	567,12	35,20%
Q9LI88	Genomic DNA, chromosome 3, P1 clone:MYF5 OS=Arabidopsis thaliana GN=GHS1 PE=3 SV=1	2	---	----	-0,224	0,20018	567,40	35,20%
O48724	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 OS=Arabidopsis thaliana GN=WEB1 PE=1 SV=1	1	---	----	-0,472	0,20018	567,40	35,20%
O80977	Vacuolar-sorting receptor 3 OS=Arabidopsis thaliana GN=VSR3 PE=2 SV=1	2	---	----	0,238	0,20062	568,64	35,30%
Q43870	ATP sulfurylase 2 OS=Arabidopsis thaliana GN=APS2 PE=1 SV=1	3	---	----	0,181	0,20101	569,75	35,30%
Q9ZUX4	Uncharacterized protein At2g27730, mitochondrial OS=Arabidopsis thaliana GN=At2g27730 PE=1 SV=1	3	---	----	0,128	0,20082	569,21	35,30%
Q9LDY2	2-oxoisovalerate dehydrogenase subunit beta 2, mitochondrial OS=Arabidopsis thaliana GN=DIN4 PE=1 SV=1	2	---	----	-0,293	0,20221	573,15	35,30%
Q38970	Acetyl-CoA carboxylase 1 OS=Arabidopsis thaliana GN=ACC1 PE=1 SV=1	2	---	----	-0,369	0,20208	572,78	35,30%
F4KHY8	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g65440 PE=1 SV=1	1	---	----	0,574	0,20161	571,45	35,40%
F4I7X1;O65449	SKU5 similar 6 OS=Arabidopsis thaliana GN=SKS6 PE=4 SV=1	1	---	----	0,49	0,20208	572,78	35,40%
Q9FKC0	60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	1	---	----	0,399	0,20208	572,78	35,40%
O48726	26S proteasome regulatory subunit RPN13 OS=Arabidopsis thaliana GN=RPN13 PE=1 SV=2	4	---	----	-0,224	0,20208	572,78	35,40%
Q9S9W2	Short-chain dehydrogenase/reductase SDRA OS=Arabidopsis thaliana GN=SDRA PE=1 SV=1	1	---	----	-0,424	0,20208	572,78	35,40%
Q9ZVD0	Serrate RNA effector molecule OS=Arabidopsis thaliana GN=SE PE=1 SV=2	1	DRSPLPPPR	Phospho S3	-0,592	0,20208	572,78	35,40%
Q9M7T0	Peroxiredoxin-2F, mitochondrial OS=Arabidopsis thaliana GN=PRXIIF PE=1 SV=2	9	---	----	0,092	0,20361	577,12	35,50%
O81629	AT4g10840/F25I24_50 OS=Arabidopsis thaliana GN=F8M12.21 PE=2 SV=1	1	---	----	0,313	0,20361	577,12	35,60%
Q9CA59	NAP1-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=1 SV=1	2	---	----	0,248	0,20422	578,84	35,60%
O64866	Calcium-binding EF-hand-containing protein OS=Arabidopsis thaliana GN=At2g44310 PE=2 SV=1	3	---	----	0,206	0,20401	578,25	35,60%
Q94A97;Q9FZ48	Ubiquitin-conjugating enzyme E2 35 OS=Arabidopsis thaliana GN=UBC35 PE=1 SV=1	3	---	----	0,192	0,20421	578,82	35,60%
Q94BZ0	At1g50450/F11F12_20 OS=Arabidopsis thaliana GN=At1g50450 PE=2 SV=1	2	---	----	-0,257	0,20408	578,45	35,60%
P60039;P60040	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	1	---	----	0,243	0,20502	581,11	35,70%
Q9ZVJ2	Uncharacterized protein At2g38710 OS=Arabidopsis thaliana GN=At2g38710 PE=2 SV=1	1	---	----	0,518	0,20608	584,12	35,80%
Q8LC83;Q9SS17	40S ribosomal protein S24-2 OS=Arabidopsis thaliana GN=RPS24B PE=2 SV=2	1	---	----	0,418	0,20601	583,92	35,80%
Q9FV52	Methionine aminopeptidase 1B, chloroplastic OS=Arabidopsis thaliana GN=MAP1B PE=2 SV=2	1	---	----	0,404	0,20618	584,40	35,80%
Q39255	SKP1-like protein 1A OS=Arabidopsis thaliana GN=SKP1A PE=1 SV=1	1	---	----	0,37	0,20601	583,92	35,80%
Q66GR6	Single-stranded DNA-binding protein WHY3, chloroplastic OS=Arabidopsis thaliana GN=WHY3 PE=1 SV=1	5	---	----	-0,165	0,20618	584,40	35,80%
B9DGD6	Acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal OS=Arabidopsis thaliana GN=ACS PE=1 SV=1	4	---	----	0,17	0,20762	588,48	35,90%
F4JVN6	Tripeptidyl-peptidase 2 OS=Arabidopsis thaliana GN=TPP2 PE=1 SV=1	16	---	----	-0,09	0,20701	586,75	35,90%
Q9LHB9	Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3	1	---	----	-0,5	0,20702	586,78	35,90%
P29513;P29514	Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1	1	---	----	0,28	0,20781	589,02	36,00%
Q8GUN7;Q8RY94	Adenylosuccinate lyase OS=Arabidopsis thaliana GN=At1g36280 PE=2 SV=1	3	---	----	0,201	0,20841	590,72	36,00%
Q0WNJ6	Clathrin heavy chain 1 OS=Arabidopsis thaliana GN=CHC1 PE=1 SV=1	10	---	----	0,123	0,20818	590,07	36,00%
Q9SF29	Syntaxin-71 OS=Arabidopsis thaliana GN=SYP71 PE=1 SV=1	2	---	----	-0,221	0,20818	590,07	36,00%
Q8H103	Glucose-6-phosphate isomerase 1, chloroplastic OS=Arabidopsis thaliana GN=PGI1 PE=1 SV=1	3	---	----	-0,265	0,20881	591,85	36,00%
Q84JF2	Class I peptide chain release factor OS=Arabidopsis thaliana GN=At1g62850 PE=2 SV=1	1	---	----	-0,61	0,21008	595,46	36,20%
Q9LW15	Cytochrome c oxidase subunit 5b-1, mitochondrial OS=Arabidopsis thaliana GN=COX5B-1 PE=2 SV=1	1	---	----	0,171	0,21081	597,52	36,30%
F4JW99	TOMV RNA binding protein OS=Arabidopsis thaliana GN=BTR1L PE=1 SV=1	8	---	----	0,114	0,21141	599,22	36,40%
Q9LZI4	At3g62810 OS=Arabidopsis thaliana GN=F26K9_240 PE=2 SV=1	1	---	----	0,385	0,21242	602,09	36,50%
Q9FGS0	RNA-binding protein CP31B, chloroplastic OS=Arabidopsis thaliana GN=CP31B PE=1 SV=1	4	---	----	-0,16	0,21208	601,13	36,50%

Q940N7	AT4g05150/C17L7_70 OS=Arabidopsis thaliana GN=At4g05150 PE=1 SV=1	1	---	----	-0,42	0,21218	601,41	36,50%
Q9LFA3	Probable monodehydroascorbate reductase, cytoplasmic isoform 3 OS=Arabidopsis thaliana GN=At3g52880 PE=1 SV=1	17	---	----	-0,06	0,21281	603,19	36,60%
Q9M328	AT3G53990 protein OS=Arabidopsis thaliana GN=F5K20_290 PE=2 SV=1	3	---	----	0,223	0,21361	605,46	36,70%
Q9LZM6	At5g02050 OS=Arabidopsis thaliana GN=T7H20_100 PE=2 SV=1	1	---	----	0,396	0,21461	608,29	36,80%
F4KE63	ATP binding/valine-tRNA ligase/aminoacyl-tRNA ligase OS=Arabidopsis thaliana GN=EMB2247 PE=3 SV=1	8	---	----	-0,128	0,21408	606,79	36,80%
Q42449	Profilin-1 OS=Arabidopsis thaliana GN=PRO1 PE=1 SV=1	4	---	----	0,149	0,21608	612,46	36,90%
Q9ASV6	30S ribosomal protein S20, chloroplastic OS=Arabidopsis thaliana GN=RPS20 PE=2 SV=1	4	---	----	-0,146	0,21608	612,46	36,90%
Q9M9S3	Single-stranded DNA-binding protein WHY1, chloroplastic OS=Arabidopsis thaliana GN=WHY1 PE=1 SV=1	2	---	----	-0,345	0,21618	612,75	36,90%
Q9FFQ8	DEK domain-containing chromatin associated protein OS=Arabidopsis thaliana GN=At5g63550 PE=4 SV=1	1	---	----	0,577	0,21682	614,56	37,00%
Q9SHH6	Glutathione S-transferase U24 OS=Arabidopsis thaliana GN=GSTU24 PE=2 SV=1	1	---	----	0,392	0,21581	611,70	37,00%
Q70E96	Aldehyde dehydrogenase family 3 member F1 OS=Arabidopsis thaliana GN=ALDH3F1 PE=2 SV=2	2	---	----	0,248	0,21581	611,70	37,00%
P40941	ADP,ATP carrier protein 2, mitochondrial OS=Arabidopsis thaliana GN=AAC2 PE=2 SV=2	1	---	----	0,245	0,21608	612,46	37,00%
O65378;Q06588;Q41931	1-aminocyclopropane-1-carboxylate oxidase 3 OS=Arabidopsis thaliana GN=At1g12010 PE=2 SV=1	1	---	----	0,209	0,21582	611,72	37,00%
Q39242;Q39243	Thioredoxin reductase 2 OS=Arabidopsis thaliana GN=NTR2 PE=2 SV=2	2	---	----	0,185	0,21601	612,26	37,00%
Q93ZN2	Probable aldo-keto reductase 4 OS=Arabidopsis thaliana GN=At1g60710 PE=2 SV=1	7	---	----	0,128	0,21808	618,13	37,10%
Q9S7N7	Photosystem I reaction center subunit V, chloroplastic OS=Arabidopsis thaliana GN=PSAG PE=2 SV=1	5	---	----	0,112	0,21808	618,13	37,10%
P93832;Q9FMT1	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1	1	---	----	0,504	0,21902	620,79	37,20%
Q8VX13	Protein disulfide isomerase-like 1-3 OS=Arabidopsis thaliana GN=PDIL1-3 PE=2 SV=1	1	---	----	0,374	0,21861	619,63	37,20%
Q8LEK2	Golgi apparatus membrane protein-like protein ECHIDNA OS=Arabidopsis thaliana GN=ECH PE=1 SV=1	1	---	----	0,276	0,21808	618,13	37,20%
Q8W471	Long-chain-fatty-acid--[acyl-carrier-protein] ligase AEE15, chloroplastic OS=Arabidopsis thaliana GN=AAE15 PE=1 SV=1	8	---	----	-0,127	0,21802	617,96	37,20%
Q9LK96	AT3g15090/K15M2_24 OS=Arabidopsis thaliana GN=At3g15090 PE=2 SV=1	6	---	----	-0,132	0,21881	620,20	37,20%
Q945K7	Isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial OS=Arabidopsis thaliana GN=IDH5 PE=2 SV=1	4	---	----	0,2	0,22008	623,80	37,30%
Q9FIE8	UDP-glucuronic acid decarboxylase 3 OS=Arabidopsis thaliana GN=UXS3 PE=1 SV=1	5	---	----	0,181	0,22041	624,73	37,30%
Q43314	Glutamate dehydrogenase 1 OS=Arabidopsis thaliana GN=GDH1 PE=2 SV=1	5	---	----	-0,148	0,22082	625,90	37,30%
Q9MB58	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase OS=Arabidopsis thaliana GN=FKFBP PE=1 SV=1	4	---	----	-0,2	0,22008	623,80	37,30%
Q94A32	Protein FATTY ACID EXPORT 2, chloroplastic OS=Arabidopsis thaliana GN=FAX2 PE=2 SV=1	1	---	----	-0,282	0,22061	625,30	37,30%
Q9SK82	UDP-glycosyltransferase 85A1 OS=Arabidopsis thaliana GN=UGT85A1 PE=2 SV=1	1	---	----	-0,389	0,22008	623,80	37,30%
Q8H1Q2	Cytosolic Fe-S cluster assembly factor NBP35 OS=Arabidopsis thaliana GN=NBP35 PE=1 SV=1	1	---	----	0,367	0,22008	623,80	37,40%
Q9LNJ3	Aspartyl protease family protein OS=Arabidopsis thaliana GN=F6F3.10 PE=2 SV=1	3	---	----	0,294	0,22141	627,57	37,40%
P56820;Q9FKV6	Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=TIF3D1 PE=1 SV=1	1	---	----	-0,373	0,22002	623,63	37,40%
F4HWS2	Calcium-dependent lipid-binding family protein OS=Arabidopsis thaliana GN=At1g48090 PE=4 SV=1	1	---	----	0,796	0,22208	629,47	37,50%
Q9LV03	Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana GN=GLT1 PE=2 SV=2	26	---	----	0,079	0,22222	629,86	37,50%
Q9S757	Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial OS=Arabidopsis thaliana GN=CYSC1 PE=1 S	11	---	----	0,075	0,22218	629,75	37,50%
Q9FNF6	Dipeptidyl peptidase IV-like protein OS=Arabidopsis thaliana GN=At5g24260 PE=2 SV=1	1	---	----	-0,631	0,22222	629,86	37,50%
Q9XJ27	30S ribosomal protein S9, chloroplastic OS=Arabidopsis thaliana GN=RPS9 PE=2 SV=1	5	---	----	-0,126	0,22401	634,94	37,70%
Q9ZVA1;Q9ZVA2	D-mannose binding lectin protein with Apple-like carbohydrate-binding domain OS=Arabidopsis thaliana GN=F9K20.13	3	---	----	-0,132	0,22408	635,14	37,70%
Q9ZSA2	Calcium-dependent protein kinase 21 OS=Arabidopsis thaliana GN=CPK21 PE=1 SV=1	4	---	----	-0,187	0,22421	635,50	37,70%
Q9XIN6	At2g27290 OS=Arabidopsis thaliana GN=At2g27290 PE=2 SV=1	1	---	----	-0,287	0,22422	635,53	37,70%
F4J8D3	Protein TPLATE OS=Arabidopsis thaliana GN=TPLATE PE=1 SV=1	1	---	----	-0,473	0,22418	635,42	37,70%
Q9LRX8	60S ribosomal protein L13a-2 OS=Arabidopsis thaliana GN=RPL13AB PE=1 SV=1	2	---	----	0,125	0,22522	638,37	37,80%
Q9LZI2	UDP-glucuronic acid decarboxylase 2 OS=Arabidopsis thaliana GN=UXS2 PE=1 SV=1	1	---	----	0,412	0,22601	640,61	37,90%
O64644	Histone deacetylase complex subunit SAP18 OS=Arabidopsis thaliana GN=At2g45640 PE=1 SV=1	1	---	----	0,389	0,22608	640,80	37,90%
P42748	Ubiquitin-conjugating enzyme E2 4 OS=Arabidopsis thaliana GN=UBC4 PE=2 SV=2	2	---	----	0,281	0,22601	640,61	37,90%
F4JGR5	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 2 OS=Arabidopsis thaliana GN=PFP-BETA2 P	2	---	----	0,266	0,22542	638,93	37,90%
Q9ZVH7	Protein FATTY ACID EXPORT 3, chloroplastic OS=Arabidopsis thaliana GN=FAX3 PE=2 SV=2	5	---	----	-0,147	0,22661	642,31	37,90%
P59169	Histone H3.3 OS=Arabidopsis thaliana GN=HTR4 PE=1 SV=2	1	---	----	-0,795	0,22618	641,09	37,90%
O22791	Putative RNA-binding protein OS=Arabidopsis thaliana GN=At2g33410 PE=2 SV=1	3	---	----	-0,293	0,22721	644,01	38,00%
P56804	30S ribosomal protein S14, chloroplastic OS=Arabidopsis thaliana GN=rps14 PE=2 SV=2	1	---	----	0,374	0,22808	646,47	38,10%
Q9ZW35	Proliferating cell nuclear antigen 2 OS=Arabidopsis thaliana GN=PCNA2 PE=1 SV=1	1	---	----	0,279	0,22808	646,47	38,10%
P42697	Dynamin-related protein 1A OS=Arabidopsis thaliana GN=DRP1A PE=1 SV=3	11	---	----	0,103	0,22761	645,14	38,10%
Q84P23	4-coumarate--CoA ligase-like 9 OS=Arabidopsis thaliana GN=4CLL9 PE=1 SV=2	1	---	----	-0,516	0,22808	646,47	38,10%
Q8L9R6	At1g68680 OS=Arabidopsis thaliana GN=At1g68680 PE=2 SV=1	1	---	----	0,965	0,23002	651,97	38,20%
Q9FNM7	DEAD-box ATP-dependent RNA helicase 26 OS=Arabidopsis thaliana GN=RH26 PE=1 SV=2	1	---	----	0,381	0,23022	652,54	38,20%
O22715	AP-1 complex subunit mu-2 OS=Arabidopsis thaliana GN=AP1M2 PE=1 SV=1	1	---	----	0,364	0,22921	649,68	38,20%
O81299	AT4g02340 protein OS=Arabidopsis thaliana GN=T14P8.15 PE=2 SV=1	1	---	----	0,344	0,23008	652,14	38,20%

Q94AC8	AT4g28030/T13J8_140 OS=Arabidopsis thaliana GN=At4g28030 PE=2 SV=1	1	---	----	0,267	0,23002	651,97	38,20%
Q9C514	40S ribosomal protein S7-1 OS=Arabidopsis thaliana GN=RPS7A PE=2 SV=1	5	---	----	0,189	0,22942	650,27	38,20%
F4JRE0	Transmembrane 9 superfamily member 12 OS=Arabidopsis thaliana GN=TMN12 PE=2 SV=1	4	---	----	0,184	0,22881	648,54	38,20%
Q38833	Chlorophyll synthase, chloroplastic OS=Arabidopsis thaliana GN=CHLG PE=2 SV=1	4	---	----	0,164	0,22882	648,57	38,20%
Q9M5K3	Dihydrolipoyl dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana GN=LPD1 PE=1 SV=2	9	---	----	-0,1	0,23008	652,14	38,20%
Q94F10	Putative uncharacterized protein At1g74730 OS=Arabidopsis thaliana GN=At1g74730 PE=1 SV=1	1	---	----	-0,176	0,22961	650,81	38,20%
Q9LYE7	Putative uncharacterized protein At5g11420 OS=Arabidopsis thaliana GN=F15N18_10 PE=2 SV=1	3	---	----	-0,196	0,22942	650,27	38,20%
Q8S8F1	Expressed protein OS=Arabidopsis thaliana GN=At2g36885 PE=2 SV=1	1	---	----	-0,27	0,23018	652,42	38,20%
Q8LPS1	Long chain acyl-CoA synthetase 6, peroxisomal OS=Arabidopsis thaliana GN=LACS6 PE=1 SV=1	1	---	----	-0,496	0,23062	653,67	38,20%
Q8LAD2	Succinyl-CoA ligase [ADP-forming] subunit alpha-2, mitochondrial OS=Arabidopsis thaliana GN=At5g23250 PE=2 SV=2	1	---	----	0,409	0,23208	657,81	38,40%
O65398;Q8W593	Lactoylglutathione lyase OS=Arabidopsis thaliana GN=F12F1.32 PE=2 SV=1	1	---	----	0,394	0,23181	657,05	38,40%
P93824	1-aminocyclopropane-1-carboxylate oxidase homolog 6 OS=Arabidopsis thaliana GN=At1g04350 PE=2 SV=1	1	---	----	-0,401	0,23218	658,09	38,40%
P10795	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1A PE=1 SV=2	1	EHGNSPGYYDGR	Phospho S5	0,77	0,23418	663,76	38,60%
P93736	Valine--tRNA ligase OS=Arabidopsis thaliana GN=VALRS PE=2 SV=2	8	---	----	0,142	0,23418	663,76	38,60%
Q9SL67	26S proteasome regulatory subunit 4 homolog B OS=Arabidopsis thaliana GN=RPT2B PE=1 SV=1	9	---	----	0,125	0,23408	663,48	38,60%
Q9M153	GDSL esterase/lipase At4g01130 OS=Arabidopsis thaliana GN=At4g01130 PE=2 SV=1	2	---	----	-0,268	0,23341	661,58	38,60%
Q9LX99	Kinesin-like protein KCA1 OS=Arabidopsis thaliana GN=KCA1 PE=1 SV=1	6	---	----	-0,161	0,23401	663,28	38,70%
Q96283	Ras-related protein RABA2c OS=Arabidopsis thaliana GN=RABA2C PE=2 SV=4	1	---	----	0,784	0,23641	670,08	38,80%
Q8L633	Ribonuclease Z, chloroplastic OS=Arabidopsis thaliana GN=CPZ PE=2 SV=1	1	---	----	0,382	0,23561	667,82	38,80%
rev_Q9M2Q4	reversed UPF0202 protein At3g57940 OS=Arabidopsis thaliana GN=At3g57940 PE=2 SV=2	1	---	----	0,373	0,23608	669,15	38,80%
Q8H118	Probable methyltransferase PMT1 OS=Arabidopsis thaliana GN=At3g23300 PE=2 SV=2	2	---	----	0,306	0,23682	671,25	38,80%
F4HS99;F4JKH6	Tetratricopeptide repeat-containing protein OS=Arabidopsis thaliana GN=At1g01320 PE=1 SV=1	3	---	----	0,164	0,23608	669,15	38,80%
Q9SW96	Asparagine--tRNA ligase, cytoplasmic 1 OS=Arabidopsis thaliana GN=SYNC1 PE=1 SV=1	6	---	----	0,143	0,23661	670,65	38,80%
P21238	Chaperonin 60 subunit alpha 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60A1 PE=1 SV=2	28	---	----	0,04	0,23661	670,65	38,80%
Q9SYI0	Protein translocase subunit SECA1, chloroplastic OS=Arabidopsis thaliana GN=SECA1 PE=2 SV=2	25	---	----	-0,066	0,23618	669,43	38,80%
D7SFH9;Q7Y208;Q9SZ11	Glycerophosphodiester phosphodiesterase protein kinase domain-containing GDPDL2 OS=Arabidopsis thaliana GN=GD	1	---	----	-0,269	0,23608	669,15	38,80%
F4JBL2	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At3g47560 PE=1 SV=1	1	---	----	-0,377	0,23618	669,43	38,80%
Q9C9Y6	Thioredoxin H9 OS=Arabidopsis thaliana GN=TRX9 PE=1 SV=1	1	VTSIIDSVPESPQRP	Phospho S11	0,497	0,23608	669,15	38,90%
Q9LVC5	Apospory-associated protein C OS=Arabidopsis thaliana GN=At5g57330 PE=1 SV=1	3	---	----	0,206	0,23842	675,78	38,90%
Q94AW8	Chaperone protein dnaJ 3 OS=Arabidopsis thaliana GN=ATJ3 PE=1 SV=2	5	---	----	0,136	0,23808	674,81	38,90%
F4IT21;Q9M1Y7	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g43945 PE=4 SV=1	2	---	----	-0,206	0,23818	675,10	38,90%
F4IPY2	Cysteinyl-tRNA synthetase OS=Arabidopsis thaliana GN=SYCO ARATH PE=3 SV=1	2	---	----	-0,285	0,23608	669,15	38,90%
P48578	Serine/threonine-protein phosphatase PP2A-3 catalytic subunit OS=Arabidopsis thaliana GN=PP2A3 PE=2 SV=1	1	---	----	-0,375	0,23741	672,92	38,90%
Q9LK23	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform 1 OS=Arabidopsis thaliana GN=ACG9 PE=2 SV=1	4	---	----	0,228	0,23901	677,45	39,00%
Q9SUI4	Photosystem I reaction center subunit XI, chloroplastic OS=Arabidopsis thaliana GN=PSAL PE=1 SV=2	6	---	----	-0,088	0,23881	676,89	39,00%
Q9C8E6	Plastid movement impaired1 OS=Arabidopsis thaliana GN=T8D8.2 PE=1 SV=1	6	---	----	-0,155	0,23881	676,89	39,00%
Q9S756	Ferritin-4, chloroplastic OS=Arabidopsis thaliana GN=FER4 PE=2 SV=1	3	---	----	-0,193	0,23941	678,59	39,00%
Q9ZUS0	Histone H2B.4 OS=Arabidopsis thaliana GN=At2g37470 PE=1 SV=3	1	---	----	0,361	0,24008	680,48	39,10%
Q9SL05	Protein PROTON GRADIENT REGULATION 5, chloroplastic OS=Arabidopsis thaliana GN=PGR5 PE=1 SV=1	1	---	----	-0,207	0,24008	680,48	39,10%
P11035	Nitrate reductase [NADH] 2 OS=Arabidopsis thaliana GN=NIA2 PE=1 SV=1	1	SVSTPFMNTTAK	Phospho S3	-0,351	0,24018	680,77	39,10%
Q5PP23	At4g28370 OS=Arabidopsis thaliana GN=At4g28370 PE=1 SV=1	1	---	----	-0,358	0,24008	680,48	39,10%
Q9SKQ0	Peptidyl-prolyl cis-trans isomerase CYP19-2 OS=Arabidopsis thaliana GN=CYP19-2 PE=1 SV=1	1	---	----	0,372	0,24161	684,82	39,30%
A8MR80	Uncharacterized protein OS=Arabidopsis thaliana GN=At4g30845 PE=4 SV=1	1	---	----	-0,363	0,24218	686,43	39,30%
rev_A4IJ32	reversed At3g12940 OS=Arabidopsis thaliana GN=At3g12940 PE=2 SV=1	1	---	----	-0,775	0,24221	686,52	39,30%
Q9FT52	ATP synthase subunit d, mitochondrial OS=Arabidopsis thaliana GN=At3g52300 PE=1 SV=3	11	---	----	0,088	0,24341	689,93	39,50%
Q9LZJ5	ABC transporter C family member 14 OS=Arabidopsis thaliana GN=ABCC14 PE=1 SV=1	1	---	----	0,386	0,24408	691,82	39,60%
O22822	UDP-glycosyltransferase 74F2 OS=Arabidopsis thaliana GN=UGT74F2 PE=1 SV=1	5	---	----	-0,16	0,24421	692,19	39,60%
Q9FF75	Protein SAD1/UNC-84 domain protein 1 OS=Arabidopsis thaliana GN=SUN1 PE=1 SV=1	1	---	----	-0,375	0,24408	691,82	39,60%
P25818	Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1	1	---	----	-0,222	0,24501	694,46	39,70%
Q8LAD4	At5g57345 OS=Arabidopsis thaliana GN=At5g57345 PE=2 SV=1	2	---	----	0,239	0,24642	698,46	39,80%
Q9LX65	V-type proton ATPase subunit H OS=Arabidopsis thaliana GN=VHA-H PE=1 SV=1	5	---	----	0,116	0,24618	697,77	39,80%
Q9C8G9	ABC transporter C family member 1 OS=Arabidopsis thaliana GN=ABCC1 PE=1 SV=1	3	---	----	-0,24	0,24608	697,49	39,80%
F4JK28	Mitochondrial transcription termination factor family protein OS=Arabidopsis thaliana GN=At4g09620 PE=4 SV=1	1	---	----	-0,348	0,24608	697,49	39,80%
Q9FLI7	CDGSH iron-sulfur domain-containing protein NEET OS=Arabidopsis thaliana GN=NEET PE=1 SV=1	3	---	----	-0,162	0,24741	701,26	39,90%
Q93Z34	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g24280 PE=2 SV=1	3	---	----	0,231	0,24882	705,26	40,00%

Q9LPU8	Indole glucosinolate O-methyltransferase 4 OS=Arabidopsis thaliana GN=T22I11.4 PE=4 SV=1	7	---	----	0,127	0,24841	704,10	40,00%
Q9SKP6	Triosephosphate isomerase, chloroplastic OS=Arabidopsis thaliana GN=TIM PE=1 SV=1	13	---	----	0,065	0,24808	703,16	40,00%
Q9SGH4	Photosynthetic NDH subunit of lumenal location 3, chloroplastic OS=Arabidopsis thaliana GN=PNSL3 PE=1 SV=1	2	---	----	-0,199	0,24781	702,40	40,00%
Q9SIM4;Q9T043	60S ribosomal protein L14-1 OS=Arabidopsis thaliana GN=RPL14A PE=2 SV=1	4	---	----	0,112	0,24882	705,26	40,10%
Q94BY7	AT3g17930/MEB5_15 OS=Arabidopsis thaliana GN=At3g17930 PE=2 SV=1	2	---	----	0,478	0,25007	708,82	40,20%
Q9FJZ7	AT5G66420 protein OS=Arabidopsis thaliana GN=At5g66420 PE=2 SV=1	4	---	----	0,161	0,25002	708,66	40,20%
Q8LDI5	Thioredoxin-like protein CXXS1 OS=Arabidopsis thaliana GN=CXXS1 PE=2 SV=2	1	---	----	-0,39	0,25017	709,11	40,20%
O82233	Eukaryotic translation initiation factor isoform 4G-2 OS=Arabidopsis thaliana GN=EIF(ISO)4G2 PE=1 SV=1	1	---	----	0,454	0,25217	714,78	40,30%
Q9FF91	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g23890 PE=1 SV=1	1	---	----	0,358	0,25207	714,49	40,30%
Q9SRH6	Hypersensitive-induced response protein 3 OS=Arabidopsis thaliana GN=HIR3 PE=1 SV=1	3	---	----	-0,185	0,25121	712,03	40,30%
Q9MA92	Filament-like plant protein 3 OS=Arabidopsis thaliana GN=FPP3 PE=2 SV=2	1	---	----	-0,301	0,25101	711,47	40,30%
F4K4N0	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g43240 PE=4 SV=1	1	---	----	0,354	0,25201	714,30	40,40%
Q9XI87	At1g14000 OS=Arabidopsis thaliana GN=F7A19.9 PE=1 SV=1	2	---	----	0,251	0,25161	713,17	40,40%
P24636;P29513;P29517	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	1	---	----	0,216	0,25322	717,73	40,40%
O24496	Hydroxyacylglutathione hydrolase cytoplasmic OS=Arabidopsis thaliana GN=GLX2-2 PE=1 SV=2	4	---	----	0,19	0,25207	714,49	40,40%
P51427	40S ribosomal protein S5-2 OS=Arabidopsis thaliana GN=RPS5B PE=1 SV=2	2	---	----	0,157	0,25242	715,46	40,40%
O50039	Ornithine carbamoyltransferase, chloroplastic OS=Arabidopsis thaliana GN=OTC PE=2 SV=2	6	---	----	0,098	0,25282	716,60	40,40%
Q9LTX3	Pyridoxine/pyridoxamine 5'-phosphate oxidase 1, chloroplastic OS=Arabidopsis thaliana GN=PPOX1 PE=1 SV=1	5	---	----	-0,135	0,25207	714,49	40,40%
F4I0B5	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein OS=Arabidopsis thaliana GN=At1g55450 F	2	---	----	-0,226	0,25341	718,27	40,40%
P41377	Eukaryotic initiation factor 4A-2 OS=Arabidopsis thaliana GN=TIF4A-2 PE=1 SV=1	1	---	----	0,325	0,25407	720,16	40,50%
Q9SL15	Glycine-rich protein 3 OS=Arabidopsis thaliana GN=GRP3 PE=1 SV=1	1	---	----	0,25	0,25407	720,16	40,50%
Q9SIL6	Prohibitin-6, mitochondrial OS=Arabidopsis thaliana GN=PHB6 PE=1 SV=1	3	---	----	-0,206	0,25417	720,44	40,50%
F4HUK6	Probable acyl-activating enzyme 1, peroxisomal OS=Arabidopsis thaliana GN=AAE1 PE=2 SV=1	2	---	----	-0,327	0,25407	720,16	40,50%
P59229	V-type proton ATPase subunit c4 OS=Arabidopsis thaliana GN=VHA-c4 PE=2 SV=1	1	---	----	0,219	0,25617	726,11	40,60%
P56766	Photosystem I P700 chlorophyll a apoprotein A1 OS=Arabidopsis thaliana GN=psaA PE=2 SV=1	13	---	----	-0,061	0,25501	722,80	40,60%
Q9S850	Sulfite oxidase OS=Arabidopsis thaliana GN=SOX PE=1 SV=1	8	---	----	-0,108	0,25607	725,83	40,60%
Q9LZD4	Ras-related protein RABE1d OS=Arabidopsis thaliana GN=RABE1D PE=1 SV=1	1	---	----	-0,336	0,25617	726,11	40,60%
Q9SSR2	Signal peptidase I OS=Arabidopsis thaliana GN=F6D8.18 PE=2 SV=1	2	---	----	0,26	0,25607	725,83	40,70%
Q9SH69	6-phosphogluconate dehydrogenase, decarboxylating 1, chloroplastic OS=Arabidopsis thaliana GN=At1g64190 PE=1 SV	4	---	----	0,134	0,25701	728,47	40,70%
Q1JPL7	Pectinesterase/pectinesterase inhibitor 18 OS=Arabidopsis thaliana GN=PME18 PE=1 SV=3	5	---	----	0,131	0,25581	725,07	40,70%
Q42512	Protein COLD-REGULATED 15A, chloroplastic OS=Arabidopsis thaliana GN=COR15A PE=1 SV=1	5	---	----	-0,093	0,25561	724,51	40,70%
Q9SVG4	Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2	7	---	----	-0,127	0,25607	725,83	40,70%
Q9M8L4	Glycerol kinase OS=Arabidopsis thaliana GN=GLPK PE=1 SV=1	3	---	----	-0,181	0,25807	731,50	40,80%
Q0PGJ6	Aldo-keto reductase family 4 member C9 OS=Arabidopsis thaliana GN=AKR4C9 PE=1 SV=1	3	---	----	-0,208	0,25781	730,74	40,80%
Q9FLP0	65-kDa microtubule-associated protein 1 OS=Arabidopsis thaliana GN=MAP65-1 PE=1 SV=1	2	---	----	0,339	0,26017	737,45	41,10%
Q9M1C2	At3g60210 OS=Arabidopsis thaliana GN=T2O9.190 PE=2 SV=1	2	---	----	0,233	0,25962	735,87	41,10%
O80858	Expressed protein OS=Arabidopsis thaliana GN=At2g30930 PE=1 SV=1	7	---	----	-0,105	0,26041	738,11	41,10%
Q9SD78	Putative uncharacterized protein At5g08060 OS=Arabidopsis thaliana GN=F13G24.260 PE=2 SV=1	2	---	----	-0,336	0,26017	737,45	41,10%
P92964	Serine/arginine-rich splicing factor RS31 OS=Arabidopsis thaliana GN=RS31 PE=1 SV=2	1	RRPSPDYGR	Phospho S4	0,643	0,26201	742,65	41,30%
Q9LS48	protein SLOW GREEN 1, chloroplastic OS=Arabidopsis thaliana GN=SG1 PE=1 SV=1	5	---	----	0,184	0,26181	742,08	41,30%
O64764	Thioredoxin O1, mitochondrial OS=Arabidopsis thaliana GN=At2g35010 PE=2 SV=1	4	---	----	0,148	0,26217	743,12	41,30%
F4IC59	Transaldolase-like protein OS=Arabidopsis thaliana GN=At1g12230 PE=3 SV=1	5	---	----	0,12	0,26161	741,51	41,30%
Q9SR70	Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-4 PE=1 SV=1	4	---	----	-0,126	0,26141	740,94	41,30%
Q8GUK5	At3g05625 OS=Arabidopsis thaliana GN=At3g05625 PE=2 SV=1	2	---	----	-0,248	0,26207	742,83	41,30%
Q570C8;Q8LF48	3-ketoacyl-CoA thiolase 5, peroxisomal OS=Arabidopsis thaliana GN=KAT5 PE=2 SV=2	1	---	----	0,275	0,26362	747,21	41,50%
Q8L5U0	COP9 signalosome complex subunit 4 OS=Arabidopsis thaliana GN=CSN4 PE=1 SV=2	4	---	----	0,221	0,26421	748,88	41,50%
P24636;P29517	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	2	---	----	0,148	0,26402	748,34	41,50%
P62095	Cytochrome b559 subunit beta OS=Arabidopsis thaliana GN=psbF PE=3 SV=1	1	---	----	-0,145	0,26417	748,79	41,50%
Q9FFD8	At5g16470 OS=Arabidopsis thaliana GN=At5g16470 PE=1 SV=1	1	---	----	-0,368	0,26407	748,50	41,50%
Q8LFK2	AT3G03270 protein OS=Arabidopsis thaliana GN=At3g03270 PE=2 SV=1	1	---	----	0,773	0,26561	752,85	41,70%
P46248;P46644	Aspartate aminotransferase, chloroplastic OS=Arabidopsis thaliana GN=ASP5 PE=1 SV=2	1	---	----	0,131	0,26607	754,17	41,70%
Q94A28	Aconitate hydratase 3, mitochondrial OS=Arabidopsis thaliana GN=ACO3 PE=2 SV=3	15	---	----	0,084	0,26617	754,45	41,70%
Q6TBX7	Carotene epsilon-monooxygenase, chloroplastic OS=Arabidopsis thaliana GN=CYP97C1 PE=1 SV=1	3	---	----	-0,215	0,26617	754,45	41,70%
Q9C8M2	Peptide methionine sulfoxide reductase B1, chloroplastic OS=Arabidopsis thaliana GN=MSRB1 PE=1 SV=1	1	---	----	0,245	0,26681	756,25	41,80%
Q9FJR0	Regulator of nonsense transcripts 1 homolog OS=Arabidopsis thaliana GN=UPF1 PE=1 SV=2	1	---	----	0,423	0,26807	759,84	41,90%

Q93Y06	Probable inactive receptor kinase At5g67200 OS=Arabidopsis thaliana GN=At5g67200 PE=1 SV=1	1	---	----	0,351	0,26807	759,84	41,90%
Q39173;Q93Z72	NADP-dependent alkenal double bond reductase P2 OS=Arabidopsis thaliana GN=P2 PE=2 SV=2	1	---	----	0,26	0,26817	760,12	41,90%
Q9LF79	Calcium-transporting ATPase 8, plasma membrane-type OS=Arabidopsis thaliana GN=ACA8 PE=1 SV=1	2	---	----	-0,214	0,26881	761,92	41,90%
Q9SYP1	F9H16.5 protein OS=Arabidopsis thaliana GN=F9H16.5 PE=4 SV=1	3	---	----	-0,217	0,26807	759,84	41,90%
Q9FND9	Probable galactinol--sucrose galactosyltransferase 5 OS=Arabidopsis thaliana GN=RFS5 PE=1 SV=1	1	SDSGINGVDFTEK	Phospho S1	-0,843	0,26807	759,84	41,90%
Q8LAJ9	At1g22520 OS=Arabidopsis thaliana GN=At1g22520 PE=2 SV=1	1	---	----	0,925	0,27007	765,51	42,10%
Q9LFE4	WEB family protein At5g16730, chloroplastic OS=Arabidopsis thaliana GN=At5g16730 PE=1 SV=1	2	---	----	0,646	0,27042	766,48	42,10%
Q67XJ2	Nuclear transcription factor Y subunit B-10 OS=Arabidopsis thaliana GN=NFYB10 PE=2 SV=1	1	---	----	0,338	0,27061	767,02	42,10%
P93014	30S ribosomal protein S5, chloroplastic OS=Arabidopsis thaliana GN=rps5 PE=2 SV=1	13	---	----	-0,069	0,27007	765,51	42,10%
F4JZ24	Probable prolyl 4-hydroxylase 10 OS=Arabidopsis thaliana GN=P4H10 PE=2 SV=1	1	---	----	0,432	0,27101	768,16	42,20%
O65719;P22953;Q8GUM2	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	1	---	----	0,532	0,27207	771,18	42,30%
Q9LMU0	Putative GDP-L-fucose synthase 2 OS=Arabidopsis thaliana GN=GER2 PE=1 SV=1	2	---	----	0,303	0,27301	773,82	42,30%
Q9C8H3	Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein OS=Arabidopsis thalian	1	---	----	0,245	0,27282	773,29	42,30%
Q9FIX1	AIG2-like protein OS=Arabidopsis thaliana GN=At5g39730 PE=2 SV=1	5	---	----	0,137	0,27217	771,46	42,30%
Q42589	Non-specific lipid-transfer protein 1 OS=Arabidopsis thaliana GN=LTP1 PE=2 SV=1	3	---	----	0,121	0,27281	773,26	42,30%
Q42533	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=BCCP1 PE=1 SV=2	5	---	----	-0,101	0,27217	771,46	42,30%
Q9ZUU4	RNA-binding protein CP29B, chloroplastic OS=Arabidopsis thaliana GN=CP29B PE=1 SV=1	6	---	----	-0,082	0,27461	778,36	42,50%
Q39172;Q39173;Q93Z72	NADP-dependent alkenal double bond reductase P1 OS=Arabidopsis thaliana GN=P1 PE=1 SV=1	1	---	----	-0,258	0,27442	777,82	42,50%
Q9LTQ5	AT3g20370/MQC12_13 OS=Arabidopsis thaliana GN=At3g20370 PE=2 SV=1	1	---	----	0,351	0,27501	779,49	42,60%
Q9SSK9	MLP-like protein 28 OS=Arabidopsis thaliana GN=MLP28 PE=1 SV=1	1	---	----	0,34	0,27701	785,16	42,60%
Q9T0K7	3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial OS=Arabidopsis thaliana GN=At4g13360 PE=2 SV=2	4	---	----	0,184	0,27617	782,80	42,60%
Q84W65	SufE-like protein 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=SUFE1 PE=1 SV=2	8	---	----	0,105	0,27607	782,51	42,60%
Q8W593	Probable lactoylglutathione lyase, chloroplast OS=Arabidopsis thaliana GN=At1g67280 PE=1 SV=1	8	---	----	-0,085	0,27617	782,80	42,60%
Q9LIC2	Transmembrane 9 superfamily member 7 OS=Arabidopsis thaliana GN=TMN7 PE=2 SV=1	1	---	----	-0,516	0,27661	784,03	42,60%
Q9FGL9	Polypyrimidine tract-binding protein homolog 2 OS=Arabidopsis thaliana GN=At5g53180 PE=1 SV=1	1	---	----	-0,573	0,27617	782,80	42,60%
P93655	Lon protease homolog 1, mitochondrial OS=Arabidopsis thaliana GN=LON1 PE=1 SV=2	2	---	----	0,311	0,27817	788,46	42,70%
Q9SK66	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Arabidopsis thaliana GN=At2g203	6	---	----	-0,132	0,27701	785,16	42,70%
O81884	L-galactose dehydrogenase OS=Arabidopsis thaliana GN=LGALDH PE=1 SV=1	4	---	----	-0,136	0,27742	786,32	42,70%
Q9M2D8	Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1	1	IALESESPAK	none	-0,225	0,27601	782,33	42,70%
Q9FG36	Thioredoxin-like 3-1, chloroplastic OS=Arabidopsis thaliana GN=WCRKC1 PE=2 SV=3	3	---	----	-0,241	0,27782	787,46	42,70%
Q8VYI0	Sm-like protein LSM8 OS=Arabidopsis thaliana GN=LSM8 PE=1 SV=1	1	---	----	-0,334	0,27607	782,51	42,70%
Q9LK94	Probable monodehydroascorbate reductase, cytoplasmic isoform 2 OS=Arabidopsis thaliana GN=At3g27820 PE=2 SV=1	2	---	----	-0,35	0,27607	782,51	42,70%
P49572	Indole-3-glycerol phosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=At2g04400 PE=2 SV=2	10	---	----	0,099	0,27902	790,86	42,80%
Q8H1E2	Lactate/malate dehydrogenase family protein OS=Arabidopsis thaliana GN=At5g58330 PE=2 SV=1	13	---	----	0,077	0,27817	788,46	42,80%
Q94K36	Putative uncharacterized protein AT3g24100 OS=Arabidopsis thaliana GN=At3g24100 PE=2 SV=1	2	---	----	0,242	0,28021	794,23	42,90%
O22793	Multiple organellar RNA editing factor 2, chloroplastic OS=Arabidopsis thaliana GN=MORF2 PE=1 SV=1	3	---	----	0,192	0,28017	794,13	42,90%
O04921	Ferrochelatase-2, chloroplastic OS=Arabidopsis thaliana GN=At2g30390 PE=2 SV=1	2	---	----	-0,31	0,28017	794,13	43,00%
Q9SKZ0	At2g32090/F22D22.16 OS=Arabidopsis thaliana GN=At2g32090 PE=2 SV=2	1	---	----	-0,546	0,28007	793,85	43,00%
rev_B6IDH3	reversed Protein root UVB sensitive 5 OS=Arabidopsis thaliana GN=RUS5 PE=2 SV=1	1	---	----	-0,348	0,28207	799,52	43,20%
Q9FY71	Protein EXORDIUM-like 4 OS=Arabidopsis thaliana GN=EXL4 PE=2 SV=1	1	---	----	-0,384	0,28207	799,52	43,20%
P29516	Tubulin beta-8 chain OS=Arabidopsis thaliana GN=TUBB8 PE=2 SV=2	1	---	----	0,371	0,28417	805,47	43,40%
P34790	Peptidyl-prolyl cis-trans isomerase CYP18-3 OS=Arabidopsis thaliana GN=CYP18-3 PE=1 SV=1	2	---	----	-0,17	0,28417	805,47	43,40%
P42036	40S ribosomal protein S14-3 OS=Arabidopsis thaliana GN=RPS14C PE=2 SV=2	1	---	----	-0,237	0,28401	805,00	43,40%
Q8LBN7	Costars family protein At4g33640 OS=Arabidopsis thaliana GN=At4g33640 PE=1 SV=1	1	---	----	-0,405	0,28407	805,19	43,40%
P30302;P43286;P43287	Aquaporin PIP2-3 OS=Arabidopsis thaliana GN=PIP2-3 PE=1 SV=1	1	---	----	-0,413	0,28407	805,19	43,40%
Q6NMA9	At5g45170 OS=Arabidopsis thaliana GN=At5g45170 PE=2 SV=1	9	---	----	-0,088	0,28521	808,40	43,50%
P92966	Serine/arginine-rich splicing factor RS41 OS=Arabidopsis thaliana GN=RS41 PE=1 SV=2	1	ARLSPDYK	Phospho S4	0,382	0,28602	810,70	43,60%
P68209	Succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1	3	---	----	0,18	0,28617	811,14	43,60%
Q9SCV3	Beta-galactosidase 9 OS=Arabidopsis thaliana GN=BGAL9 PE=2 SV=1	1	---	----	-0,304	0,28607	810,85	43,60%
P38605	Cycloartenol synthase OS=Arabidopsis thaliana GN=CAS1 PE=1 SV=2	2	---	----	0,239	0,28817	816,81	43,90%
Q9LT08	26S proteasome non-ATPase regulatory subunit 14 homolog OS=Arabidopsis thaliana GN=RPN11 PE=1 SV=1	4	---	----	0,138	0,28841	817,47	43,90%
Q9LF30	40S ribosomal protein S19-2 OS=Arabidopsis thaliana GN=RPS19B PE=2 SV=1	1	---	----	0,251	0,28921	819,74	44,00%
Q8L7R2	Homoserine kinase OS=Arabidopsis thaliana GN=HSK PE=1 SV=1	2	---	----	0,182	0,29001	822,01	44,00%
Q9SDM9	Nitrile-specifier protein 1 OS=Arabidopsis thaliana GN=NSP1 PE=2 SV=2	4	---	----	0,154	0,29002	822,04	44,00%
Q9SSK5;Q9SSK7	MLP-like protein 43 OS=Arabidopsis thaliana GN=MLP43 PE=1 SV=1	2	---	----	0,141	0,29007	822,19	44,00%

Q9SSB5	26S protease regulatory subunit 7 homolog A OS=Arabidopsis thaliana GN=RPT1A PE=1 SV=1	9	---	----	0,126	0,29007	822,19	44,00%
Q9S713	Serine/threonine-protein kinase STN7, chloroplastic OS=Arabidopsis thaliana GN=STN7 PE=1 SV=1	6	---	----	0,126	0,29062	823,74	44,00%
Q8GUM2;Q9LDZ0	Heat shock 70 kDa protein 9, mitochondrial OS=Arabidopsis thaliana GN=HSP70-9 PE=2 SV=1	3	---	----	0,119	0,28921	819,74	44,00%
Q9M2E2	(+)-neomenthol dehydrogenase OS=Arabidopsis thaliana GN=SDR1 PE=1 SV=1	8	---	----	-0,121	0,28961	820,88	44,00%
Q9FLW9	Plastidial pyruvate kinase 2 OS=Arabidopsis thaliana GN=PKP2 PE=1 SV=1	6	---	----	0,135	0,29141	825,98	44,10%
O22265	Signal recognition particle 43 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=CAO PE=1 SV=2	3	---	----	0,173	0,29262	829,41	44,20%
P56771	Cytochrome f OS=Arabidopsis thaliana GN=petA PE=3 SV=1	14	---	----	-0,044	0,29207	827,86	44,20%
Q9M236	Putative uncharacterized protein At3g43540 OS=Arabidopsis thaliana GN=T18D12_110 PE=2 SV=1	4	---	----	-0,165	0,29201	827,68	44,20%
Q9CAP1	At1g77670 OS=Arabidopsis thaliana GN=T5M16.26 PE=2 SV=1	1	---	----	0,336	0,29407	833,53	44,30%
Q9M158	Rhodanese-like domain-containing protein 4, chloroplastic OS=Arabidopsis thaliana GN=STR4 PE=1 SV=2	10	---	----	-0,071	0,29407	833,53	44,30%
Q9M1J6	Protein STRICTOSIDINE SYNTHASE-LIKE 9 OS=Arabidopsis thaliana GN=SSL9 PE=2 SV=1	5	---	----	-0,196	0,29321	831,08	44,30%
Q9S7J7	At2g05070/F1O13.20 OS=Arabidopsis thaliana GN=LHCB2.2 PE=2 SV=1	1	---	----	-0,234	0,29442	834,51	44,30%
rev_F4J7Q4	reversed Late embryogenesis abundant protein, group 2 OS=Arabidopsis thaliana GN=At3g24600 PE=4 SV=1	1	---	----	-0,338	0,29407	833,53	44,30%
P92966	Serine/arginine-rich splicing factor RS41 OS=Arabidopsis thaliana GN=RS41 PE=1 SV=2	1	ERGSPDYGR	Phospho S4	0,715	0,29407	833,53	44,40%
Q9M291	Protein transport protein Sec24-like CEF OS=Arabidopsis thaliana GN=CEF PE=2 SV=3	1	---	----	0,333	0,29407	833,53	44,40%
Q9S714;Q9S831	Photosystem I reaction center subunit IV B, chloroplastic OS=Arabidopsis thaliana GN=PSAE2 PE=2 SV=1	2	---	----	-0,111	0,29407	833,53	44,40%
Q9XIK0	At1g10522 OS=Arabidopsis thaliana GN=At1g10522 PE=2 SV=1	1	---	----	0,313	0,29617	839,48	44,50%
Q501F7	At1g21440 OS=Arabidopsis thaliana GN=At1g21440 PE=2 SV=1	8	---	----	0,113	0,29607	839,20	44,50%
Q8GW78	Clp protease-related protein At4g12060, chloroplastic OS=Arabidopsis thaliana GN=At4g12060 PE=1 SV=1	4	---	----	-0,146	0,29607	839,20	44,50%
Q9LXA8	Probable beta-D-xylosidase 6 OS=Arabidopsis thaliana GN=BXL6 PE=2 SV=1	3	---	----	-0,177	0,29617	839,48	44,50%
Q9FVQ4	Plastidal glycolate/glycerate translocator 1, chloroplastic OS=Arabidopsis thaliana GN=PLGG1 PE=2 SV=1	3	---	----	-0,197	0,29662	840,74	44,50%
Q9SSD2	F18B13.15 protein OS=Arabidopsis thaliana GN=F18B13.15 PE=4 SV=1	1	---	----	0,341	0,29817	845,15	44,60%
Q9LXC9	Soluble inorganic pyrophosphatase 6, chloroplastic OS=Arabidopsis thaliana GN=PPA6 PE=1 SV=1	13	---	----	0,067	0,29817	845,15	44,60%
F4K2Y3	Putative S9 Tyrosyl aminopeptidase OS=Arabidopsis thaliana GN=At5g36210 PE=4 SV=1	7	---	----	-0,123	0,29882	846,98	44,60%
D7SFH9	Glycerophosphodiester phosphodiesterase protein kinase domain-containing GDPDL2 OS=Arabidopsis thaliana GN=GD	2	---	----	-0,177	0,29842	845,85	44,60%
F4ITX5	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g38780 PE=4 SV=1	1	---	----	-0,328	0,29817	845,15	44,60%
Q9ZUT9	40S ribosomal protein S5-1 OS=Arabidopsis thaliana GN=RPS5A PE=1 SV=1	1	---	----	0,644	0,29807	844,86	44,70%
A1L4Y4	At5g61510 OS=Arabidopsis thaliana GN=At5g61510 PE=2 SV=1	1	---	----	0,403	0,29807	844,86	44,70%
Q9LW15;Q9SSB8	Cytochrome c oxidase subunit 5b-1, mitochondrial OS=Arabidopsis thaliana GN=COX5B-1 PE=2 SV=1	1	---	----	0,345	0,30007	850,53	44,70%
Q9ZSJ7	AT3g24160/MUJ8_16 OS=Arabidopsis thaliana GN=PMP PE=2 SV=1	1	---	----	0,343	0,29941	848,65	44,70%
Q9FZ48	Ubiquitin-conjugating enzyme E2 36 OS=Arabidopsis thaliana GN=UBC36 PE=1 SV=1	2	---	----	0,192	0,30007	850,53	44,70%
Q9FKA5	Uncharacterized protein At5g39570 OS=Arabidopsis thaliana GN=At5g39570 PE=1 SV=1	7	---	----	0,082	0,30022	850,95	44,70%
Q6DBN2;Q9LU85	Probable plastid-lipid-associated protein 5, chloroplastic OS=Arabidopsis thaliana GN=PAP5 PE=2 SV=1	1	---	----	-0,198	0,29807	844,86	44,70%
Q9M2N5	Zinc finger BED domain-containing protein DAYSLEEPER OS=Arabidopsis thaliana GN=HAT PE=1 SV=1	2	---	----	-0,202	0,29807	844,86	44,70%
Q38950	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Arabidopsis thaliana GN=PP2A	3	---	----	-0,222	0,30017	850,82	44,70%
Q8H183	Beta-ureidopropionase OS=Arabidopsis thaliana GN=PYD3 PE=1 SV=1	1	---	----	-0,424	0,29941	848,65	44,70%
Q84LM4	Acylamino acid-releasing enzyme OS=Arabidopsis thaliana GN=aare PE=2 SV=1	1	---	----	0,235	0,30007	850,53	44,80%
Q9LJR2;Q9LK72	Lectin-like protein LEC OS=Arabidopsis thaliana GN=LEC PE=1 SV=1	3	---	----	-0,139	0,30081	852,62	44,80%
P54888	Delta-1-pyrroline-5-carboxylate synthase B OS=Arabidopsis thaliana GN=P5CSB PE=2 SV=1	2	---	----	-0,192	0,30217	856,48	44,80%
O78310	Superoxide dismutase [Cu-Zn] 2, chloroplastic OS=Arabidopsis thaliana GN=CSD2 PE=1 SV=2	1	---	----	-0,435	0,30217	856,48	44,80%
F4K455	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein OS=Arabidopsis thaliana GN=At5g20160 PE=4 SV=1	2	---	----	0,233	0,30207	856,20	44,90%
P30186	Proteasome subunit alpha type-7-A OS=Arabidopsis thaliana GN=PAD1 PE=1 SV=1	3	---	----	0,16	0,30281	858,29	44,90%
Q9LY74	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic OS=Arabidopsis thaliana GN=VTE3 PE=1 SV=1	7	---	----	0,093	0,30282	858,32	44,90%
rev_F4K493	reversed SNF2 domain-containing protein CLASSY 2 OS=Arabidopsis thaliana GN=CLSY2 PE=1 SV=1	1	---	----	-0,315	0,30207	856,20	44,90%
Q94BT0;Q9FY54	Sucrose-phosphate synthase 1 OS=Arabidopsis thaliana GN=SPS1 PE=1 SV=1	1	---	----	-0,328	0,30201	856,02	44,90%
Q9CAU9	Contains similarity to O-linked GlcNAc transferases OS=Arabidopsis thaliana GN=T9J14.22 PE=2 SV=1	1	---	----	-0,504	0,30182	855,48	44,90%
Q94KD3	Vacuolar protein sorting-associated protein 52 A OS=Arabidopsis thaliana GN=VPS52 PE=1 SV=1	1	---	----	0,415	0,30407	861,87	45,00%
O23647	1,4-alpha-glucan-branching enzyme 2-1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SBE2.1 PE=2 SV=1	3	---	----	0,185	0,30441	862,82	45,00%
P35614	Eukaryotic peptide chain release factor subunit 1-3 OS=Arabidopsis thaliana GN=ERF1-3 PE=1 SV=1	3	---	----	0,162	0,30407	861,87	45,00%
Q9ZQ80	Nodulin-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=2 SV=1	4	---	----	-0,114	0,30362	860,59	45,00%
Q9T0I9	EF-Hand containing protein-like OS=Arabidopsis thaliana GN=At4g38810 PE=2 SV=1	1	---	----	0,223	0,30607	867,54	45,20%
P48484	Serine/threonine-protein phosphatase PP1 isozyme 4 OS=Arabidopsis thaliana GN=TOPP4 PE=1 SV=1	1	---	----	0,318	0,30817	873,49	45,30%
O65272	K(+) efflux antiporter 2, chloroplastic OS=Arabidopsis thaliana GN=KEA2 PE=1 SV=2	1	---	----	0,254	0,30841	874,16	45,30%
O81644	Villin-2 OS=Arabidopsis thaliana GN=VLN2 PE=1 SV=2	8	---	----	0,116	0,30681	869,63	45,30%
Q94CE4	Beta carbonic anhydrase 4 OS=Arabidopsis thaliana GN=BCA4 PE=1 SV=1	10	---	----	-0,073	0,30722	870,79	45,30%

Q9FM11	Phosphoglycerate mutase family protein OS=Arabidopsis thaliana GN=At5g62840 PE=2 SV=1	1	---	----	-0,352	0,30721	870,76	45,30%
Q9SGY2	ATP-citrate synthase alpha chain protein 1 OS=Arabidopsis thaliana GN=ACLA-1 PE=1 SV=1	1	---	----	0,487	0,30921	876,43	45,40%
Q9LEY9	H/ACA ribonucleoprotein complex subunit 2-like protein OS=Arabidopsis thaliana GN=At5g08180 PE=1 SV=1	1	---	----	0,22	0,31017	879,16	45,40%
Q9LK29	Cytochrome c1 1, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC11 PE=1 SV=1	3	---	----	0,184	0,30882	875,32	45,40%
Q9SW21	Acyl carrier protein 4, chloroplastic OS=Arabidopsis thaliana GN=ACP4 PE=2 SV=1	2	---	----	0,137	0,31022	879,29	45,40%
Q9FI56	Chaperone protein ClpC1, chloroplastic OS=Arabidopsis thaliana GN=CLPC1 PE=1 SV=1	16	---	----	0,052	0,30942	877,03	45,40%
O64730	Probable protein phosphatase 2C 26 OS=Arabidopsis thaliana GN=At2g30170 PE=2 SV=2	6	---	----	-0,139	0,30802	873,06	45,40%
Q7Y208	Glycerophosphodiester phosphodiesterase GDPDL1 OS=Arabidopsis thaliana GN=GDPDL1 PE=1 SV=2	5	---	----	-0,151	0,30721	870,76	45,40%
Q94F00	Phosphatase IMPL1, chloroplastic OS=Arabidopsis thaliana GN=IMPL1 PE=1 SV=2	3	---	----	-0,158	0,30817	873,49	45,40%
Q84J81	Protein Fes1A OS=Arabidopsis thaliana GN=Fes1A PE=2 SV=1	2	---	----	-0,214	0,30807	873,21	45,40%
F4J117	Phosphoglucan phosphatase LSF1, chloroplastic OS=Arabidopsis thaliana GN=LSF1 PE=1 SV=1	2	---	----	-0,262	0,30801	873,03	45,40%
F4IW47	Transketolase-2, chloroplastic OS=Arabidopsis thaliana GN=TKL-2 PE=2 SV=1	1	---	----	0,339	0,31017	879,16	45,50%
Q9FJN8;Q9SIP0	Ras-related protein RABA4a OS=Arabidopsis thaliana GN=RABA4A PE=1 SV=1	1	---	----	0,317	0,31017	879,16	45,50%
F4JCX1	Glycoside hydrolase family 2 protein OS=Arabidopsis thaliana GN=At3g54440 PE=3 SV=1	2	---	----	0,232	0,31007	878,87	45,50%
Q9M0X9	4-coumarate--CoA ligase-like 7 OS=Arabidopsis thaliana GN=4CLL7 PE=1 SV=1	4	---	----	-0,171	0,31217	884,83	45,50%
Q8GSJ1;Q9S762	ATP phosphoribosyltransferase 2, chloroplastic OS=Arabidopsis thaliana GN=HISN1B PE=1 SV=1	1	---	----	0,36	0,31207	884,54	45,60%
Q941A7	AT4g20760/F21C20_110 OS=Arabidopsis thaliana GN=At4g20760 PE=2 SV=1	1	---	----	0,332	0,31217	884,83	45,60%
Q9SIH0	40S ribosomal protein S14-1 OS=Arabidopsis thaliana GN=RPS14A PE=1 SV=1	1	---	----	0,206	0,31341	888,33	45,60%
Q09152	Farnesyl pyrophosphate synthase 1, mitochondrial OS=Arabidopsis thaliana GN=FPS1 PE=2 SV=2	3	---	----	0,172	0,31262	886,10	45,60%
Q6XJG8;Q9SIV2	26S proteasome non-ATPase regulatory subunit 2 homolog B OS=Arabidopsis thaliana GN=RPN1B PE=1 SV=1	5	---	----	0,129	0,31322	887,80	45,60%
P56792	50S ribosomal protein L14, chloroplastic OS=Arabidopsis thaliana GN=rpl14 PE=3 SV=1	5	---	----	-0,09	0,31417	890,49	45,60%
F4J7G5	MD-2-related lipid recognition domain-containing protein OS=Arabidopsis thaliana GN=At3g11780 PE=4 SV=1	2	---	----	-0,165	0,31217	884,83	45,60%
O82762	F17H15.1/F17H15.1 OS=Arabidopsis thaliana GN=At2g25970 PE=2 SV=1	3	---	----	-0,167	0,31207	884,54	45,60%
Q9LM02	Cycloartenol-C-24-methyltransferase OS=Arabidopsis thaliana GN=SMT1 PE=1 SV=1	1	---	----	-0,451	0,31207	884,54	45,60%
O65655	Putative uncharacterized protein AT4g39680 OS=Arabidopsis thaliana GN=At4g39680 PE=1 SV=1	2	---	----	0,347	0,31407	890,21	45,70%
F4IRR2;F4J738	Importin beta-like SAD2 OS=Arabidopsis thaliana GN=SAD2 PE=1 SV=1	2	---	----	0,189	0,31202	884,39	45,70%
Q9SRR8	2Fe-2S ferredoxin-like protein OS=Arabidopsis thaliana GN=F21O3.19 PE=2 SV=1	3	---	----	-0,146	0,31407	890,21	45,70%
P92963;Q38922	Ras-related protein RABB1c OS=Arabidopsis thaliana GN=RABB1C PE=1 SV=1	3	---	----	-0,154	0,31417	890,49	45,70%
O23628	Histone H2A variant 1 OS=Arabidopsis thaliana GN=H2AV PE=1 SV=1	2	---	----	-0,177	0,31417	890,49	45,70%
Q9FZI8	Lecithin-cholesterol acyltransferase-like 1 OS=Arabidopsis thaliana GN=LCAT1 PE=2 SV=1	2	---	----	0,238	0,31621	896,27	45,80%
F4I420	Eukaryotic translation initiation factor 2 (EIF-2) family protein OS=Arabidopsis thaliana GN=At1g76810 PE=1 SV=1	1	---	----	0,224	0,31607	895,88	45,80%
Q39196	Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1	3	---	----	0,223	0,31607	895,88	45,80%
F4JHW1	Phenazine biosynthesis PhzC/PhzF protein OS=Arabidopsis thaliana GN=At4g02860 PE=4 SV=1	1	---	----	-0,301	0,31607	895,88	45,80%
Q9SJI7	Phospholipase A1-IIdelta OS=Arabidopsis thaliana GN=At2g42690 PE=1 SV=1	6	---	----	-0,108	0,31607	895,88	45,90%
Q9XJ36	ATP-dependent Clp protease proteolytic subunit-related protein 2, chloroplastic OS=Arabidopsis thaliana GN=CLPR2 PE	4	---	----	-0,128	0,31701	898,54	45,90%
O49290	Carboxyvinyl-carboxyphosphonate phosphorylmutase, chloroplastic OS=Arabidopsis thaliana GN=At1g77060 PE=2 SV=	2	---	----	-0,201	0,31607	895,88	45,90%
Q9LY82	Probable glucuronokinase 2 OS=Arabidopsis thaliana GN=GLCAK2 PE=2 SV=1	1	---	----	0,315	0,31882	903,67	46,10%
Q8W4A0	Eukaryotic translation initiation factor 3 subunit M OS=Arabidopsis thaliana GN=F14P3.15 PE=2 SV=1	6	---	----	0,119	0,31922	904,80	46,10%
Q93Y35	26S proteasome non-ATPase regulatory subunit 6 homolog OS=Arabidopsis thaliana GN=RPN7 PE=1 SV=1	7	---	----	0,108	0,31921	904,77	46,10%
O23657	Ras-related protein RABC1 OS=Arabidopsis thaliana GN=RABC1 PE=1 SV=1	2	---	----	-0,2	0,31882	903,67	46,10%
Q9SUC6	Berberine bridge enzyme-like protein OS=Arabidopsis thaliana GN=T13K14.20 PE=4 SV=1	1	---	----	-0,404	0,31941	905,34	46,10%
Q9FGW9	Transcription factor GTE10 OS=Arabidopsis thaliana GN=GTE10 PE=1 SV=2	1	---	----	0,334	0,32041	908,18	46,20%
P0CJ46;P53492;Q96292	Actin-1 OS=Arabidopsis thaliana GN=ACT1 PE=1 SV=1	4	---	----	0,084	0,32007	907,21	46,20%
P28185	Ras-related protein RABA1a OS=Arabidopsis thaliana GN=RABA1A PE=1 SV=1	4	---	----	-0,116	0,32017	907,50	46,20%
Q0WUI9	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 8 OS=Arabidopsis thaliana GN=TPS8 PE=2 SV=1	1	---	----	-0,324	0,32081	909,31	46,20%
F4IA48	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g78150 PE=1 SV=1	1	---	----	0,576	0,32261	914,41	46,40%
Q9FGX1	ATP-citrate synthase beta chain protein 2 OS=Arabidopsis thaliana GN=ACLB-2 PE=1 SV=1	1	---	----	0,224	0,32261	914,41	46,40%
Q9SZD6	Elongation factor Ts OS=Arabidopsis thaliana GN=F19B15.90 PE=2 SV=1	31	---	----	0,044	0,32207	912,88	46,40%
O64740	Protein transport protein SEC13 homolog B OS=Arabidopsis thaliana GN=SEC13B PE=1 SV=1	1	---	----	0,313	0,32341	916,68	46,50%
Q9SMX3;Q9SRH5	Mitochondrial outer membrane protein porin 3 OS=Arabidopsis thaliana GN=VDAC3 PE=1 SV=3	2	---	----	-0,136	0,32301	915,54	46,50%
Q9ZPI1	Lysine--tRNA ligase OS=Arabidopsis thaliana GN=At3g11710 PE=1 SV=1	11	---	----	0,081	0,32462	920,11	46,60%
P41568	Protein translation factor SUI1 homolog 1 OS=Arabidopsis thaliana GN=At4g27130 PE=1 SV=2	1	---	----	0,222	0,32641	925,18	46,80%
F4I3N6	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g63610 PE=4 SV=1	3	---	----	0,175	0,32701	926,88	46,80%
Q94C59	Patellin-4 OS=Arabidopsis thaliana GN=PATL4 PE=1 SV=2	7	---	----	-0,129	0,32617	924,50	46,80%
Q9CA23	Ubiquitin-fold modifier 1 OS=Arabidopsis thaliana GN=At1g77710 PE=3 SV=1	2	---	----	-0,208	0,32621	924,61	46,80%

Q9M9Q6	Serine carboxypeptidase-like 50 OS=Arabidopsis thaliana GN=SCPL50 PE=2 SV=1	1	---	----	-0,372	0,32607	924,22	46,80%
Q940N7	AT4g05150/C17L7_70 OS=Arabidopsis thaliana GN=At4g05150 PE=1 SV=1	1	EVSTLSDPGSPRR	Phospho S10	-0,86	0,32607	924,22	46,80%
O82209	Copia-like retroelement pol polyprotein OS=Arabidopsis thaliana GN=At2g19680 PE=2 SV=1	1	---	----	0,303	0,32817	930,17	46,90%
Q8VYP7	Putative Sar1 GTP binding protein OS=Arabidopsis thaliana GN=At3g62560 PE=2 SV=1	1	---	----	-0,67	0,32807	929,89	46,90%
Q9FJE8	Probable histone H2A.7 OS=Arabidopsis thaliana GN=At5g59870 PE=1 SV=1	2	---	----	0,183	0,32807	929,89	47,00%
Q9C8L2	Fatty-acid-binding protein 3 OS=Arabidopsis thaliana GN=FAP3 PE=1 SV=1	5	---	----	-0,126	0,33017	935,84	47,00%
Q94AI6	Exocyst complex component SEC6 OS=Arabidopsis thaliana GN=SEC6 PE=1 SV=1	2	---	----	0,282	0,33017	935,84	47,10%
Q9LNU3	Expansin-A11 OS=Arabidopsis thaliana GN=EXPA11 PE=2 SV=1	2	---	----	-0,154	0,33007	935,56	47,10%
Q9S7E9	Glutamate--glyoxylate aminotransferase 2 OS=Arabidopsis thaliana GN=GGAT2 PE=1 SV=1	4	---	----	-0,173	0,32962	934,28	47,10%
B9DHA5	AT3G28760 protein OS=Arabidopsis thaliana GN=At3g28760 PE=2 SV=1	2	---	----	-0,344	0,33007	935,56	47,10%
Q9FHX2	Protein MITOFERRINLIKE 1, chloroplastic OS=Arabidopsis thaliana GN=MFL1 PE=2 SV=1	2	---	----	-0,53	0,33007	935,56	47,10%
F4J8C7	Phosphoglycerate mutase-like protein OS=Arabidopsis thaliana GN=At3g01310 PE=1 SV=1	1	QGSGIIGTFGQSEELF	Phospho S3	-1,012	0,33007	935,56	47,10%
F4IRR2	Importin beta-like SAD2 OS=Arabidopsis thaliana GN=SAD2 PE=1 SV=1	3	---	----	0,201	0,33217	941,51	47,20%
Q9SJT9	Coatomer subunit alpha-2 OS=Arabidopsis thaliana GN=At2g21390 PE=2 SV=1	6	---	----	0,151	0,33142	939,38	47,20%
O48963	Phototropin-1 OS=Arabidopsis thaliana GN=PHOT1 PE=1 SV=1	5	---	----	-0,117	0,33217	941,51	47,20%
Q8LBS4	Monothiol glutaredoxin-S12, chloroplastic OS=Arabidopsis thaliana GN=GRXS12 PE=2 SV=2	3	---	----	-0,12	0,33207	941,22	47,20%
Q9SF23	Dihydroneopterin aldolase 1 OS=Arabidopsis thaliana GN=FOLB1 PE=1 SV=1	3	---	----	-0,191	0,33302	943,92	47,20%
Q8VZS7	AT4G18070 protein OS=Arabidopsis thaliana GN=At4g18070 PE=1 SV=1	1	---	----	-0,333	0,33207	941,22	47,20%
Q9SVQ9	AT4g13180/F17N18_70 OS=Arabidopsis thaliana GN=F17N18.70 PE=1 SV=1	1	---	----	-0,363	0,33007	935,56	47,20%
O23034	Ubiquitin-like modifier-activating enzyme 5 OS=Arabidopsis thaliana GN=At1g05350 PE=3 SV=2	1	---	----	0,504	0,33421	947,29	47,30%
Q9FME2	AT5g60980/MSL3_100 OS=Arabidopsis thaliana GN=At5g60980 PE=2 SV=1	4	---	----	0,15	0,33302	943,92	47,30%
Q9ZW24	Glutathione S-transferase U7 OS=Arabidopsis thaliana GN=GSTU7 PE=2 SV=1	4	---	----	-0,155	0,33361	945,59	47,30%
P24102	Peroxidase 22 OS=Arabidopsis thaliana GN=PER22 PE=1 SV=2	1	---	----	-0,629	0,33207	941,22	47,30%
Q9FXB0	At1g56580/F25P12_18 OS=Arabidopsis thaliana GN=F25P12.97 PE=2 SV=1	1	---	----	0,296	0,33521	950,12	47,40%
Q9SJU4	Probable fructose-bisphosphate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=FBA1 PE=1 SV=2	8	---	----	-0,058	0,33462	948,45	47,40%
Q9FNC4	HAD superfamily, subfamily IIIB acid phosphatase OS=Arabidopsis thaliana GN=At5g44020 PE=2 SV=1	6	---	----	-0,087	0,33417	947,18	47,40%
Q39258	V-type proton ATPase subunit E1 OS=Arabidopsis thaliana GN=VHA-E1 PE=1 SV=2	8	---	----	0,065	0,33617	952,84	47,50%
Q96242	Allene oxide synthase, chloroplastic OS=Arabidopsis thaliana GN=CYP74A PE=1 SV=3	22	---	----	-0,05	0,33622	952,99	47,50%
Q93W22	60S ribosomal protein L10-3 OS=Arabidopsis thaliana GN=RPL10C PE=2 SV=1	2	---	----	-0,158	0,33601	952,39	47,50%
A7WM73;Q8L7S6	Beta-hexosaminidase 1 OS=Arabidopsis thaliana GN=HEXO1 PE=1 SV=1	1	---	----	-0,291	0,33607	952,56	47,50%
Q9SJZ2	Peroxidase 17 OS=Arabidopsis thaliana GN=PER17 PE=2 SV=1	1	---	----	-0,293	0,33607	952,56	47,50%
O80526;Q9SGY2	ATP-citrate synthase alpha chain protein 3 OS=Arabidopsis thaliana GN=ACLA-3 PE=2 SV=1	1	---	----	0,213	0,33807	958,23	47,60%
F4JFN3;Q9SIF2;Q9STX5	HEAT SHOCK PROTEIN 89.1 OS=Arabidopsis thaliana GN=Hsp89.1 PE=3 SV=1	1	---	----	0,212	0,33741	956,36	47,60%
Q9FYF8	At1g67350 OS=Arabidopsis thaliana GN=At1g67350 PE=2 SV=1	1	---	----	0,171	0,33721	955,79	47,60%
P49040	Sucrose synthase 1 OS=Arabidopsis thaliana GN=SUS1 PE=1 SV=3	2	---	----	0,155	0,33821	958,63	47,60%
B3LF83	Probable inactive linolenate hydroperoxide lyase OS=Arabidopsis thaliana GN=CYP74B2 PE=2 SV=1	3	---	----	-0,174	0,33802	958,09	47,60%
Q8L745	AT5g42220/K5J14_2 OS=Arabidopsis thaliana GN=At5g42220 PE=2 SV=1	1	---	----	0,407	0,34007	963,90	47,80%
Q9LT77	Probable cysteine proteinase At3g19400 OS=Arabidopsis thaliana GN=At3g19400 PE=2 SV=1	1	---	----	-0,307	0,34007	963,90	47,80%
F4K7W6	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g01010 PE=1 SV=1	3	---	----	0,241	0,34007	963,90	47,90%
F4JCU3	Diphosphomevalonate decarboxylase OS=Arabidopsis thaliana GN=At3g54250 PE=4 SV=1	2	---	----	0,238	0,34207	969,57	48,00%
Q94A52	DEAD-box ATP-dependent RNA helicase 2 OS=Arabidopsis thaliana GN=RH2 PE=2 SV=2	2	---	----	0,183	0,34207	969,57	48,00%
O80452	AMP deaminase OS=Arabidopsis thaliana GN=AMPD PE=1 SV=2	2	---	----	0,238	0,34407	975,23	48,10%
P21240	Chaperonin 60 subunit beta 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60B1 PE=1 SV=3	11	---	----	-0,075	0,34301	972,23	48,10%
Q8GZQ3	Polyribonucleotide nucleotidyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PNP1 PE=1 SV=1	11	---	----	-0,088	0,34407	975,23	48,10%
O82261	Protease Do-like 2, chloroplastic OS=Arabidopsis thaliana GN=DEGP2 PE=1 SV=2	9	---	----	-0,102	0,34207	969,57	48,10%
Q6NMC1	At1g72640 OS=Arabidopsis thaliana GN=At1g72640 PE=2 SV=1	4	---	----	-0,13	0,34301	972,23	48,10%
Q9C5D6	Cationic amino acid transporter 9, chloroplastic OS=Arabidopsis thaliana GN=CAT9 PE=2 SV=1	1	---	----	-0,206	0,34422	975,66	48,10%
P47999;Q43725	Cysteine synthase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=OASB PE=1 SV=2	1	---	----	-0,21	0,34301	972,23	48,10%
O23676	Protein mago nashi homolog OS=Arabidopsis thaliana GN=At1g02140 PE=1 SV=1	1	---	----	0,3	0,34381	974,50	48,20%
Q9STY6	40S ribosomal protein S20-2 OS=Arabidopsis thaliana GN=RPS20B PE=2 SV=1	1	---	----	0,265	0,34502	977,93	48,20%
Q9ZQ26	AT2G24420 protein OS=Arabidopsis thaliana GN=At2g24420 PE=2 SV=2	2	---	----	0,21	0,34681	983,00	48,20%
O81146;O81147	Proteasome subunit alpha type-6-A OS=Arabidopsis thaliana GN=PAA1 PE=1 SV=2	3	---	----	0,152	0,34407	975,23	48,20%
Q9FH82	Pectin acetylesterase 11 OS=Arabidopsis thaliana GN=PAE11 PE=2 SV=1	4	---	----	0,146	0,34407	975,23	48,20%
Q8RWT5	AICARFT/IMPCHase bienzyme family protein OS=Arabidopsis thaliana GN=At2g35040 PE=2 SV=1	10	---	----	0,094	0,34702	983,60	48,20%
Q42592	L-ascorbate peroxidase S, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=APXS PE=1 SV=2	8	---	----	0,09	0,34641	981,87	48,20%

F4I907	Glyoxylate/succinic semialdehyde reductase 2, chloroplastic OS=Arabidopsis thaliana GN=GLYR2 PE=1 SV=1	6	---	----	-0,098	0,34617	981,19	48,20%
P0DKC3;Q8GWU0	Phosphoglycolate phosphatase 1A, chloroplastic OS=Arabidopsis thaliana GN=PGLP1A PE=1 SV=1	1	---	----	-0,219	0,34617	981,19	48,20%
Q9M1Q9	ABC transporter B family member 21 OS=Arabidopsis thaliana GN=ABCB21 PE=1 SV=2	1	---	----	-0,313	0,34607	980,90	48,20%
Q84WS0	Subtilisin-like protease SBT1.1 OS=Arabidopsis thaliana GN=SBTI1.1 PE=1 SV=1	1	---	----	-0,356	0,34661	982,44	48,20%
F4JY76	Eukaryotic translation initiation factor 3 subunit L OS=Arabidopsis thaliana GN=At5g25754 PE=3 SV=1	4	---	----	0,198	0,34602	980,76	48,30%
Q9FM65	Fasciclin-like arabinogalactan protein 1 OS=Arabidopsis thaliana GN=FLA1 PE=1 SV=1	3	---	----	0,144	0,34602	980,76	48,30%
Q9ZVQ3	Glutathione S-transferase Z1 OS=Arabidopsis thaliana GN=GSTZ1 PE=1 SV=1	1	---	----	-0,302	0,34607	980,90	48,30%
Q9SHJ8	3-hydroxyisobutyryl-CoA hydrolase-like protein 5 OS=Arabidopsis thaliana GN=At1g06550 PE=1 SV=2	1	---	----	0,407	0,34807	986,57	48,40%
Q9SII8	Ubiquitin domain-containing protein DSK2b OS=Arabidopsis thaliana GN=DSK2B PE=1 SV=1	2	---	----	0,215	0,34822	987,00	48,40%
Q058N4	Magnesium transporter MRS2-11, chloroplastic OS=Arabidopsis thaliana GN=MRS2-11 PE=2 SV=1	3	---	----	0,144	0,35061	993,77	48,50%
rev_Q5BPN1	reversed UPF0725 protein At3g57210 OS=Arabidopsis thaliana GN=At3g57210 PE=2 SV=1	1	---	----	-0,281	0,35016	992,52	48,50%
F4JWS8	Cytochrome b-c1 complex subunit 7-2 OS=Arabidopsis thaliana GN=QCR7-2 PE=1 SV=1	1	---	----	-0,393	0,35016	992,52	48,50%
F4IAX0;F4IAX1	Putative copper amine oxidase OS=Arabidopsis thaliana GN=At1g31690 PE=3 SV=1	1	---	----	-0,471	0,35022	992,67	48,50%
Q1G3F7	Transferases/nucleotidyltransferases OS=Arabidopsis thaliana GN=At5g19485 PE=2 SV=1	1	---	----	0,486	0,35006	992,24	48,60%
Q9FVR1	At1g32160/F3C3_6 OS=Arabidopsis thaliana GN=F3C3.6 PE=2 SV=1	2	---	----	0,224	0,35016	992,52	48,60%
Q94AU2	25.3 kDa vesicle transport protein OS=Arabidopsis thaliana GN=SEC22 PE=2 SV=1	2	---	----	0,211	0,35006	992,24	48,60%
Q9M5P2	Secretory carrier-associated membrane protein 3 OS=Arabidopsis thaliana GN=SCAMP3 PE=1 SV=1	2	---	----	-0,198	0,35216	998,19	48,60%
Q56Y42	Pyridoxal reductase, chloroplastic OS=Arabidopsis thaliana GN=PLR1 PE=1 SV=1	3	---	----	-0,251	0,35221	998,31	48,60%
Q9LHK9	Cofactor-independent phosphoglycerate mutase OS=Arabidopsis thaliana GN=At3g30841 PE=2 SV=1	1	---	----	0,29	0,35206	997,91	48,70%
Q9STX2	3-oxo-Delta(4,5)-steroid 5-beta-reductase OS=Arabidopsis thaliana GN=VEP1 PE=1 SV=1	3	---	----	-0,205	0,35261	999,44	48,70%
Q6NKW9	Glucan endo-1,3-beta-glucosidase 8 OS=Arabidopsis thaliana GN=At1g64760 PE=1 SV=2	1	---	----	-0,312	0,35206	997,91	48,70%
Q9SRU2	Auxin transport protein BIG OS=Arabidopsis thaliana GN=BIG PE=1 SV=2	1	---	----	-0,378	0,35206	997,91	48,70%
Q8RXU5	60S ribosomal protein L37a-2 OS=Arabidopsis thaliana GN=RPL37AC PE=3 SV=1	2	---	----	0,155	0,35406	1003,58	48,80%
Q93YZ7	Acetolactate synthase small subunit 2, chloroplastic OS=Arabidopsis thaliana GN=At2g31810 PE=1 SV=1	7	---	----	0,11	0,35361	1002,28	48,80%
Q6NL08	At1g29530 OS=Arabidopsis thaliana GN=At1g29530 PE=1 SV=1	1	---	----	0,294	0,35606	1009,24	48,90%
Q43292	60S ribosomal protein L37-2 OS=Arabidopsis thaliana GN=RPL37B PE=3 SV=2	1	---	----	0,293	0,35481	1005,68	48,90%
Q9SEE5	Galactokinase OS=Arabidopsis thaliana GN=GAL1 PE=1 SV=2	6	---	----	0,126	0,35606	1009,24	48,90%
P56785	Protein TIC 214 OS=Arabidopsis thaliana GN=TIC214 PE=1 SV=1	3	---	----	-0,166	0,35606	1009,24	48,90%
rev_Q96291	reversed 2-Cys peroxiredoxin BAS1, chloroplastic OS=Arabidopsis thaliana GN=BAS1 PE=1 SV=2	1	---	----	-0,326	0,35641	1010,21	48,90%
F4IFC5	Putative threonyl-tRNA synthetase / threonine--tRNA ligase OS=Arabidopsis thaliana GN=EMB2761 PE=3 SV=1	4	---	----	0,138	0,35722	1012,51	49,00%
Q9M5K2	Dihydrolipoyl dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=LPD2 PE=1 SV=1	7	---	----	0,126	0,35542	1007,41	49,00%
Q9LTX9	Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana GN=HSP70-7 PE=2 SV=1	11	---	----	-0,065	0,35606	1009,24	49,00%
P31169	Stress-induced protein KIN2 OS=Arabidopsis thaliana GN=KIN2 PE=2 SV=1	3	---	----	-0,109	0,35741	1013,05	49,00%
Q8VZB1	Putative uncharacterized protein At2g39070:At2g39080; T7F6.24:T7F6.25 OS=Arabidopsis thaliana GN=At2g39070At2g	3	---	----	-0,149	0,35816	1015,20	49,00%
Q9FMC7	Nuclear transport factor 2 (NTF2) family protein OS=Arabidopsis thaliana GN=At5g04830 PE=2 SV=1	1	---	----	-0,203	0,35606	1009,24	49,00%
Q9SE45	Annexin D3 OS=Arabidopsis thaliana GN=ANN3 PE=2 SV=2	1	---	----	-0,623	0,35606	1009,24	49,00%
O23617	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabidopsis thaliana GN=TPS5 PE=1 SV=2	1	---	----	0,299	0,35806	1014,91	49,10%
P47998	Cysteine synthase 1 OS=Arabidopsis thaliana GN=OASA1 PE=1 SV=2	12	---	----	0,054	0,35842	1015,91	49,10%
Q9C7F7	Non-specific lipid transfer protein GPI-anchored 1 OS=Arabidopsis thaliana GN=LTPG1 PE=1 SV=1	1	---	----	-0,19	0,35816	1015,20	49,10%
P42742	Proteasome subunit beta type-1 OS=Arabidopsis thaliana GN=PBF1 PE=1 SV=2	5	---	----	0,11	0,36016	1020,86	49,20%
P93832	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1	6	---	----	0,102	0,35962	1019,31	49,20%
P38389	Protein transport protein Sec61 subunit beta OS=Arabidopsis thaliana GN=At2g45070 PE=1 SV=1	2	---	----	0,209	0,36222	1026,68	49,30%
P50318;Q9SAJ4	Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=2 SV=3	1	---	----	-0,111	0,36216	1026,53	49,30%
A4IJ41	Alpha/beta-hydrolase domain-containing protein OS=Arabidopsis thaliana GN=At3g10840 PE=2 SV=1	1	---	----	-0,305	0,36222	1026,68	49,30%
Q8L798	Inter-alpha-trypsin inhibitor heavy chain-like protein OS=Arabidopsis thaliana GN=At1g19110 PE=2 SV=1	1	---	----	0,781	0,36206	1026,25	49,40%
rev_F4IDG2	reversed Adenine nucleotide alpha hydrolases-domain containing protein kinase OS=Arabidopsis thaliana GN=At1g789	1	---	----	0,401	0,36216	1026,53	49,40%
P32068	Anthranilate synthase alpha subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ASA1 PE=1 SV=1	3	---	----	0,174	0,36342	1030,08	49,40%
Q42340	40S ribosomal protein S16-3 OS=Arabidopsis thaliana GN=RPS16C PE=2 SV=1	1	---	----	0,158	0,36141	1024,39	49,40%
O82230;Q9M098	At2g24020/T29E15.22 OS=Arabidopsis thaliana GN=At2g24020 PE=2 SV=2	2	---	----	0,128	0,36216	1026,53	49,40%
Q02971	Cinnamyl alcohol dehydrogenase 7 OS=Arabidopsis thaliana GN=CAD7 PE=1 SV=2	7	---	----	0,085	0,36416	1032,20	49,40%
A8MS68	Dihydrolipoyl dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=LPD1 PE=2 SV=1	2	---	----	-0,126	0,36406	1031,92	49,40%
Q9STM6	GDSL esterase/lipase At3g48460 OS=Arabidopsis thaliana GN=At3g48460 PE=2 SV=1	2	---	----	-0,173	0,36206	1026,25	49,40%
Q9FJ62	Glycerophosphodiester phosphodiesterase GDPDL4 OS=Arabidopsis thaliana GN=GDPDL4 PE=1 SV=1	4	---	----	-0,205	0,36206	1026,25	49,40%
O80983	ATP-dependent zinc metalloprotease FTSH 4, mitochondrial OS=Arabidopsis thaliana GN=FTSH4 PE=1 SV=2	1	---	----	-0,348	0,36406	1031,92	49,40%
Q9STZ8	At4g12880 OS=Arabidopsis thaliana GN=T20K18.230 PE=2 SV=1	1	---	----	0,293	0,36502	1034,62	49,50%

Q9LJQ3	AT3g18280/MIE15_7 OS=Arabidopsis thaliana GN=At3g18280 PE=2 SV=1	1	---	----	0,272	0,36621	1037,99	49,50%
Q9FFP9	Serine/threonine-protein kinase SRK2H OS=Arabidopsis thaliana GN=SRK2H PE=1 SV=1	1	---	----	0,206	0,36406	1031,92	49,50%
Q9M330	Probable proteasome inhibitor OS=Arabidopsis thaliana GN=At3g53970 PE=1 SV=1	4	---	----	0,172	0,36401	1031,76	49,50%
P51407;Q9SLF7	60S acidic ribosomal protein P2-1 OS=Arabidopsis thaliana GN=RPP2A PE=2 SV=2	2	---	----	0,094	0,36206	1026,25	49,50%
Q94B78	Glycine dehydrogenase (decarboxylating) 1, mitochondrial OS=Arabidopsis thaliana GN=GLDP1 PE=1 SV=2	16	---	----	0,049	0,36621	1037,99	49,50%
Q9STT2	Vacuolar protein sorting-associated protein 29 OS=Arabidopsis thaliana GN=VPS29 PE=2 SV=1	3	---	----	-0,172	0,36522	1035,19	49,50%
Q8VYH2	Squalene epoxidase 3 OS=Arabidopsis thaliana GN=SQE3 PE=1 SV=1	1	---	----	0,477	0,36721	1040,83	49,60%
Q9ZU66	Putative spliceosome associated protein OS=Arabidopsis thaliana GN=emb2444 PE=2 SV=1	1	---	----	0,296	0,36816	1043,54	49,60%
Q94CE4-2	Isoform 2 of Beta carbonic anhydrase 4 OS=Arabidopsis thaliana GN=BCA4	1	---	----	0,269	0,36616	1037,87	49,60%
Q9FM97	Pyruvate kinase OS=Arabidopsis thaliana GN=At5g56350 PE=2 SV=1	3	---	----	0,159	0,36616	1037,87	49,60%
P56807	30S ribosomal protein S18, chloroplastic OS=Arabidopsis thaliana GN=rps18 PE=3 SV=1	3	---	----	0,135	0,36816	1043,54	49,60%
Q93YR3	FAM10 family protein At4g22670 OS=Arabidopsis thaliana GN=At4g22670 PE=1 SV=1	8	---	----	0,087	0,36606	1037,59	49,60%
Q9SUI6;Q9SUI7	Photosystem I reaction center subunit VI-2, chloroplastic OS=Arabidopsis thaliana GN=PSAH2 PE=2 SV=1	4	---	----	-0,079	0,36681	1039,69	49,60%
Q9ZPY5	At2g46540/F11C10.23 OS=Arabidopsis thaliana GN=At2g46540 PE=2 SV=2	1	---	----	0,234	0,36806	1043,25	49,70%
P41088	Chalcone--flavonone isomerase 1 OS=Arabidopsis thaliana GN=CHI1 PE=1 SV=2	3	---	----	0,154	0,36862	1044,82	49,70%
P10795;P10796;P10797	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1A PE=1 SV=2	1	---	----	0,152	0,36922	1046,52	49,70%
Q8L7C9;Q9ZRW8	Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1	2	---	----	0,12	0,36806	1043,25	49,70%
Q8LD49	Thioredoxin X, chloroplastic OS=Arabidopsis thaliana GN=ATHX PE=2 SV=2	5	---	----	0,103	0,37006	1048,92	49,70%
O65719	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	11	---	----	0,059	0,36801	1043,09	49,70%
Q56WF8	Serine carboxypeptidase-like 48 OS=Arabidopsis thaliana GN=SCPL48 PE=2 SV=2	1	---	----	-0,345	0,36942	1047,09	49,70%
Q7DLS1	Proteasome subunit beta type-7-B OS=Arabidopsis thaliana GN=PBB2 PE=1 SV=2	1	---	----	0,185	0,37006	1048,92	49,80%
Q9FFK3	Probable zinc metalloprotease EGY2, chloroplastic OS=Arabidopsis thaliana GN=EGY2 PE=2 SV=1	3	---	----	-0,196	0,37006	1048,92	49,80%
P28186;Q9FJF1	Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	2	---	----	0,211	0,37301	1057,27	50,00%
Q9C6B3	Gamma carbonic anhydrase 2, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA2 PE=1 SV=1	2	---	----	0,139	0,37341	1058,40	50,00%
Q9SA14	3-isopropylmalate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=IMDH1 PE=2 SV=2	5	---	----	0,089	0,37216	1054,87	50,00%
O80501	Ras-related protein RABH1b OS=Arabidopsis thaliana GN=RABH1B PE=1 SV=1	5	---	----	0,084	0,37242	1055,59	50,00%
Q9M081	Protein transport protein Sec24-like At4g32640 OS=Arabidopsis thaliana GN=At4g32640 PE=2 SV=3	2	---	----	-0,275	0,37216	1054,87	50,00%
Q9LH52	Leucine-rich repeat protein FLOR1 OS=Arabidopsis thaliana GN=FLR1 PE=2 SV=1	1	---	----	0,298	0,37402	1060,13	50,10%
Q8L794	Putative xylulose kinase OS=Arabidopsis thaliana GN=XK-1 PE=2 SV=1	3	---	----	0,182	0,37341	1058,40	50,10%
F4J9K9	Neurofilament protein-related protein OS=Arabidopsis thaliana GN=At3g05900 PE=1 SV=1	10	---	----	0,085	0,37406	1060,26	50,10%
P92959	50S ribosomal protein L24, chloroplastic OS=Arabidopsis thaliana GN=RPL24 PE=2 SV=2	6	---	----	-0,084	0,37406	1060,26	50,10%
O81127	Serine/arginine-rich splicing factor RSZ21 OS=Arabidopsis thaliana GN=RSZ21 PE=1 SV=1	1	RRSPDYGYAR	Phospho S3	-0,607	0,37481	1062,37	50,10%
Q9SRE0	5-formyltetrahydrofolate cyclo-ligase-like protein COG0212 OS=Arabidopsis thaliana GN=COG0212 PE=2 SV=1	1	---	----	0,292	0,37616	1066,21	50,20%
Q38845;Q38951	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Arabidopsis thaliana GN=PP2	1	---	----	0,205	0,37602	1065,80	50,20%
O22860	60S ribosomal protein L38 OS=Arabidopsis thaliana GN=RPL38A PE=3 SV=1	2	---	----	0,17	0,37582	1065,23	50,20%
P61845	50S ribosomal protein L23, chloroplastic OS=Arabidopsis thaliana GN=rpl23-A PE=3 SV=1	3	---	----	-0,126	0,37662	1067,50	50,20%
Q9C5I1	UDP-sugar pyrophosphorylase OS=Arabidopsis thaliana GN=USP PE=1 SV=1	1	---	----	-0,282	0,37606	1065,93	50,20%
Q9SRQ1	Cytochrome P450 89A9 OS=Arabidopsis thaliana GN=CYP89A9 PE=2 SV=1	1	---	----	-0,285	0,37606	1065,93	50,20%
Q39096	Protein EARLY RESPONSIVE TO DEHYDRATION 15 OS=Arabidopsis thaliana GN=ERD15 PE=1 SV=1	1	---	----	-0,311	0,37606	1065,93	50,20%
F4K2A1	Folylpolyglutamate synthase OS=Arabidopsis thaliana GN=FPGS1 PE=1 SV=1	1	---	----	0,302	0,37801	1071,44	50,30%
P59169;Q9FX60	Histone H3.3 OS=Arabidopsis thaliana GN=HTR4 PE=1 SV=2	1	---	----	0,204	0,37806	1071,60	50,30%
Q9ZP06	Malate dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana GN=At1g53240 PE=1 SV=1	4	---	----	0,074	0,37781	1070,87	50,30%
P33207	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic OS=Arabidopsis thaliana GN=At1g24360 PE=2 SV=2	8	---	----	-0,075	0,37882	1073,73	50,30%
Q94AQ8	Photosynthetic NDH subunit of subcomplex B 2, chloroplastic OS=Arabidopsis thaliana GN=PNSB2 PE=2 SV=1	6	---	----	-0,095	0,37781	1070,87	50,30%
O82234	Translation initiation factor IF-3 OS=Arabidopsis thaliana GN=At2g24060 PE=2 SV=1	2	---	----	-0,154	0,37761	1070,30	50,30%
Q8VYN6;Q9M0F9	ATP-dependent 6-phosphofructokinase 5, chloroplastic OS=Arabidopsis thaliana GN=PFK5 PE=1 SV=1	1	---	----	-0,261	0,37806	1071,60	50,30%
Q9FID2	Acyltransferase-like protein OS=Arabidopsis thaliana GN=At5g39080 PE=2 SV=1	1	---	----	-0,194	0,37922	1074,87	50,40%
Q9LHB9;Q9SMU8	Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3	1	---	----	-0,196	0,38006	1077,26	50,40%
P50546	DNA-directed RNA polymerase subunit beta OS=Arabidopsis thaliana GN=rpoB PE=3 SV=4	3	---	----	-0,227	0,38016	1077,55	50,40%
Q9SIQ8	AT2G31490 protein OS=Arabidopsis thaliana GN=At2g31490 PE=2 SV=1	1	---	----	0,29	0,38006	1077,26	50,50%
P46422;Q96266	Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3	1	---	----	-0,196	0,38122	1080,54	50,50%
F4IGM4	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g21385 PE=4 SV=1	8	---	----	-0,085	0,38182	1082,24	50,60%
Q4V3C7	DUF21 domain-containing protein At4g14230 OS=Arabidopsis thaliana GN=CBSDUF2 PE=2 SV=1	1	---	----	-0,223	0,38222	1083,37	50,60%
Q9XI10;Q9XI11	DPP6 N-terminal domain-like protein OS=Arabidopsis thaliana GN=F8K7.10 PE=2 SV=1	1	---	----	0,253	0,38406	1088,60	50,80%
Q8LB02	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial OS=Arabidopsis thaliana GN=SDH2-2 PE=1	2	---	----	0,191	0,38406	1088,60	50,80%

F4I448	Pre-mRNA-processing factor 39 OS=Arabidopsis thaliana GN=PRP39 PE=1 SV=1	3	---	----	0,164	0,38362	1087,34	50,80%
Q6ICZ8;Q9LHG9	Nascent polypeptide-associated complex subunit alpha-like protein 3 OS=Arabidopsis thaliana GN=At5g13850 PE=1 SV	2	---	----	0,137	0,38481	1090,71	50,80%
Q8GWB3	Protein YIPF OS=Arabidopsis thaliana GN=At3g05280 PE=1 SV=1	1	---	----	-0,337	0,38416	1088,88	50,80%
Q9SMU7	Signal recognition particle 9 kDa protein OS=Arabidopsis thaliana GN=SRP9 PE=3 SV=1	1	---	----	0,316	0,38616	1094,55	50,90%
Q9STI0	At4g12310 OS=Arabidopsis thaliana GN=T4C9.150 PE=2 SV=1	1	---	----	0,275	0,38606	1094,27	50,90%
Q93ZC5;Q9LS02;Q9LS03	Allene oxide cyclase 4, chloroplastic OS=Arabidopsis thaliana GN=AOC4 PE=2 SV=1	1	---	----	0,197	0,38642	1095,28	50,90%
P40940	ADP-ribosylation factor 3 OS=Arabidopsis thaliana GN=ARF3 PE=1 SV=2	2	---	----	0,19	0,38682	1096,41	50,90%
Q949P2;Q94AM1	Probable cytosolic oligopeptidase A OS=Arabidopsis thaliana GN=CYOP PE=1 SV=1	8	---	----	0,074	0,38522	1091,87	50,90%
P42643;P42644;P42645;P	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	---	----	-0,127	0,38606	1094,27	50,90%
F4JM15	PfkB-like carbohydrate kinase family protein OS=Arabidopsis thaliana GN=At4g28706 PE=3 SV=1	3	---	----	-0,162	0,38701	1096,95	50,90%
P94014	Germin-like protein subfamily 2 member 1 OS=Arabidopsis thaliana GN=GLP4 PE=2 SV=2	1	---	----	-0,265	0,38582	1093,57	50,90%
Q38900;Q42406	Peptidyl-prolyl cis-trans isomerase CYP19-1 OS=Arabidopsis thaliana GN=CYP19-1 PE=1 SV=1	1	---	----	0,258	0,38722	1097,54	51,00%
Q42605;Q8LDN8	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 OS=Arabidopsis thaliana GN=UGE1 PE=1 SV=2	4	---	----	-0,118	0,38782	1099,24	51,00%
Q93Z84	At2g04039/At2g04039 OS=Arabidopsis thaliana GN=At2g04039 PE=2 SV=1	5	---	----	-0,121	0,38761	1098,65	51,00%
Q6DBN2	Probable plastid-lipid-associated protein 5, chloroplastic OS=Arabidopsis thaliana GN=PAP5 PE=2 SV=1	2	---	----	-0,195	0,38806	1099,94	51,00%
Q9ZNS2	Auxin-responsive GH3 family protein OS=Arabidopsis thaliana GN=F4C21.36 PE=2 SV=1	1	---	----	-0,602	0,38861	1101,48	51,00%
Q9SK86	Alcohol dehydrogenase-like 1 OS=Arabidopsis thaliana GN=At1g22430 PE=2 SV=1	1	---	----	0,608	0,39061	1107,15	51,20%
F4K0V9	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g12240 PE=4 SV=1	1	---	----	0,296	0,39006	1105,61	51,20%
Q9M3D2	60S ribosomal protein L35-3 OS=Arabidopsis thaliana GN=RPL35C PE=2 SV=1	1	---	----	0,274	0,39422	1117,38	51,20%
rev_Q9M366	reversed Ca2+dependent plant phosphoribosyltransferase family protein OS=Arabidopsis thaliana GN=F15G16.110 PE=	1	---	----	0,272	0,39006	1105,61	51,20%
Q9LFX8	Putative uncharacterized protein At1g27090 OS=Arabidopsis thaliana GN=At1g27090 PE=2 SV=1	3	---	----	0,195	0,39081	1107,72	51,20%
Q9S7D2	Putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I OS=Arabidopsis thalian	2	---	----	0,172	0,39016	1105,89	51,20%
O65570;O81644;O81645	Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1	1	---	----	0,155	0,39041	1106,58	51,20%
F4JL11	Importin subunit alpha-2 OS=Arabidopsis thaliana GN=IMPA2 PE=1 SV=1	6	---	----	0,138	0,39216	1111,56	51,20%
Q42479	Calcium-dependent protein kinase 3 OS=Arabidopsis thaliana GN=CPK3 PE=1 SV=1	7	---	----	0,098	0,39416	1117,23	51,20%
Q9LIR4	Dihydroxy-acid dehydratase, chloroplastic OS=Arabidopsis thaliana GN=DHAD PE=2 SV=1	7	---	----	0,086	0,39101	1108,29	51,20%
O48646	Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial OS=Arabidopsis thaliana GN=GPX6 PE=2	7	---	----	0,068	0,39216	1111,56	51,20%
Q9C5M0	Mitochondrial dicarboxylate/tricarboxylate transporter DTC OS=Arabidopsis thaliana GN=DTC PE=1 SV=1	10	---	----	0,056	0,39206	1111,27	51,20%
P25819;Q42547;Q96528	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=2 SV=3	1	---	----	-0,097	0,39281	1113,39	51,20%
Q8LCE1	Glutamine synthetase cytosolic isozyme 1-2 OS=Arabidopsis thaliana GN=GLN1-2 PE=1 SV=2	5	---	----	-0,114	0,39122	1108,88	51,20%
C0LGK9	Probable LRR receptor-like serine/threonine-protein kinase At2g24230 OS=Arabidopsis thaliana GN=At2g24230 PE=2 S	1	---	----	-0,182	0,39206	1111,27	51,20%
B3H6G9	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein OS=Arabidopsis thaliana GN=At4g02405	1	---	----	-0,255	0,39121	1108,85	51,20%
P61837	Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1	1	---	----	-0,351	0,39206	1111,27	51,20%
Q9LQ55	Dynamin-2B OS=Arabidopsis thaliana GN=DRP2B PE=1 SV=2	1	TSPQPDGPSSTGGS	Phospho S3	0,738	0,39406	1116,94	51,30%
Q8W493;Q9FKW6	Ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic OS=Arabidopsis thaliana GN=LFNR2 PE=1 SV=1	1	---	----	0,591	0,39406	1116,94	51,30%
Q9LF21	Eukaryotic translation initiation factor 3 subunit M OS=Arabidopsis thaliana GN=T20K14_220 PE=2 SV=1	1	---	----	0,312	0,39521	1120,19	51,30%
F4JRN8	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At4g18810 PE=4 SV=1	10	---	----	-0,081	0,39382	1116,25	51,30%
Q9C5G6	Peptidase C15, pyroglutamyl peptidase I-like protein OS=Arabidopsis thaliana GN=At1g23430 PE=2 SV=1	2	---	----	-0,15	0,39206	1111,27	51,30%
P56758	ATP synthase subunit a, chloroplastic OS=Arabidopsis thaliana GN=atpI PE=3 SV=1	1	---	----	-0,164	0,39406	1116,94	51,30%
O49339	PTI1-like tyrosine-protein kinase 2 OS=Arabidopsis thaliana GN=PTI12 PE=1 SV=1	2	---	----	-0,175	0,39406	1116,94	51,30%
Q9T042	Protein disulfide-isomerase 5-4 OS=Arabidopsis thaliana GN=PDIL5-4 PE=2 SV=1	1	---	----	0,291	0,39606	1122,61	51,40%
P92974;P93028	Ubiquitin-activating enzyme E1 2 OS=Arabidopsis thaliana GN=UBA2 PE=1 SV=1	1	---	----	0,185	0,39601	1122,46	51,40%
Q6NLB6	At4g13220 OS=Arabidopsis thaliana GN=At4g13220 PE=2 SV=1	1	---	----	-0,345	0,39616	1122,89	51,40%
Q8S9J8	Probable clathrin assembly protein At4g32285 OS=Arabidopsis thaliana GN=At4g32285 PE=1 SV=2	1	SRSFGDVNEIGAR	Phospho S3	0,543	0,39806	1128,28	51,50%
Q9LK39	Probable acyl-activating enzyme 16, chloroplastic OS=Arabidopsis thaliana GN=AAE16 PE=2 SV=1	1	---	----	0,352	0,39806	1128,28	51,50%
Q9M879	Acyl-[acyl-carrier-protein] desaturase 5, chloroplastic OS=Arabidopsis thaliana GN=S-ACP-DES5 PE=1 SV=1	3	---	----	0,222	0,39702	1125,32	51,50%
F4JXW9	PQQ_DH domain-containing protein OS=Arabidopsis thaliana GN=At5g11560 PE=4 SV=1	3	---	----	0,164	0,39782	1127,59	51,50%
Q570B4	3-ketoacyl-CoA synthase 10 OS=Arabidopsis thaliana GN=FDH PE=1 SV=2	1	---	----	-0,258	0,39802	1128,15	51,50%
Q9XI98	Ras-related protein RABG3e OS=Arabidopsis thaliana GN=RABG3E PE=2 SV=1	1	---	----	-0,28	0,39816	1128,56	51,50%
Q42512;Q9SIN5	Protein COLD-REGULATED 15A, chloroplastic OS=Arabidopsis thaliana GN=COR15A PE=1 SV=1	1	---	----	-0,297	0,39806	1128,28	51,50%
P28186;Q9FJF1;Q9FPJ4;Q	Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	1	---	----	0,156	0,39782	1127,59	51,60%
Q9ZSD4	Syntaxin-121 OS=Arabidopsis thaliana GN=SYP121 PE=1 SV=1	1	---	----	-0,29	0,40016	1134,23	51,70%
F4J9G6	LETM1-like protein OS=Arabidopsis thaliana GN=At3g59820 PE=4 SV=1	1	---	----	-0,639	0,40006	1133,95	51,70%
Q8VZS8	Abscisic acid receptor PYL1 OS=Arabidopsis thaliana GN=PYL1 PE=1 SV=1	1	---	----	0,201	0,40206	1139,62	51,80%
Q9SLF7	60S acidic ribosomal protein P2-2 OS=Arabidopsis thaliana GN=RPP2B PE=1 SV=1	4	---	----	0,104	0,40421	1145,70	51,80%

O64835	At2g23670/F26B6.32 OS=Arabidopsis thaliana GN=YCF37 PE=2 SV=1	2	---	----	-0,118	0,40122	1137,22	51,80%
O22218	Calcium-transporting ATPase 4, plasma membrane-type OS=Arabidopsis thaliana GN=ACA4 PE=1 SV=1	4	---	----	-0,148	0,40206	1139,62	51,80%
Q9C7T2	At1g72230/T9N14_17 OS=Arabidopsis thaliana GN=T9N14.17 PE=2 SV=1	1	---	----	-0,292	0,40416	1145,57	51,80%
Q9SEE9	Serine/arginine-rich splicing factor SR45 OS=Arabidopsis thaliana GN=SR45 PE=1 SV=1	1	GRSPPPPPSK	Phospho S3	-0,345	0,40206	1139,62	51,80%
Q9CAR3	SNF1-related protein kinase regulatory subunit gamma-1-like OS=Arabidopsis thaliana GN=CBSCBS2 PE=1 SV=1	1	---	----	0,335	0,40302	1142,33	51,90%
O24633	Proteasome subunit beta type-2-B OS=Arabidopsis thaliana GN=PBD2 PE=1 SV=1	1	---	----	0,163	0,40342	1143,46	51,90%
Q8RWF0	26S proteasome non-ATPase regulatory subunit 13 homolog A OS=Arabidopsis thaliana GN=RPN9A PE=1 SV=1	4	---	----	0,121	0,40206	1139,62	51,90%
P61847	50S ribosomal protein L32, chloroplastic OS=Arabidopsis thaliana GN=rpl32 PE=3 SV=2	2	---	----	0,115	0,40301	1142,30	51,90%
Q2HIR7	At5g38660 OS=Arabidopsis thaliana GN=APE1 PE=2 SV=1	8	---	----	0,084	0,40406	1145,28	51,90%
O80504	Chloroplast chaperonin 10 OS=Arabidopsis thaliana GN=CHL-CPN10 PE=2 SV=1	2	---	----	-0,094	0,40406	1145,28	51,90%
Q8S3U9	Exocyst complex component SEC5A OS=Arabidopsis thaliana GN=SEC5A PE=1 SV=1	3	---	----	-0,152	0,40416	1145,57	51,90%
Q9SEU7	Thioredoxin M3, chloroplastic OS=Arabidopsis thaliana GN=GAT1 PE=2 SV=2	1	---	----	-0,242	0,40406	1145,28	51,90%
F4JK84	Monooxygenase 1 OS=Arabidopsis thaliana GN=MO1 PE=4 SV=1	1	---	----	-0,248	0,40416	1145,57	51,90%
B4F7N8	At5g18420 OS=Arabidopsis thaliana GN=At5g18420 PE=2 SV=1	1	---	----	0,285	0,40616	1151,24	52,00%
Q9C8D3	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=F15E12.2 PE=4 SV=1	2	---	----	0,191	0,40616	1151,24	52,00%
Q9SEL7	Protease Do-like 5, chloroplastic OS=Arabidopsis thaliana GN=DEGP5 PE=1 SV=3	4	---	----	0,118	0,40406	1145,28	52,00%
P56765	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=accD PE=	8	---	----	-0,094	0,40616	1151,24	52,00%
Q8VZU2	Syntaxin-132 OS=Arabidopsis thaliana GN=SYP132 PE=1 SV=1	5	---	----	-0,109	0,40701	1153,64	52,00%
Q93Z11	AT5g37360/MNJ8_150 OS=Arabidopsis thaliana GN=At5g37360 PE=2 SV=1	3	---	----	-0,14	0,40616	1151,24	52,00%
Q9S7Q2	Pentatricopeptide repeat-containing protein At1g74850, chloroplastic OS=Arabidopsis thaliana GN=PTAC2 PE=2 SV=1	2	---	----	-0,236	0,40606	1150,95	52,00%
Q00874	DNA-damage-repair/toleration protein DRT100 OS=Arabidopsis thaliana GN=DRT100 PE=2 SV=2	2	---	----	0,156	0,40816	1156,90	52,10%
P62090	Photosystem I iron-sulfur center OS=Arabidopsis thaliana GN=psaC PE=3 SV=2	2	---	----	0,118	0,40862	1158,20	52,10%
F4IXW2	Brefeldin A-inhibited guanine nucleotide-exchange protein 5 OS=Arabidopsis thaliana GN=BIG5 PE=1 SV=2	7	---	----	0,104	0,40741	1154,77	52,10%
Q940J8	Pectin acetylesterase 7 OS=Arabidopsis thaliana GN=PAE7 PE=2 SV=1	8	---	----	-0,068	0,40816	1156,90	52,10%
Q9SAA2	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic OS=Arabidopsis thaliana GN=CLPP6 PE=1 SV=1	4	---	----	-0,096	0,40861	1158,17	52,10%
Q93Y09	Serine carboxypeptidase-like 45 OS=Arabidopsis thaliana GN=SCPL45 PE=2 SV=1	1	---	----	0,312	0,41016	1162,57	52,20%
Q9XGX9	Mitochondrial import inner membrane translocase subunit TIM9 OS=Arabidopsis thaliana GN=TIM9 PE=1 SV=2	1	---	----	0,186	0,40941	1160,44	52,20%
F4IWV2	2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=At3g55410 PE=4 SV=1	9	---	----	0,075	0,41021	1162,71	52,20%
Q9LV91	4-alpha-glucanotransferase DPE1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=DPE1 PE=2 SV=1	4	---	----	-0,13	0,41016	1162,57	52,20%
Q8S8L4	At2g37510 OS=Arabidopsis thaliana GN=At2g37510 PE=2 SV=1	1	---	----	-0,243	0,41006	1162,29	52,20%
Q6DBH4	At2g23820 OS=Arabidopsis thaliana GN=At2g23820 PE=2 SV=1	1	---	----	-0,25	0,41006	1162,29	52,20%
Q6XJG8	26S proteasome non-ATPase regulatory subunit 2 homolog B OS=Arabidopsis thaliana GN=RPN1B PE=1 SV=1	1	---	----	0,308	0,41206	1167,96	52,30%
F4J738	Importin beta-like SAD2 homolog OS=Arabidopsis thaliana GN=At3g59020 PE=1 SV=1	1	---	----	0,246	0,41206	1167,96	52,30%
Q39002	ADP,ATP carrier protein 1, chloroplastic OS=Arabidopsis thaliana GN=AATP1 PE=1 SV=2	8	---	----	0,089	0,41122	1165,57	52,30%
Q949Y3	Bifunctional purple acid phosphatase 26 OS=Arabidopsis thaliana GN=PAP26 PE=1 SV=1	7	---	----	0,08	0,41201	1167,81	52,30%
O23715	Proteasome subunit alpha type-3 OS=Arabidopsis thaliana GN=PAG1 PE=1 SV=2	7	---	----	0,079	0,41206	1167,96	52,30%
rev_O82484	reversed Putative disease resistance protein At4g10780 OS=Arabidopsis thaliana GN=At4g10780 PE=3 SV=1	1	---	----	-0,231	0,41216	1168,24	52,30%
Q9SKI2	Vacuolar protein sorting-associated protein 2 homolog 1 OS=Arabidopsis thaliana GN=VPS2.1 PE=1 SV=2	1	---	----	-0,334	0,41006	1162,29	52,30%
B3H5K3	Uncharacterized binding protein OS=Arabidopsis thaliana GN=At5g47690 PE=1 SV=1	4	---	----	-0,155	0,41416	1173,91	52,40%
F4JQ90	FGGY family of carbohydrate kinase OS=Arabidopsis thaliana GN=At4g30310 PE=1 SV=1	1	---	----	-0,251	0,41406	1173,63	52,40%
Q75W54	Mannosylglycoprotein endo-beta-mannosidase OS=Arabidopsis thaliana GN=EBM PE=1 SV=3	2	---	----	-0,267	0,41406	1173,63	52,50%
Q6IDC7	At1g77550 OS=Arabidopsis thaliana GN=At1g77550 PE=2 SV=1	1	---	----	-0,458	0,41406	1173,63	52,50%
rev_Q5E916	reversed ATP-dependent protease La (LON) domain protein OS=Arabidopsis thaliana GN=At2g25740 PE=2 SV=1	1	LPTSLSATGLPYR	Phospho S4	0,772	0,41606	1179,29	52,60%
rev_Q5S4X4	reversed Uncharacterized protein OS=Arabidopsis thaliana GN=At2g28580 PE=2 SV=1	1	---	----	0,268	0,41606	1179,29	52,60%
Q9ZQQ0	Serine carboxypeptidase-like 26 OS=Arabidopsis thaliana GN=SCPL26 PE=2 SV=1	3	---	----	0,165	0,41661	1180,85	52,60%
Q8GSJ1	ATP phosphoribosyltransferase 2, chloroplastic OS=Arabidopsis thaliana GN=HISN1B PE=1 SV=1	4	---	----	0,121	0,41642	1180,31	52,60%
Q93VS8	Protein EMBRYO DEFECTIVE 2734 OS=Arabidopsis thaliana GN=emb2734 PE=2 SV=1	11	---	----	0,079	0,41616	1179,58	52,60%
Q9FN08	Beta-galactosidase 10 OS=Arabidopsis thaliana GN=BGAL10 PE=2 SV=1	4	---	----	-0,195	0,41616	1179,58	52,60%
O22993	Cell division protein isolog OS=Arabidopsis thaliana GN=T19F6.22 PE=4 SV=1	1	---	----	0,437	0,41781	1184,25	52,70%
Q38931	Peptidyl-prolyl cis-trans isomerase FKBP62 OS=Arabidopsis thaliana GN=FKBP62 PE=1 SV=2	10	---	----	0,058	0,41816	1185,25	52,70%
Q9STG3	Putative cullin-like protein 4 OS=Arabidopsis thaliana GN=At3g46910 PE=3 SV=1	1	---	----	-0,247	0,41806	1184,96	52,70%
O65569	40S ribosomal protein S11-2 OS=Arabidopsis thaliana GN=RPS11B PE=2 SV=2	1	---	----	0,466	0,42042	1191,65	52,90%
O81027	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Arabidopsis thaliana GN=HMGCL PE=1 SV=2	2	---	----	0,179	0,42022	1191,08	52,90%
F4K4Y5	DEK domain-containing chromatin associated protein OS=Arabidopsis thaliana GN=At5g55660 PE=1 SV=1	1	---	----	-0,258	0,42006	1190,63	52,90%
Q9SIU8	Probable protein phosphatase 2C 20 OS=Arabidopsis thaliana GN=PPC3-1.2 PE=1 SV=3	7	---	----	0,085	0,42216	1196,58	53,00%

Q9LVJ1	At3g14067 OS=Arabidopsis thaliana GN=At3g14067 PE=2 SV=1	8	---	----	0,069	0,42122	1193,91	53,00%
Q8VYL1;Q9FIJ7	Adenylate kinase 5, chloroplastic OS=Arabidopsis thaliana GN=At5g35170 PE=1 SV=1	1	---	----	-0,226	0,42241	1197,29	53,00%
Q9SP35	Mitochondrial import inner membrane translocase subunit TIM17-2 OS=Arabidopsis thaliana GN=TIM17-2 PE=1 SV=2	1	---	----	0,261	0,42206	1196,30	53,10%
Q8LAZ7	COP9 signalosome complex subunit 5b OS=Arabidopsis thaliana GN=CSN5B PE=1 SV=2	1	---	----	0,246	0,42206	1196,30	53,10%
Q9SFV3	At3g07230 OS=Arabidopsis thaliana GN=T1B9.10 PE=2 SV=1	2	---	----	0,181	0,42341	1200,12	53,10%
Q9LU01	Putative uncharacterized protein At5g44650 OS=Arabidopsis thaliana GN=CEST PE=2 SV=1	4	---	----	-0,118	0,42416	1202,25	53,10%
Q9SJT7	V-type proton ATPase subunit a2 OS=Arabidopsis thaliana GN=VHA-a2 PE=1 SV=1	3	---	----	-0,177	0,42216	1196,58	53,10%
P92966	Serine/arginine-rich splicing factor RS41 OS=Arabidopsis thaliana GN=RS41 PE=1 SV=2	1	---	----	0,248	0,42616	1207,92	53,20%
Q94AJ9	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=At1g12800 PE=2 SV=1	6	---	----	0,104	0,42616	1207,92	53,20%
Q93VT6	Putative uncharacterized protein At5g08540 OS=Arabidopsis thaliana GN=At5g08540 PE=1 SV=1	7	---	----	-0,085	0,42406	1201,97	53,20%
Q8VZE9	UDP-glycosyltransferase 73B1 OS=Arabidopsis thaliana GN=UGT73B1 PE=2 SV=1	2	---	----	-0,157	0,42406	1201,97	53,20%
O22874	Expansin-A8 OS=Arabidopsis thaliana GN=EXPA8 PE=2 SV=1	2	---	----	-0,204	0,42406	1201,97	53,20%
Q8L540	Thiol-disulfide oxidoreductase LTO1 OS=Arabidopsis thaliana GN=LTO1 PE=1 SV=1	1	---	----	-0,248	0,42616	1207,92	53,20%
Q9M028	LIMR family protein At5g01460 OS=Arabidopsis thaliana GN=At5g01460 PE=2 SV=1	1	---	----	0,245	0,42606	1207,64	53,30%
Q93W77	NifU-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=NIFU1 PE=1 SV=1	2	---	----	0,196	0,42616	1207,92	53,30%
Q8VZ21	Putative uncharacterized protein At5g61820 OS=Arabidopsis thaliana GN=At5g61820 PE=2 SV=1	2	---	----	0,194	0,42606	1207,64	53,30%
Q9XI93	At1g13930/F16A14.27 OS=Arabidopsis thaliana GN=F7A19.2 PE=2 SV=1	4	---	----	0,07	0,42742	1211,49	53,30%
Q8W4K6	At4g13350 OS=Arabidopsis thaliana GN=T9E8.90 PE=1 SV=1	1	---	----	-0,182	0,42606	1207,64	53,30%
Q9LRW6	F-box protein At3g13820 OS=Arabidopsis thaliana GN=At3g13820 PE=2 SV=1	1	---	----	-0,296	0,42606	1207,64	53,30%
Q8L637	Putative uncharacterized protein At3g21140 OS=Arabidopsis thaliana GN=At3g21140 PE=2 SV=1	1	---	----	0,274	0,42816	1213,59	53,40%
Q93ZH0	LysM domain-containing GPI-anchored protein 1 OS=Arabidopsis thaliana GN=LYM1 PE=1 SV=1	1	---	----	-0,163	0,42602	1207,52	53,40%
rev_Q9SN15	reversed Putative uncharacterized protein F3A4.110 OS=Arabidopsis thaliana GN=F3A4.110 PE=4 SV=1	1	---	----	-0,568	0,42816	1213,59	53,40%
O64740;Q9SRI1	Protein transport protein SEC13 homolog B OS=Arabidopsis thaliana GN=SEC13B PE=1 SV=1	1	---	----	0,273	0,43041	1219,96	53,50%
O81488	PHD finger protein ALFIN-LIKE 4 OS=Arabidopsis thaliana GN=AL4 PE=1 SV=2	1	---	----	0,241	0,43041	1219,96	53,50%
Q9SUW2	Adenine phosphoribosyltransferase 3 OS=Arabidopsis thaliana GN=APT3 PE=1 SV=1	1	---	----	0,233	0,43016	1219,26	53,50%
P56788	Photosystem I assembly protein Ycf4 OS=Arabidopsis thaliana GN=ycf4 PE=3 SV=1	3	---	----	0,112	0,43206	1224,64	53,50%
Q42560;Q9SIB9	Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2	7	---	----	0,084	0,43181	1223,93	53,50%
Q9SR37	Beta-glucosidase 23 OS=Arabidopsis thaliana GN=BGLU23 PE=1 SV=1	12	---	----	0,059	0,43102	1221,69	53,50%
P00761	Trypsin OS=Sus scrofa PE=1 SV=1	4	---	----	-0,052	0,43016	1219,26	53,50%
F4J9G2	Rhodanese/cell cycle control phosphatase superfamily protein OS=Arabidopsis thaliana GN=At3g59780 PE=4 SV=1	14	---	----	-0,061	0,42921	1216,56	53,50%
Q8RUF8	Omega-amidase,chloroplastic OS=Arabidopsis thaliana GN=NLP3 PE=1 SV=1	6	---	----	-0,088	0,43016	1219,26	53,50%
Q94K30	AT1G01800 protein OS=Arabidopsis thaliana GN=At1g01800 PE=2 SV=1	8	---	----	-0,088	0,43016	1219,26	53,50%
Q8H0W0	Protein LOW PSII ACCUMULATION 3, chloroplastic OS=Arabidopsis thaliana GN=LPA3 PE=1 SV=1	9	---	----	-0,09	0,43162	1223,39	53,50%
Q94A40	Coatomer subunit alpha-1 OS=Arabidopsis thaliana GN=At1g62020 PE=2 SV=2	6	---	----	-0,098	0,43141	1222,80	53,50%
F4JRQ4	Protein kinase family protein OS=Arabidopsis thaliana GN=At4g24810 PE=4 SV=1	1	---	----	-0,257	0,43216	1224,92	53,50%
O49305	At1g23120 OS=Arabidopsis thaliana GN=T26J12.11 PE=2 SV=1	1	---	----	-0,573	0,43206	1224,64	53,50%
Q9SIM4	60S ribosomal protein L14-1 OS=Arabidopsis thaliana GN=RPL14A PE=2 SV=1	2	---	----	0,159	0,43006	1218,97	53,60%
Q8RWR1-2	Isoform 2 of Putative lysine-specific demethylase JMJD5 OS=Arabidopsis thaliana GN=JMJD5	2	---	----	0,228	0,43406	1230,31	53,70%
Q9FJW4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Arabidopsis thaliana GN=FRO1 PE=2 SV=1	3	---	----	0,113	0,43421	1230,73	53,70%
F4K0M7	Maf-like protein OS=Arabidopsis thaliana GN=At5g66550 PE=4 SV=1	1	---	----	-0,236	0,43406	1230,31	53,70%
Q9SYA9	AT1G61730 protein OS=Arabidopsis thaliana GN=T13M11.9 PE=1 SV=1	1	---	----	-0,243	0,43406	1230,31	53,70%
Q9SJF3	mRNA-decapping enzyme-like protein OS=Arabidopsis thaliana GN=At1g08370 PE=1 SV=2	1	---	----	0,28	0,43581	1235,27	53,80%
Q9C901	DNA-binding enhancer-like protein OS=Arabidopsis thaliana GN=F5E6.6 PE=2 SV=1	1	---	----	0,24	0,43561	1234,70	53,80%
Q9FH13	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3 OS=Arabidopsis thaliana GN=At5g56260 PE=1 SV=1	2	---	----	0,148	0,43821	1242,07	53,80%
Q9FFR3;Q9FWA3;Q9SH69	6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV	2	---	----	0,109	0,43616	1236,26	53,80%
Q9XGM1	V-type proton ATPase subunit D OS=Arabidopsis thaliana GN=VHA-D PE=1 SV=2	12	---	----	0,057	0,43822	1242,10	53,80%
Q9LVI9	Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic OS=Arabidopsis thaliana GN=PYD1 PE=1 SV=1	5	---	----	-0,089	0,43521	1233,57	53,80%
O81014	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic OS=Arabidopsis thaliana GN=ISPE PE=2 SV=1	3	---	----	-0,135	0,43606	1235,98	53,80%
Q8GYN5	RPM1-interacting protein 4 OS=Arabidopsis thaliana GN=RIN4 PE=1 SV=1	1	ADESPEKVTVVPK	Phospho S4	-0,4	0,43606	1235,98	53,80%
P82874	Mitochondrial import receptor subunit TOM20-3 OS=Arabidopsis thaliana GN=TOM20-3 PE=1 SV=1	1	---	----	0,31	0,43806	1241,65	53,90%
Q9LFM4	At5g11330 OS=Arabidopsis thaliana GN=F2I11_220 PE=2 SV=1	2	---	----	0,198	0,43806	1241,65	53,90%
Q09152;Q43315	Farnesyl pyrophosphate synthase 1, mitochondrial OS=Arabidopsis thaliana GN=FPS1 PE=2 SV=2	1	---	----	0,171	0,44006	1247,31	53,90%
Q8LFS6	RNA-binding protein BRN1 OS=Arabidopsis thaliana GN=BRN1 PE=2 SV=1	3	---	----	0,153	0,43816	1241,93	53,90%
P49078;Q9LV77	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Arabidopsis thaliana GN=ASN1 PE=2 SV=2	2	---	----	0,139	0,44006	1247,31	53,90%
O65258	Beta-amylase 2, chloroplastic OS=Arabidopsis thaliana GN=BAM2 PE=1 SV=2	3	---	----	0,13	0,43806	1241,65	53,90%

O80988	Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana GN=GLDP2 PE=2 SV=1	10	---	----	0,063	0,43762	1240,40	53,90%
Q8W456	Putative uncharacterized protein At1g20220 OS=Arabidopsis thaliana GN=T20H2.2 PE=2 SV=1	3	---	----	-0,153	0,43806	1241,65	53,90%
F4J3N2	FtsH extracellular protease family protein OS=Arabidopsis thaliana GN=emb2458 PE=4 SV=1	1	---	----	-0,243	0,44016	1247,60	53,90%
Q9LYT2	Pentatricopeptide repeat-containing protein At3g59040 OS=Arabidopsis thaliana GN=At3g59040 PE=2 SV=2	1	---	----	0,431	0,44006	1247,31	54,00%
O22224	Nuclear pore complex protein NUP93A OS=Arabidopsis thaliana GN=NUP93A PE=1 SV=2	1	---	----	0,247	0,44082	1249,47	54,00%
A8MRP2	AIG2-like family protein OS=Arabidopsis thaliana GN=At2g24390 PE=4 SV=1	1	---	----	-0,24	0,44006	1247,31	54,00%
Q9FZ27	Germin-like protein subfamily 2 member 2 OS=Arabidopsis thaliana GN=At1g02335 PE=2 SV=1	1	---	----	-0,324	0,43806	1241,65	54,00%
Q949Y5	Probable zinc metalloprotease EGY1, chloroplastic OS=Arabidopsis thaliana GN=EGY1 PE=2 SV=1	1	---	----	-0,407	0,44006	1247,31	54,00%
Q93W30	Expressed protein OS=Arabidopsis thaliana GN=At2g35605 PE=2 SV=1	1	---	----	0,248	0,44262	1254,57	54,10%
O82462	Glutamyl-tRNA synthetase OS=Arabidopsis thaliana GN=At5g26707 PE=2 SV=1	9	---	----	0,086	0,44216	1253,27	54,10%
Q8GYI4	Phosphoenolpyruvate carboxylase-like protein OS=Arabidopsis thaliana GN=At2g43180 PE=2 SV=1	4	---	----	-0,111	0,44206	1252,98	54,10%
Q9XFS7	Non-specific lipid-transfer protein 5 OS=Arabidopsis thaliana GN=LTP5 PE=1 SV=1	1	---	----	-0,127	0,44181	1252,27	54,10%
Q9ZPI6	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 OS=Arabidopsis thaliana GN=AIM1 PE=1 SV=1	12	---	----	-0,069	0,44416	1258,93	54,20%
Q8VY52	PsbP domain-containing protein 2, chloroplastic OS=Arabidopsis thaliana GN=PPD2 PE=1 SV=1	3	---	----	-0,156	0,44416	1258,93	54,20%
O49553	AT4g21110/F7J7_50 OS=Arabidopsis thaliana GN=F7J7.50 PE=2 SV=1	2	---	----	0,172	0,44616	1264,60	54,30%
Q9SQT8	Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=EMB	5	---	----	0,092	0,44616	1264,60	54,30%
F4ICG2	Putative tRNA-glutamine ligase OS=Arabidopsis thaliana GN=OVA9 PE=4 SV=1	1	---	----	-0,231	0,44406	1258,65	54,30%
Q8RYC3	Expressed protein OS=Arabidopsis thaliana GN=At2g33845 PE=2 SV=1	1	---	----	0,298	0,44616	1264,60	54,40%
Q84JM6	Putative uncharacterized protein At2g25310 OS=Arabidopsis thaliana GN=At2g25310 PE=2 SV=1	1	---	----	0,24	0,44816	1270,27	54,40%
Q66GN9	ATP-dependent Clp protease OS=Arabidopsis thaliana GN=At1g33360 PE=2 SV=1	1	---	----	0,239	0,44606	1264,32	54,40%
Q9FND9	Probable galactinol--sucrose galactosyltransferase 5 OS=Arabidopsis thaliana GN=RFS5 PE=1 SV=1	2	---	----	0,225	0,44601	1264,18	54,40%
Q9S7L9	Cytochrome c oxidase subunit 6b-1 OS=Arabidopsis thaliana GN=COX6B-1 PE=1 SV=1	4	---	----	0,103	0,44816	1270,27	54,40%
P42799	Glutamate-1-semialdehyde 2,1-aminomutase 1, chloroplastic OS=Arabidopsis thaliana GN=GSA1 PE=2 SV=1	5	---	----	0,085	0,44816	1270,27	54,40%
Q9SJ89	Ferredoxin-thioredoxin reductase catalytic chain, chloroplastic OS=Arabidopsis thaliana GN=FTRC PE=2 SV=1	2	---	----	-0,121	0,44816	1270,27	54,40%
F4JTL0	Uncharacterized protein OS=Arabidopsis thaliana GN=At4g38225 PE=4 SV=1	2	---	----	-0,189	0,44582	1263,64	54,40%
Q9FHD7	Probable serine/threonine-protein kinase At5g41260 OS=Arabidopsis thaliana GN=At5g41260 PE=1 SV=1	1	---	----	-0,275	0,44816	1270,27	54,40%
O80950	Jacalin-related lectin 22 OS=Arabidopsis thaliana GN=JAL22 PE=1 SV=1	1	---	----	0,313	0,44922	1273,28	54,50%
rev_Q8L7L8	reversed Telomere repeat-binding protein 1 OS=Arabidopsis thaliana GN=TRP1 PE=1 SV=2	1	---	----	0,244	0,44806	1269,99	54,50%
Q9SKK4	Probable 2-oxoacid dependent dioxygenase OS=Arabidopsis thaliana GN=GSL-OH PE=2 SV=1	3	---	----	0,109	0,44806	1269,99	54,50%
Q9LZS3	1,4-alpha-glucan-branching enzyme 2-2, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SBE2.2 PE=2 SV=1	9	---	----	0,078	0,45015	1275,94	54,50%
O22941	Zinc-metallopeptidase, peroxisomal OS=Arabidopsis thaliana GN=PXM16 PE=2 SV=1	10	---	----	0,075	0,45015	1275,94	54,50%
P52410	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic OS=Arabidopsis thaliana GN=KAS1 PE=2 SV=2	10	---	----	-0,055	0,45015	1275,94	54,50%
Q9LFD5	Binding partner of ACD11 1 OS=Arabidopsis thaliana GN=BPA1 PE=1 SV=1	4	---	----	-0,09	0,45005	1275,66	54,50%
Q9FNX5	Dynamin-related protein 1E OS=Arabidopsis thaliana GN=DRP1E PE=1 SV=1	4	---	----	-0,167	0,44806	1269,99	54,50%
P27140-2	Isoform 2 of Beta carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=BCA1	1	---	----	-0,547	0,44816	1270,27	54,50%
Q9ZUC1	Quinone oxidoreductase-like protein At1g23740, chloroplastic OS=Arabidopsis thaliana GN=At1g23740 PE=2 SV=2	11	---	----	-0,052	0,45142	1279,51	54,60%
Q43349;Q9ZUU4	29 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP29A PE=2 SV=2	2	---	----	0,1	0,45321	1284,59	54,70%
Q8RY11	AT3g05350/T12H1_32 OS=Arabidopsis thaliana GN=At3g05350 PE=2 SV=1	6	---	----	-0,113	0,45281	1283,45	54,70%
Q945Q5	At2g30700/T11J7.9 OS=Arabidopsis thaliana GN=At2g30695 PE=2 SV=1	2	---	----	-0,168	0,45215	1281,61	54,70%
Q9LFM3	At5g11340 OS=Arabidopsis thaliana GN=F2I11_230 PE=2 SV=1	1	---	----	-0,319	0,45215	1281,61	54,70%
Q9LHP1	60S ribosomal protein L7-4 OS=Arabidopsis thaliana GN=RPL7D PE=2 SV=1	1	---	----	0,241	0,45405	1286,99	54,80%
Q9FIW4	Beta-glucosidase 42 OS=Arabidopsis thaliana GN=BGLU42 PE=2 SV=1	1	---	----	-0,251	0,45415	1287,28	54,80%
Q9T0A0	Long chain acyl-CoA synthetase 4 OS=Arabidopsis thaliana GN=LACS4 PE=2 SV=1	8	---	----	0,066	0,45481	1289,12	54,90%
P93025	Phototropin-2 OS=Arabidopsis thaliana GN=PHOT2 PE=1 SV=2	8	---	----	0,079	0,45815	1298,61	55,00%
O04450	T-complex protein 1 subunit epsilon OS=Arabidopsis thaliana GN=CCT5 PE=1 SV=1	9	---	----	0,071	0,45621	1293,09	55,00%
Q9FHM7	Hypersensitive-induced response protein 4 OS=Arabidopsis thaliana GN=HIR4 PE=1 SV=1	1	---	----	0,235	0,45805	1298,33	55,10%
Q43348	Acid beta-fructofuranosidase 3, vacuolar OS=Arabidopsis thaliana GN=BFRUCT3 PE=2 SV=1	3	---	----	0,159	0,45815	1298,61	55,10%
O04904	Dihydroorotase, mitochondrial OS=Arabidopsis thaliana GN=PYR4 PE=2 SV=1	3	---	----	-0,187	0,45805	1298,33	55,10%
Q9FFA5	Putative uncharacterized protein At5g23750 OS=Arabidopsis thaliana GN=MRO11.3 PE=2 SV=1	1	---	----	-0,269	0,45815	1298,61	55,10%
P51430	40S ribosomal protein S6-2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=3	1	SRLSSAPAKPVAA	Phospho S4	0,624	0,46015	1304,28	55,20%
P57720	Chorismate synthase, chloroplastic OS=Arabidopsis thaliana GN=EMB1144 PE=2 SV=2	4	---	----	0,117	0,46002	1303,89	55,20%
Q9LUB2	AT5g48220/MIF21_11 OS=Arabidopsis thaliana GN=At5g48220 PE=2 SV=1	5	---	----	-0,081	0,46015	1304,28	55,20%
Q8VZ93	Allyl alcohol dehydrogenase-like protein OS=Arabidopsis thaliana GN=F24G16.11 PE=2 SV=1	1	---	----	-0,134	0,46005	1304,00	55,20%
O23401	UDP-glycosyltransferase 84A3 OS=Arabidopsis thaliana GN=UGT84A3 PE=1 SV=1	2	---	----	-0,135	0,45805	1298,33	55,20%
Q9LXJ2	Putative ubiquinol-cytochrome c reductase subunit 9 OS=Arabidopsis thaliana GN=F3C22_130 PE=2 SV=1	2	---	----	-0,167	0,45805	1298,33	55,20%

Q9SLC8	Putative uncharacterized protein At2g42310 OS=Arabidopsis thaliana GN=At2g42310 PE=2 SV=1	1	---	----	-0,24	0,46061	1305,56	55,20%
P38025	Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic OS=Arabidopsis thaliana GN=PUR7 PE=2 S	1	---	----	-0,282	0,46005	1304,00	55,20%
Q8GWU0	Phosphoglycolate phosphatase 2 OS=Arabidopsis thaliana GN=PGLP2 PE=1 SV=1	1	---	----	-0,576	0,45805	1298,33	55,20%
Q9LSA9	Genomic DNA, chromosome 3, P1 clone: MVE11 OS=Arabidopsis thaliana GN=At3g18680 PE=1 SV=1	1	---	----	0,243	0,46415	1315,62	55,30%
Q9SVM9	Protein ECERIFERUM 26 OS=Arabidopsis thaliana GN=CER26 PE=2 SV=1	1	---	----	0,242	0,46121	1307,26	55,30%
Q8W575	COP9 signalosome complex subunit 3 OS=Arabidopsis thaliana GN=CSN3 PE=1 SV=2	2	---	----	0,152	0,46215	1309,95	55,30%
Q9FFT4	Pyruvate decarboxylase 2 OS=Arabidopsis thaliana GN=PDC2 PE=2 SV=1	5	---	----	-0,091	0,46215	1309,95	55,30%
Q93Z83	AT5g26280/T19G15_130 OS=Arabidopsis thaliana GN=At5g26280 PE=2 SV=1	3	---	----	-0,127	0,46422	1315,79	55,30%
Q93Z53	Plastidial pyruvate kinase 3, chloroplastic OS=Arabidopsis thaliana GN=PKP3 PE=1 SV=1	2	---	----	-0,203	0,46215	1309,95	55,30%
Q9FJ81	At5g52110 OS=Arabidopsis thaliana GN=HCF208 PE=2 SV=1	1	---	----	-0,274	0,46222	1310,12	55,30%
rev_Q940Y1	reversed Oxysterol-binding protein-related protein 2A OS=Arabidopsis thaliana GN=ORP2A PE=2 SV=1	1	---	----	0,261	0,46415	1315,62	55,40%
Q8L719	THO complex subunit 4B OS=Arabidopsis thaliana GN=ALY2 PE=1 SV=1	2	---	----	0,145	0,46321	1312,93	55,40%
Q940V1	AT4g39960/T5J17_130 OS=Arabidopsis thaliana GN=At4g39960 PE=2 SV=1	4	---	----	0,131	0,46415	1315,62	55,40%
Q38893	Zeta-carotene desaturase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=ZDS1 PE=1 SV=3	9	---	----	-0,066	0,46302	1312,39	55,40%
Q8VYY8	Putative uncharacterized protein At2g43630 OS=Arabidopsis thaliana GN=At2g43630 PE=2 SV=1	1	---	----	-0,227	0,46415	1315,62	55,40%
Q8VZT0	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 OS=Arabidopsis thaliana GN=At3g03920 PE=2 SV=1	1	---	----	-0,293	0,46361	1314,06	55,40%
Q94A97	Ubiquitin-conjugating enzyme E2 35 OS=Arabidopsis thaliana GN=UBC35 PE=1 SV=1	1	---	----	0,25	0,46615	1321,29	55,50%
O23647;Q9LZS3	1,4-alpha-glucan-branching enzyme 2-1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SBE2.1 PE=2 SV=1	1	---	----	0,134	0,46641	1322,00	55,50%
Q8RYE9	Haloacid dehalogenase-like hydrolase domain-containing protein At2g33255 OS=Arabidopsis thaliana GN=At2g33255 P	5	---	----	0,118	0,46615	1321,29	55,50%
Q9FE78	AT5g05470 OS=Arabidopsis thaliana GN=EIF2 ALPHA PE=2 SV=1	1	---	----	0,234	0,46815	1326,95	55,60%
Q9LSQ5	NAD(P)H dehydrogenase (quinone) FQR1 OS=Arabidopsis thaliana GN=FQR1 PE=1 SV=1	4	---	----	0,078	0,46761	1325,40	55,60%
Q9FMF1	AT5g64380/MSJ1_22 OS=Arabidopsis thaliana GN=At5g64380 PE=2 SV=1	5	---	----	-0,095	0,46762	1325,43	55,60%
Q9M2W2	Glutathione S-transferase L2, chloroplastic OS=Arabidopsis thaliana GN=GSTL2 PE=2 SV=1	3	---	----	-0,131	0,46815	1326,95	55,60%
Q9M1E7	Tetraspanin-3 OS=Arabidopsis thaliana GN=TET3 PE=2 SV=1	2	---	----	-0,15	0,46815	1326,95	55,60%
C0Z2J1	AT1G11360 protein OS=Arabidopsis thaliana GN=At1g11360 PE=1 SV=1	1	SPTVVTVQPSSPR	Phospho S10	-0,519	0,47005	1332,34	55,60%
Q38864	Expansin-A5 OS=Arabidopsis thaliana GN=EXPA5 PE=2 SV=1	1	---	----	0,414	0,46982	1331,67	55,70%
Q9XII1	Plastid division protein PDV2 OS=Arabidopsis thaliana GN=PDV2 PE=1 SV=1	1	---	----	0,345	0,46815	1326,95	55,70%
Q5M729	Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial OS=Ar	2	---	----	0,153	0,47005	1332,34	55,70%
Q9FNF2	Starch synthase 1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SS1 PE=2 SV=1	3	---	----	0,109	0,47005	1332,34	55,70%
F4IW47;Q8RWV0	Transketolase-2, chloroplastic OS=Arabidopsis thaliana GN=TKL-2 PE=2 SV=1	7	---	----	-0,05	0,46962	1331,10	55,70%
Q9SCL7	Acetylglutamate kinase, chloroplastic OS=Arabidopsis thaliana GN=NAGK PE=1 SV=1	4	---	----	-0,106	0,46961	1331,07	55,70%
Q94FB9	ABC transporter D family member 1 OS=Arabidopsis thaliana GN=ABCC1 PE=1 SV=1	2	---	----	-0,237	0,47005	1332,34	55,70%
Q8GYC7;Q8H112	PGR5-like protein 1B, chloroplastic OS=Arabidopsis thaliana GN=PGRL1B PE=1 SV=1	1	---	----	-0,526	0,47005	1332,34	55,70%
Q9LQL0	Glycine cleavage system H protein 3, mitochondrial OS=Arabidopsis thaliana GN=GDH3 PE=1 SV=1	1	---	----	0,087	0,47205	1338,01	55,80%
Q8RW90	At1g12050/F12F1_8 OS=Arabidopsis thaliana GN=At1g12050 PE=2 SV=1	5	---	----	-0,085	0,47205	1338,01	55,80%
O81147	Proteasome subunit alpha type-6-B OS=Arabidopsis thaliana GN=PAA2 PE=1 SV=1	2	---	----	-0,112	0,47215	1338,29	55,80%
Q8L7A9	AP-4 complex subunit epsilon OS=Arabidopsis thaliana GN=At1g31730 PE=1 SV=1	2	---	----	-0,167	0,47202	1337,90	55,80%
O81845	Mitochondrial uncoupling protein 1 OS=Arabidopsis thaliana GN=PUMP1 PE=1 SV=1	7	---	----	0,088	0,47415	1343,96	55,90%
Q9LZ08	Protein MODIFIER OF SNC1 11 OS=Arabidopsis thaliana GN=MOS11 PE=1 SV=1	1	---	----	-0,215	0,47405	1343,68	55,90%
Q9LFY3	At1g27030/T7N9_9 OS=Arabidopsis thaliana GN=At1g27030 PE=2 SV=1	1	---	----	0,325	0,47381	1342,97	56,00%
Q9LXS6;Q9SJH7	Citrate synthase 2, peroxisomal OS=Arabidopsis thaliana GN=CSY2 PE=2 SV=1	2	---	----	-0,108	0,47405	1343,68	56,00%
Q945Q1	Cysteine proteinase inhibitor 1 OS=Arabidopsis thaliana GN=CYS1 PE=1 SV=2	1	---	----	-0,153	0,47481	1345,81	56,00%
Q93ZI7	AT5g35440/MOK9_2 OS=Arabidopsis thaliana GN=At5g35430 PE=2 SV=1	1	---	----	-0,31	0,47542	1347,54	56,00%
F4KEV7	Fragile histidine triad protein OS=Arabidopsis thaliana GN=FHIT PE=4 SV=1	1	---	----	0,282	0,47815	1355,30	56,10%
Q4V3D9	Protein STRICTOSIDINE SYNTHASE-LIKE 10 OS=Arabidopsis thaliana GN=SSL10 PE=2 SV=1	1	---	----	0,232	0,47721	1352,61	56,10%
Q9SYZ4	Putative uncharacterized protein AT4g34290 OS=Arabidopsis thaliana GN=At4g34290 PE=2 SV=1	1	---	----	0,13	0,47661	1350,91	56,10%
Q8L611	Protein transport protein SEC31 homolog B OS=Arabidopsis thaliana GN=SEC31B PE=1 SV=1	11	---	----	0,074	0,47601	1349,21	56,10%
Q9SS87	Protein SIEVE ELEMENT OCCLUSION B OS=Arabidopsis thaliana GN=SEOB PE=1 SV=1	2	---	----	-0,153	0,47815	1355,30	56,10%
rev_Q9SR39	reversed Protein kinase protein with tetratricopeptide repeat domain OS=Arabidopsis thaliana GN=F3L24.11 PE=4 SV=	1	---	----	-0,295	0,47605	1349,34	56,10%
P25071	Calmodulin-like protein 12 OS=Arabidopsis thaliana GN=CML12 PE=1 SV=3	1	---	----	0,464	0,47815	1355,30	56,20%
rev_F4IPJ1	reversed Phosphatidylinositol 3-and 4-kinase family protein with FAT domain OS=Arabidopsis thaliana GN=At2g17930	1	---	----	-0,218	0,47805	1355,01	56,20%
Q494P3	At3g17770 OS=Arabidopsis thaliana GN=At3g17770 PE=2 SV=1	1	---	----	-0,223	0,47815	1355,30	56,20%
Q8LDW8	Probable hydroxyacylglutathione hydrolase 2, chloroplast OS=Arabidopsis thaliana GN=GLX2-4 PE=2 SV=1	1	---	----	-0,543	0,47782	1354,34	56,20%
B9DG73	AT3G11930 protein OS=Arabidopsis thaliana GN=At3g11930 PE=2 SV=1	3	---	----	-0,098	0,47961	1359,41	56,30%
O48788	Probable inactive receptor kinase At2g26730 OS=Arabidopsis thaliana GN=At2g26730 PE=1 SV=1	3	---	----	-0,158	0,48005	1360,68	56,30%

rev_F4HU83	reversed Kinesin-like protein OS=Arabidopsis thaliana GN=ARK2 PE=3 SV=1	1	---	----	-0,261	0,48005	1360,68	56,30%
Q9SF21	At3g11770 OS=Arabidopsis thaliana GN=F26K24.6 PE=2 SV=1	1	---	----	0,226	0,48205	1366,35	56,40%
Q9SCK3	At3g49560 OS=Arabidopsis thaliana GN=T9C5.150 PE=2 SV=1	3	---	----	0,107	0,48241	1367,35	56,40%
Q94F20;Q9LYE7	At5g25460 OS=Arabidopsis thaliana GN=At5g25460 PE=2 SV=1	4	---	----	0,066	0,48215	1366,63	56,40%
P57752	Acyl-CoA-binding domain-containing protein 6 OS=Arabidopsis thaliana GN=ACBP6 PE=1 SV=1	4	---	----	-0,064	0,48205	1366,35	56,40%
P56802	30S ribosomal protein S11, chloroplastic OS=Arabidopsis thaliana GN=rps11 PE=3 SV=1	4	---	----	-0,071	0,48121	1363,95	56,40%
Q8S9J1	Protoporphyrinogen oxidase 2, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=PPOX2 PE=1 SV=1	3	---	----	-0,107	0,48205	1366,35	56,40%
A7WM73	Beta-hexosaminidase 1 OS=Arabidopsis thaliana GN=HEXO1 PE=1 SV=1	3	---	----	-0,108	0,48181	1365,65	56,40%
B9DGU7	Thiamine pyrophosphokinase 1 OS=Arabidopsis thaliana GN=TPK1 PE=2 SV=1	1	---	----	-0,453	0,48261	1367,92	56,40%
O04379	Protein argonaute 1 OS=Arabidopsis thaliana GN=AGO1 PE=1 SV=1	1	---	----	0,36	0,48405	1372,02	56,50%
Q9ZVA1	D-mannose binding lectin protein with Apple-like carbohydrate-binding domain OS=Arabidopsis thaliana GN=F9K20.13	3	---	----	0,123	0,48405	1372,02	56,50%
Q9FMT8	Major facilitator protein OS=Arabidopsis thaliana GN=At5g14120 PE=1 SV=1	3	---	----	-0,101	0,48415	1372,30	56,50%
F4I7I0;Q9LVA0	Alanine aminotransferase 1, mitochondrial OS=Arabidopsis thaliana GN=ALAAT1 PE=1 SV=1	1	---	----	-0,158	0,48415	1372,30	56,50%
P56764	DNA-directed RNA polymerase subunit beta'' OS=Arabidopsis thaliana GN=rpoC2 PE=3 SV=1	2	---	----	-0,168	0,48361	1370,75	56,50%
Q8L831	Nudix hydrolase 3 OS=Arabidopsis thaliana GN=NUDT3 PE=1 SV=1	7	---	----	0,081	0,48642	1378,72	56,60%
Q8LPJ3	Alpha-mannosidase OS=Arabidopsis thaliana GN=At5g13980 PE=2 SV=1	8	---	----	-0,085	0,48615	1377,97	56,60%
O80456	At2g23390/F26B6.4 OS=Arabidopsis thaliana GN=At2g23390 PE=2 SV=1	2	---	----	-0,142	0,48605	1377,69	56,60%
Q84L33	Ubiquitin receptor RAD23b OS=Arabidopsis thaliana GN=RAD23B PE=1 SV=3	1	---	----	0,235	0,48805	1383,35	56,70%
Q9LHP2	Serine/arginine-rich SC35-like splicing factor SCL30A OS=Arabidopsis thaliana GN=SCL30A PE=1 SV=1	2	---	----	0,207	0,48815	1383,64	56,70%
Q9LXZ4	GroES-like zinc-binding alcohol dehydrogenase family protein OS=Arabidopsis thaliana GN=T5P19_110 PE=2 SV=1	2	---	----	0,161	0,48762	1382,12	56,70%
Q38929	Isopentenyl-diphosphate Delta-isomerase I, chloroplastic OS=Arabidopsis thaliana GN=IPP1 PE=2 SV=3	4	---	----	0,114	0,48722	1380,98	56,70%
Q01908	ATP synthase gamma chain 1, chloroplastic OS=Arabidopsis thaliana GN=ATPC1 PE=1 SV=1	13	---	----	-0,033	0,48722	1380,98	56,70%
Q96329	Acyl-coenzyme A oxidase 4, peroxisomal OS=Arabidopsis thaliana GN=ACX4 PE=1 SV=1	6	---	----	-0,083	0,48805	1383,35	56,70%
Q8RXS1	Photosynthetic NDH subunit of subcomplex B 4, chloroplastic OS=Arabidopsis thaliana GN=PNSB4 PE=2 SV=1	2	---	----	-0,133	0,48815	1383,64	56,70%
Q84K72	Putative uncharacterized protein At1g06510 OS=Arabidopsis thaliana GN=At1g06510 PE=2 SV=1	1	---	----	-0,232	0,48722	1380,98	56,70%
Q8W498	ARM repeat superfamily protein OS=Arabidopsis thaliana GN=T29A15.130 PE=2 SV=1	1	---	----	-0,276	0,48902	1386,09	56,70%
Q9C958	Serine/threonine-protein kinase SRK2B OS=Arabidopsis thaliana GN=SRK2B PE=1 SV=1	2	---	----	0,129	0,49001	1388,89	56,80%
P56808	30S ribosomal protein S19, chloroplastic OS=Arabidopsis thaliana GN=rps19 PE=3 SV=1	3	---	----	0,124	0,49015	1389,31	56,80%
Q9LTB2	Methionine S-methyltransferase OS=Arabidopsis thaliana GN=MMT1 PE=1 SV=1	3	---	----	0,113	0,49015	1389,31	56,80%
F4KG14	Guanylate-binding protein OS=Arabidopsis thaliana GN=At5g46070 PE=4 SV=1	1	---	----	-0,258	0,49005	1389,02	56,80%
Q9FKW6	Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=LFNR1 PE=1 SV=1	16	---	----	-0,033	0,49162	1393,46	56,90%
O04310	Jacalin-related lectin 34 OS=Arabidopsis thaliana GN=JAL34 PE=1 SV=1	8	---	----	-0,08	0,49205	1394,69	56,90%
A8MS41	Carbon catabolite repressor protein 4 homolog 4 OS=Arabidopsis thaliana GN=CCR4-4 PE=2 SV=1	1	---	----	-0,223	0,49205	1394,69	56,90%
Q9SK27	Early nodulin-like protein 1 OS=Arabidopsis thaliana GN=At2g25060 PE=1 SV=2	1	---	----	0,236	0,49405	1400,36	57,10%
Q8L719;Q8L773	THO complex subunit 4B OS=Arabidopsis thaliana GN=ALY2 PE=1 SV=1	1	---	----	0,227	0,49382	1399,69	57,10%
Q96250	ATP synthase subunit gamma, mitochondrial OS=Arabidopsis thaliana GN=ATPC PE=2 SV=1	9	---	----	-0,062	0,49415	1400,64	57,10%
Q8LCA1	Protein CURVATURE THYLAKOID 1B, chloroplastic OS=Arabidopsis thaliana GN=CURT1B PE=1 SV=2	3	---	----	-0,082	0,49415	1400,64	57,10%
Q9ZUF4	Putative uncharacterized protein At2g05940 OS=Arabidopsis thaliana GN=At2g05940 PE=2 SV=1	1	---	----	-0,23	0,49415	1400,64	57,10%
Q8W112	Beta-D-glucan exohydrolase-like protein OS=Arabidopsis thaliana GN=At5g20950 PE=2 SV=1	1	---	----	0,126	0,49582	1405,36	57,20%
Q93WL3	Double Clp-N motif protein OS=Arabidopsis thaliana GN=At4g25370 PE=2 SV=1	6	---	----	-0,077	0,49615	1406,31	57,20%
Q9CA83	NADP-dependent malic enzyme 4, chloroplastic OS=Arabidopsis thaliana GN=NADP-ME4 PE=1 SV=1	2	---	----	0,169	0,49815	1411,98	57,30%
Q949P2	Probable cytosolic oligopeptidase A OS=Arabidopsis thaliana GN=CYOP PE=1 SV=1	4	---	----	0,114	0,49821	1412,13	57,30%
Q8VZF3	Probable glutamyl endopeptidase, chloroplastic OS=Arabidopsis thaliana GN=GEP PE=2 SV=2	14	---	----	-0,053	0,49661	1407,60	57,30%
Q9SZ63	Nudix hydrolase 14, chloroplastic OS=Arabidopsis thaliana GN=NUDT14 PE=1 SV=2	2	---	----	-0,148	0,49721	1409,30	57,30%
Q9MAS9	At1g04800 OS=Arabidopsis thaliana GN=F13M7.21 PE=2 SV=1	2	---	----	-0,149	0,49702	1408,76	57,30%
Q9LN62	At1g19360 OS=Arabidopsis thaliana GN=At1g19360 PE=2 SV=1	2	---	----	-0,174	0,49815	1411,98	57,40%
O04376	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform OS=Arabidopsis thaliana GN=B'BET	2	---	----	-0,18	0,49815	1411,98	57,40%
F4IUX6	Regulator of nonsense transcripts UPF2 OS=Arabidopsis thaliana GN=UPF2 PE=2 SV=1	1	---	----	-0,328	0,50015	1417,65	57,40%
O22899	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase OS=Arabidopsis thaliana GN=At2g47250 PE=2 SV=1	2	---	----	0,139	0,50005	1417,36	57,50%
Q9C7S3	Chloroplast inner membrane localized protein OS=Arabidopsis thaliana GN=F13A11.2 PE=2 SV=1	2	---	----	-0,124	0,49981	1416,67	57,50%
Q94CB1	Probable pectinesterase/pectinesterase inhibitor 25 OS=Arabidopsis thaliana GN=PME25 PE=2 SV=1	1	---	----	-0,405	0,50005	1417,36	57,50%
Q9LDE3	F-box/kelch-repeat protein At1g23390 OS=Arabidopsis thaliana GN=At1g23390 PE=2 SV=1	1	---	----	0,221	0,50215	1423,32	57,60%
B9DHG0	AT1G22700 protein OS=Arabidopsis thaliana GN=At1g22700 PE=2 SV=1	4	---	----	0,092	0,50220	1423,47	57,60%
Q94K73	Phenylalanine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At3g58140 PE=2 SV=1	11	---	----	-0,056	0,50215	1423,32	57,60%
O80504;Q9M1C2	Chloroplast chaperonin 10 OS=Arabidopsis thaliana GN=CHL-CPN10 PE=2 SV=1	1	---	----	-0,118	0,50205	1423,03	57,60%

Q8L9M8	Putative uncharacterized protein At1g33810 OS=Arabidopsis thaliana GN=At1g33810 PE=1 SV=1	3	---	----	0,115	0,50405	1428,70	57,70%
Q9SD80	Mitochondrial import receptor subunit TOM5 homolog OS=Arabidopsis thaliana GN=TOM5 PE=1 SV=3	2	---	----	-0,147	0,50381	1428,04	57,70%
P29517	Tubulin beta-9 chain OS=Arabidopsis thaliana GN=TUBB9 PE=1 SV=1	2	---	----	0,118	0,50481	1430,87	57,80%
O04202	Eukaryotic translation initiation factor 3 subunit F OS=Arabidopsis thaliana GN=TIF3F1 PE=1 SV=1	7	---	----	0,081	0,50480	1430,84	57,80%
P25855	Glycine cleavage system H protein 1, mitochondrial OS=Arabidopsis thaliana GN=GDH1 PE=1 SV=1	1	---	----	0,06	0,50615	1434,65	57,90%
Q94C74;Q9SZJ5	Serine hydroxymethyltransferase 2, mitochondrial OS=Arabidopsis thaliana GN=SHM2 PE=2 SV=2	7	---	----	0,041	0,50605	1434,37	57,90%
A1L4X7	AT-hook motif nuclear-localized protein 14 OS=Arabidopsis thaliana GN=AHL14 PE=1 SV=1	1	---	----	0,21	0,50805	1440,04	58,00%
rev_Q8W4D6	reversed High chlorophyll fluorescence phenotype 173 protein OS=Arabidopsis thaliana GN=F17F16.7 PE=2 SV=1	1	---	----	0,203	0,50760	1438,78	58,00%
P0CJ46	Actin-1 OS=Arabidopsis thaliana GN=ACT1 PE=1 SV=1	3	---	----	0,14	0,51215	1451,66	58,00%
Q9LSP5	AT3g17020/K14A17_14 OS=Arabidopsis thaliana GN=At3g17020 PE=2 SV=1	2	---	----	0,083	0,50815	1440,32	58,00%
Q9SEI4	26S protease regulatory subunit 6B homolog OS=Arabidopsis thaliana GN=RPT3 PE=1 SV=1	6	---	----	0,079	0,50721	1437,67	58,00%
P48348;P48349	14-3-3-like protein GF14 kappa OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=2	4	---	----	-0,068	0,50815	1440,32	58,00%
Q9LQ48	Glutathione S-transferase U15 OS=Arabidopsis thaliana GN=GSTU15 PE=2 SV=1	1	---	----	-0,162	0,50821	1440,51	58,00%
Q9FJ41	GDSL esterase/lipase At5g45950 OS=Arabidopsis thaliana GN=At5g45950 PE=2 SV=1	1	---	----	0,218	0,51205	1451,37	58,10%
Q9LPU1	Putative uncharacterized protein At1g21065 OS=Arabidopsis thaliana GN=T22I11.11 PE=2 SV=1	1	---	----	0,207	0,51205	1451,37	58,10%
Q42592;Q42593	L-ascorbate peroxidase S, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=APXS PE=1 SV=2	2	---	----	0,166	0,50940	1443,88	58,10%
Q9ZNT0	Protein SUPPRESSOR OF K(+) TRANSPORT GROWTH DEFECT 1 OS=Arabidopsis thaliana GN=SKD1 PE=1 SV=1	2	---	----	0,158	0,51215	1451,66	58,10%
Q9T070	Cytochrome c oxidase subunit 6a, mitochondrial OS=Arabidopsis thaliana GN=COX6A PE=2 SV=1	1	---	----	0,153	0,51100	1448,41	58,10%
Q9SMV6	Protein EXPORTIN 1A OS=Arabidopsis thaliana GN=XPO1 PE=1 SV=1	4	---	----	0,131	0,51120	1448,98	58,10%
Q9LZR5	Histone deacetylase HDT3 OS=Arabidopsis thaliana GN=HDT3 PE=1 SV=2	3	---	----	0,126	0,51015	1445,99	58,10%
O82221	Probable small nuclear ribonucleoprotein G OS=Arabidopsis thaliana GN=At2g23930 PE=2 SV=1	2	---	----	0,11	0,50901	1442,77	58,10%
Q96292	Actin-2 OS=Arabidopsis thaliana GN=ACT2 PE=1 SV=1	9	---	----	0,044	0,51205	1451,37	58,10%
Q8GYJ9	Histidine triad nucleotide-binding 2 protein OS=Arabidopsis thaliana GN=HINT 2 PE=2 SV=1	3	---	----	-0,097	0,51421	1457,51	58,10%
Q9LTK1	At5g52190 OS=Arabidopsis thaliana GN=At5g52190 PE=2 SV=1	2	---	----	-0,112	0,51205	1451,37	58,10%
Q9LPD7	Putative uncharacterized protein At1g44920 OS=Arabidopsis thaliana GN=T12C22.21 PE=2 SV=1	2	---	----	-0,121	0,51005	1445,71	58,10%
O22809	Cinnamoyl-CoA:NADP oxidoreductase-like 1 OS=Arabidopsis thaliana GN=At2g33590 PE=2 SV=1	2	---	----	-0,141	0,51005	1445,71	58,10%
Q84VQ3	CBL-interacting serine/threonine-protein kinase 26 OS=Arabidopsis thaliana GN=CIPK26 PE=1 SV=2	2	---	----	-0,154	0,51080	1447,85	58,10%
Q9SZB9	Peroxidase 47 OS=Arabidopsis thaliana GN=PER47 PE=2 SV=2	1	---	----	-0,194	0,51015	1445,99	58,10%
Q8RVQ5	Exocyst complex component SEC10 OS=Arabidopsis thaliana GN=SEC10 PE=1 SV=2	2	---	----	0,192	0,51415	1457,33	58,20%
C0Z361;P21240;Q9LJE4	Chaperonin 60 subunit beta 3, chloroplastic OS=Arabidopsis thaliana GN=CPN60B3 PE=1 SV=1	12	---	----	-0,03	0,51420	1457,49	58,20%
Q8LPJ5	Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At5g14590 PE=2 SV=1	5	---	----	-0,074	0,51415	1457,33	58,20%
Q9FKA3	TLD-domain containing nucleolar protein OS=Arabidopsis thaliana GN=At5g39590 PE=4 SV=1	5	---	----	-0,091	0,51405	1457,04	58,20%
Q94K78	Putative uncharacterized protein At2g40765 OS=Arabidopsis thaliana GN=At2g40765 PE=2 SV=1	1	---	----	-0,153	0,51415	1457,33	58,20%
Q9LMG7	Probable inactive purple acid phosphatase 2 OS=Arabidopsis thaliana GN=PAP2 PE=2 SV=1	2	---	----	-0,168	0,51205	1451,37	58,20%
O23614	Carboxyl-terminal-processing peptidase 2, chloroplastic OS=Arabidopsis thaliana GN=CTPA2 PE=1 SV=1	1	---	----	-0,267	0,51201	1451,28	58,20%
O48802	Carboxylate clamp-tetratricopeptide repeat protein OS=Arabidopsis thaliana GN=At1g62390 PE=1 SV=1	2	---	----	0,185	0,51615	1462,99	58,30%
Q9M0Y8	Vesicle-fusing ATPase OS=Arabidopsis thaliana GN=NSF PE=2 SV=2	3	---	----	0,126	0,51621	1463,18	58,30%
Q38857	Xyloglucan endotransglucosylase/hydrolase protein 22 OS=Arabidopsis thaliana GN=XTH22 PE=1 SV=1	1	---	----	-0,196	0,51605	1462,71	58,30%
Q94K80	La-related protein 1C OS=Arabidopsis thaliana GN=LARP1C PE=1 SV=1	1	---	----	-0,309	0,51605	1462,71	58,30%
Q9XI05	Proteasome subunit beta type-3-A OS=Arabidopsis thaliana GN=PBC1 PE=1 SV=2	3	---	----	0,123	0,52015	1474,33	58,40%
Q9S7W1	Chlorophyll a-b binding protein CP29.3, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.3 PE=2 SV=1	7	---	----	0,091	0,52080	1476,19	58,40%
Q9LQ55;Q9SE83	Dynamin-2B OS=Arabidopsis thaliana GN=DRP2B PE=1 SV=2	6	---	----	0,09	0,52061	1475,65	58,40%
Q96299	14-3-3-like protein GF14 mu OS=Arabidopsis thaliana GN=GRF9 PE=1 SV=2	9	---	----	0,046	0,52015	1474,33	58,40%
Q9LVY0	Peptide chain release factor PrfB1, chloroplastic OS=Arabidopsis thaliana GN=PRFB1 PE=2 SV=1	5	---	----	-0,09	0,51805	1468,38	58,40%
Q84WK5	At1g61150 OS=Arabidopsis thaliana GN=At1g61150 PE=2 SV=1	2	---	----	-0,142	0,51815	1468,66	58,40%
Q9M0F9	ATP-dependent 6-phosphofructokinase 1 OS=Arabidopsis thaliana GN=PFK1 PE=1 SV=1	1	---	----	-0,212	0,51805	1468,38	58,40%
F4JHH5	Exocyst complex component SEC15B OS=Arabidopsis thaliana GN=SEC15B PE=1 SV=1	3	---	----	-0,227	0,52215	1480,00	58,40%
O65693	Probable ribosome-binding factor A, chloroplastic OS=Arabidopsis thaliana GN=At4g34730 PE=2 SV=2	1	---	----	0,447	0,52005	1474,05	58,50%
Q9LMR3	Arogenate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=TYRAAT2 PE=1 SV=1	1	---	----	0,279	0,52205	1479,72	58,50%
B5X565	At3g12080 OS=Arabidopsis thaliana GN=emb2738 PE=2 SV=1	1	---	----	0,218	0,52015	1474,33	58,50%
Q9ZUY3	Arogenate dehydratase 3, chloroplastic OS=Arabidopsis thaliana GN=ADT3 PE=1 SV=1	2	---	----	0,205	0,52015	1474,33	58,50%
Q39222;Q96283;Q9FIF9;C	Ras-related protein RABA1b OS=Arabidopsis thaliana GN=RABA1B PE=2 SV=1	1	---	----	0,163	0,52015	1474,33	58,50%
Q8H1S6	U2 small nuclear ribonucleoprotein B'' 2 OS=Arabidopsis thaliana GN=At1g06960 PE=1 SV=1	1	---	----	0,14	0,52205	1479,72	58,50%
P21216	Soluble inorganic pyrophosphatase 2 OS=Arabidopsis thaliana GN=PPA2 PE=2 SV=2	2	---	----	0,107	0,51940	1472,22	58,50%
O65719;P22953;Q9LHA8;	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	2	---	----	0,076	0,52015	1474,33	58,50%

O22795	50S ribosomal protein L28, chloroplastic OS=Arabidopsis thaliana GN=RPL28 PE=2 SV=2	3	---	----	-0,084	0,52215	1480,00	58,50%
Q9SHS7	Serine/threonine-protein phosphatase BSL3 OS=Arabidopsis thaliana GN=BSL3 PE=1 SV=2	3	---	----	-0,108	0,51805	1468,38	58,50%
Q8GXX7	Zinc finger CCCH domain-containing protein 33 OS=Arabidopsis thaliana GN=ZFN1 PE=1 SV=1	2	---	----	-0,151	0,52280	1481,86	58,50%
Q9ST43	Pleckstrin homology domain-containing protein 1 OS=Arabidopsis thaliana GN=PH1 PE=2 SV=2	1	---	----	-0,152	0,52215	1480,00	58,50%
P32069	Anthranilate synthase alpha subunit 2, chloroplastic OS=Arabidopsis thaliana GN=ASA2 PE=2 SV=1	2	---	----	-0,157	0,52205	1479,72	58,50%
Q9C9C9;Q9C9D0	Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1	1	---	----	0,228	0,52405	1485,38	58,60%
Q8L475	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At1g74640 PE=2 SV=1	2	---	----	0,2	0,52415	1485,67	58,60%
Q9SJ67	At2g35830/F11F19.26 OS=Arabidopsis thaliana GN=At2g35830 PE=2 SV=2	1	---	----	0,188	0,52405	1485,38	58,60%
Q38867	Peptidyl-prolyl cis-trans isomerase CYP19-3 OS=Arabidopsis thaliana GN=CYP19-3 PE=2 SV=2	2	---	----	0,095	0,52460	1486,96	58,60%
Q9LI74	Protein CHUP1, chloroplastic OS=Arabidopsis thaliana GN=CHUP1 PE=1 SV=1	3	---	----	-0,122	0,52205	1479,72	58,60%
P31168;P42763	Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2	1	---	----	-0,126	0,52615	1491,34	58,60%
Q9SU13	Fasciclin-like arabinogalactan protein 2 OS=Arabidopsis thaliana GN=FLA2 PE=1 SV=1	1	---	----	-0,138	0,52501	1488,13	58,60%
F4K1G7	P-loop containing nucleoside triphosphate hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g35970 PE=	2	---	----	-0,145	0,52005	1474,05	58,60%
F4K5T6	Cytidine/deoxycytidylate deaminase family protein OS=Arabidopsis thaliana GN=At5g28050 PE=4 SV=1	2	---	----	0,119	0,52615	1491,34	58,70%
P57751	UTP--glucose-1-phosphate uridylyltransferase 1 OS=Arabidopsis thaliana GN=At5g17310 PE=2 SV=1	8	---	----	0,066	0,52741	1494,93	58,70%
Q9STG9	Amidophosphoribosyltransferase 2, chloroplastic OS=Arabidopsis thaliana GN=ASE2 PE=1 SV=1	8	---	----	0,063	0,52721	1494,36	58,70%
Q9LS03	Allene oxide cyclase 1, chloroplastic OS=Arabidopsis thaliana GN=AOC1 PE=1 SV=1	3	---	----	-0,121	0,52561	1489,83	58,70%
Q94AI7	Protein TOPLESS OS=Arabidopsis thaliana GN=TPL PE=1 SV=1	1	APSPVNNPLLGGIPK	Phospho S3	-0,641	0,52615	1491,34	58,70%
Q9ZQ78	Putative uncharacterized protein At2g03420 OS=Arabidopsis thaliana GN=At2g03420 PE=2 SV=2	2	---	----	-0,148	0,52815	1497,00	58,80%
rev_F4ICA1	reversed BED zinc finger and hAT dimerization domain-containing protein OS=Arabidopsis thaliana GN=At1g18560 PE=	1	---	----	-0,216	0,52815	1497,00	58,80%
Q9LKA3	Malate dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=At3g15020 PE=2 SV=1	1	---	----	-0,246	0,52815	1497,00	58,80%
Q76E23	Eukaryotic translation initiation factor 4G OS=Arabidopsis thaliana GN=EIF4G PE=1 SV=2	1	---	----	0,207	0,53005	1502,39	58,90%
P54873	Hydroxymethylglutaryl-CoA synthase OS=Arabidopsis thaliana GN=HMGS PE=1 SV=2	1	---	----	0,202	0,53100	1505,10	58,90%
Q9S795	Betaine aldehyde dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=ALDH10A8 PE=2 SV=1	9	---	----	0,078	0,53061	1504,00	58,90%
O80448;Q8L940	Pyridoxal 5'-phosphate synthase subunit PDX1.1 OS=Arabidopsis thaliana GN=PDX11 PE=1 SV=1	3	---	----	0,071	0,53015	1502,67	58,90%
Q9M0F5	Acid phosphatase-like protein OS=Arabidopsis thaliana GN=At4g29260 PE=2 SV=1	3	---	----	-0,107	0,53215	1508,34	58,90%
Q9XI73	Photosynthetic NDH subunit of lumenal location 2, chloroplastic OS=Arabidopsis thaliana GN=PNSL2 PE=1 SV=1	4	---	----	-0,118	0,52981	1501,73	58,90%
O23512	Probable pheophorbidase OS=Arabidopsis thaliana GN=PPD PE=2 SV=1	1	---	----	-0,257	0,53005	1502,39	58,90%
Q9LQF2	Alkaline/neutral invertase CINV1 OS=Arabidopsis thaliana GN=CINV1 PE=1 SV=1	1	---	----	-0,647	0,53015	1502,67	58,90%
Q9MBA2	Putative septum site-determining protein minD homolog, chloroplastic OS=Arabidopsis thaliana GN=MIND1 PE=1 SV=1	1	---	----	0,22	0,53415	1514,01	59,00%
P56756	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic OS=Arabidopsis thaliana GN=ndhK PE=3 SV=1	3	---	----	0,121	0,53205	1508,06	59,00%
P42770	Glutathione reductase, chloroplastic OS=Arabidopsis thaliana GN=EMB2360 PE=2 SV=1	12	---	----	-0,041	0,53205	1508,06	59,00%
A4GNA8	Phosphatidylserine decarboxylase proenzyme 3 OS=Arabidopsis thaliana GN=PSD3 PE=1 SV=1	1	---	----	-0,205	0,53415	1514,01	59,00%
Q9LHS5	Cell division related protein-like OS=Arabidopsis thaliana GN=At5g06110 PE=4 SV=1	1	---	----	-0,487	0,53205	1508,06	59,00%
Q9T0I8	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1 OS=Arabidopsis thaliana GN=MTN1 PE=1 SV=1	1	---	----	0,199	0,53405	1513,73	59,10%
Q94BQ2;Q9MAK9;Q9SEI2	26S protease regulatory subunit 8 homolog B OS=Arabidopsis thaliana GN=RPT6B PE=1 SV=1	1	---	----	0,152	0,53615	1519,68	59,10%
P27140-3	Isoform 3 of Beta carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=BCA1	4	---	----	0,093	0,53561	1518,17	59,10%
Q9LPW0	Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic OS=Arabidopsis thaliana GN=GAPA2 PE=2 SV=1	3	---	----	-0,047	0,53615	1519,68	59,10%
Q9SKI0	At2g10940/F15K19.1 OS=Arabidopsis thaliana GN=At2g10940 PE=2 SV=1	4	---	----	-0,056	0,53605	1519,39	59,10%
Q9SHG8	At1g17100 OS=Arabidopsis thaliana GN=F20D23.21 PE=2 SV=1	5	---	----	-0,071	0,53481	1515,90	59,10%
Q9LK72	Lectin-like protein At3g16530 OS=Arabidopsis thaliana GN=At3g16530 PE=1 SV=1	5	---	----	-0,073	0,53401	1513,63	59,10%
Q8VY91	30S ribosomal protein S6 alpha, chloroplastic OS=Arabidopsis thaliana GN=RPS6 PE=2 SV=1	3	---	----	-0,093	0,53615	1519,68	59,10%
Q8LAA6	Probable aquaporin PIP1-5 OS=Arabidopsis thaliana GN=PIP1-5 PE=2 SV=2	2	---	----	-0,103	0,53501	1516,47	59,10%
P46637;Q9ZPF5	Arginase 1, mitochondrial OS=Arabidopsis thaliana GN=ARGAH1 PE=2 SV=1	2	---	----	-0,15	0,53415	1514,01	59,10%
F4J4K6	Tubulin binding cofactor C domain-containing protein OS=Arabidopsis thaliana GN=At3g57890 PE=4 SV=1	1	---	----	-0,194	0,53415	1514,01	59,10%
Q9M0V3	DNA damage-binding protein 1a OS=Arabidopsis thaliana GN=DDB1A PE=1 SV=1	3	---	----	0,109	0,53815	1525,35	59,20%
Q9LDZ0	Heat shock 70 kDa protein 10, mitochondrial OS=Arabidopsis thaliana GN=HSP70-10 PE=2 SV=1	13	---	----	0,05	0,53805	1525,06	59,20%
P28493	Pathogenesis-related protein 5 OS=Arabidopsis thaliana GN=At1g75040 PE=1 SV=1	1	---	----	-0,193	0,53815	1525,35	59,20%
Q8RWM6	Transmembrane emp24 domain-containing protein p24delta5 OS=Arabidopsis thaliana GN=At1g21900 PE=1 SV=1	1	---	----	0,217	0,54241	1537,44	59,30%
P93303	ATP synthase protein YMF19 OS=Arabidopsis thaliana GN=YMF19 PE=1 SV=1	2	---	----	0,09	0,54215	1536,68	59,30%
Q9SJU9	Epimerase family protein SDR39U1 homolog, chloroplastic OS=Arabidopsis thaliana GN=GC1 PE=2 SV=2	4	---	----	0,087	0,54180	1535,71	59,30%
Q9FUS8	Glutathione S-transferase U17 OS=Arabidopsis thaliana GN=GSTU17 PE=2 SV=1	5	---	----	-0,055	0,54015	1531,01	59,30%
Q02166	Anthranilate phosphoribosyltransferase, chloroplastic OS=Arabidopsis thaliana GN=PAT1 PE=2 SV=1	6	---	----	-0,075	0,54060	1532,31	59,30%
Q04613	ATP synthase protein MI25 OS=Arabidopsis thaliana GN=AtMg00640 PE=1 SV=2	2	---	----	-0,079	0,54020	1531,18	59,30%
Q05212	DNA-damage-repair/toleration protein DRT102 OS=Arabidopsis thaliana GN=DRT102 PE=1 SV=2	4	---	----	-0,084	0,53805	1525,06	59,30%

Q9ZTZ7	K(+) efflux antiporter 1, chloroplastic OS=Arabidopsis thaliana GN=KEA1 PE=1 SV=2	3	---	----	-0,099	0,54081	1532,91	59,30%
Q9LZQ4	Carbohydrate-binding-like fold-containing protein OS=Arabidopsis thaliana GN=T12C14_60 PE=4 SV=1	2	---	----	-0,127	0,54015	1531,01	59,30%
Q0WWT7	Rhodanese-like domain-containing protein 11, chloroplastic OS=Arabidopsis thaliana GN=STR11 PE=2 SV=1	2	---	----	-0,136	0,54015	1531,01	59,30%
Q8L604	Putative uncharacterized protein At1g65230 OS=Arabidopsis thaliana GN=At1g65230 PE=2 SV=1	2	---	----	-0,172	0,54015	1531,01	59,30%
Q42524	4-coumarate--CoA ligase 1 OS=Arabidopsis thaliana GN=4CL1 PE=1 SV=1	1	---	----	-0,232	0,54100	1533,45	59,30%
Q39243	Thioredoxin reductase 1 OS=Arabidopsis thaliana GN=NTR1 PE=1 SV=3	1	---	----	0,261	0,54405	1542,07	59,40%
Q8L5Y6	Cullin-associated NEDD8-dissociated protein 1 OS=Arabidopsis thaliana GN=CAND1 PE=1 SV=1	1	---	----	0,193	0,54415	1542,35	59,40%
O04316	Nitrile-specifier protein 4 OS=Arabidopsis thaliana GN=NSP4 PE=2 SV=1	1	---	----	0,126	0,54215	1536,68	59,40%
O22100	ATMRK1 OS=Arabidopsis thaliana GN=F16M2_110 PE=2 SV=1	5	---	----	0,112	0,54415	1542,35	59,40%
Q42064	60S ribosomal protein L8-3 OS=Arabidopsis thaliana GN=RPL8C PE=1 SV=2	2	---	----	0,087	0,54440	1543,08	59,40%
Q94C74	Serine hydroxymethyltransferase 2, mitochondrial OS=Arabidopsis thaliana GN=SHM2 PE=2 SV=2	4	---	----	0,081	0,54005	1530,73	59,40%
Q9LX13;Q9SIE3	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-like protein OS=Arabidopsis thaliana GN=T31P16_150 PE=2 SV	1	---	----	-0,124	0,54405	1542,07	59,40%
Q9FMH8	Cysteine protease component of protease-inhibitor complex OS=Arabidopsis thaliana GN=At5g43060 PE=1 SV=1	2	---	----	-0,134	0,54000	1530,61	59,40%
Q9FX60	Histone H3-like 1 OS=Arabidopsis thaliana GN=At1g13370 PE=2 SV=3	1	---	----	-0,165	0,54480	1544,22	59,40%
F4IE99	Ferredoxin C2 OS=Arabidopsis thaliana GN=At1g32550 PE=4 SV=1	1	---	----	-0,181	0,54415	1542,35	59,40%
O65023	Probable envelope ADP,ATP carrier protein, chloroplastic OS=Arabidopsis thaliana GN=EAAC PE=2 SV=2	1	---	----	-0,263	0,54005	1530,73	59,40%
O23523;Q9LVT8	AT4g16830/dl4440w OS=Arabidopsis thaliana GN=dl4440w PE=2 SV=1	1	---	----	0,128	0,54405	1542,07	59,50%
Q9C5U8	Histidinol dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=HISN8 PE=2 SV=1	7	---	----	0,061	0,54405	1542,07	59,50%
Q1WIQ6	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase OS=Arabidopsis thaliana GN=ALDH11A3 PE=1 SV=2	19	---	----	0,034	0,54615	1548,02	59,50%
O82234;Q94B52	Translation initiation factor IF-3 OS=Arabidopsis thaliana GN=At2g24060 PE=2 SV=1	1	---	----	-0,187	0,54605	1547,74	59,50%
Q9ZPY1	Pyridoxine/pyridoxamine 5'-phosphate oxidase 2 OS=Arabidopsis thaliana GN=PPOX2 PE=1 SV=2	1	---	----	-0,227	0,54815	1553,69	59,60%
Q9LHE5	Mitochondrial import receptor subunit TOM40-1 OS=Arabidopsis thaliana GN=TOM40-1 PE=1 SV=3	3	---	----	0,11	0,54805	1553,40	59,70%
O23247	Arginyl-tRNA synthetase OS=Arabidopsis thaliana GN=T25K17.110 PE=3 SV=1	10	---	----	0,056	0,54805	1553,40	59,70%
Q9M336	Uracil phosphoribosyltransferase, chloroplastic OS=Arabidopsis thaliana GN=UPP PE=1 SV=1	9	---	----	-0,052	0,55014	1559,36	59,70%
Q9FKS5	Cytochrome c1 2, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC12 PE=1 SV=1	2	---	----	-0,131	0,54861	1555,02	59,70%
Q9LZ17	40S ribosomal protein S17-4 OS=Arabidopsis thaliana GN=RPS17D PE=2 SV=3	1	---	----	0,248	0,55214	1565,02	59,80%
Q9SID0	Probable fructokinase-1 OS=Arabidopsis thaliana GN=At2g31390 PE=2 SV=1	6	---	----	0,082	0,55214	1565,02	59,80%
Q07356	15-cis-phytoene desaturase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=PDS PE=1 SV=1	7	---	----	0,071	0,54961	1557,85	59,80%
Q9SQI8	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic OS=Arab	9	---	----	0,06	0,55014	1559,36	59,80%
Q9LXS6	Citrate synthase 2, peroxisomal OS=Arabidopsis thaliana GN=CSY2 PE=2 SV=1	1	---	----	-0,177	0,55220	1565,19	59,80%
O80944;Q0PGJ6	Aldo-keto reductase family 4 member C8 OS=Arabidopsis thaliana GN=AKR4C8 PE=1 SV=2	1	---	----	-0,194	0,55004	1559,07	59,80%
Q8VZ18	Putative uncharacterized protein At3g44150 OS=Arabidopsis thaliana GN=At3g44150 PE=2 SV=1	1	---	----	0,252	0,55204	1564,74	59,90%
Q94AF7	At2g07350/T13E11.12 OS=Arabidopsis thaliana GN=PFD1 PE=2 SV=1	1	---	----	0,219	0,55404	1570,41	59,90%
Q9FHX0	Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=At5g42150 PE=2 SV=1	1	---	----	0,217	0,55361	1569,19	59,90%
Q43315	Farnesyl pyrophosphate synthase 2 OS=Arabidopsis thaliana GN=FPS2 PE=2 SV=1	1	---	----	0,193	0,55301	1567,49	59,90%
Q9ZUS6	At2g37400 OS=Arabidopsis thaliana GN=At2g37400 PE=2 SV=1	2	---	----	0,161	0,55160	1563,49	59,90%
Q9M084	AT4G31180 protein OS=Arabidopsis thaliana GN=At4g31180 PE=2 SV=1	8	---	----	0,058	0,55414	1570,69	59,90%
Q9SJZ7	Molecular chaperone DnaJ OS=Arabidopsis thaliana GN=At2g22360 PE=3 SV=2	4	---	----	-0,095	0,55204	1564,74	59,90%
Q9M2T6	Beta-1, 3-glucanase-like protein OS=Arabidopsis thaliana GN=T22E16.90 PE=2 SV=1	1	---	----	-0,195	0,55404	1570,41	59,90%
Q06850	Calcium-dependent protein kinase 1 OS=Arabidopsis thaliana GN=CPK1 PE=1 SV=1	1	---	----	-0,583	0,55204	1564,74	59,90%
P29388	NADH-ubiquinone oxidoreductase chain 5 OS=Arabidopsis thaliana GN=ND5 PE=2 SV=3	1	---	----	-0,121	0,55480	1572,56	60,00%
Q9FXA1	AT1G49750 protein OS=Arabidopsis thaliana GN=F14J22.4 PE=2 SV=1	5	---	----	0,071	0,55604	1576,08	60,10%
rev_F4I9Q5	reversed RNA helicase family protein OS=Arabidopsis thaliana GN=At1g58060 PE=4 SV=1	1	---	----	0,502	0,55880	1583,90	60,20%
P24101	Peroxidase 33 OS=Arabidopsis thaliana GN=PER33 PE=1 SV=1	1	---	----	0,225	0,55900	1584,47	60,20%
O49636	Mitochondrial pyruvate carrier 4 OS=Arabidopsis thaliana GN=MPC4 PE=3 SV=1	2	---	----	0,139	0,56014	1587,70	60,20%
Q8VZB9	60S ribosomal protein L10a-1 OS=Arabidopsis thaliana GN=RPL10AA PE=1 SV=1	2	---	----	0,092	0,55814	1582,03	60,20%
Q9SX68	50S ribosomal protein L18, chloroplastic OS=Arabidopsis thaliana GN=RPL18 PE=2 SV=1	4	---	----	0,074	0,56004	1587,41	60,20%
F4J4T3	Tryptophanyl-tRNA synthetase-like protein OS=Arabidopsis thaliana GN=At3g04600 PE=3 SV=1	6	---	----	0,071	0,56014	1587,70	60,20%
Q9SZX3	Argininosuccinate synthase, chloroplastic OS=Arabidopsis thaliana GN=At4g24830 PE=2 SV=3	11	---	----	-0,044	0,56014	1587,70	60,20%
Q43727	Glucose-6-phosphate 1-dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=APG1 PE=2 SV=2	6	---	----	-0,068	0,56004	1587,41	60,20%
Q56WN1;Q8LCE1	Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2	4	---	----	-0,087	0,55814	1582,03	60,20%
Q93Y31	ADP-ribosylation factor-like A1D OS=Arabidopsis thaliana GN=K9I9.13 PE=2 SV=1	2	---	----	-0,11	0,55814	1582,03	60,20%
Q8VWF5	Protein MEI2-like 5 OS=Arabidopsis thaliana GN=ML5 PE=1 SV=1	1	---	----	-0,279	0,55814	1582,03	60,20%
F4JUG0	Glycine-rich protein OS=Arabidopsis thaliana GN=At4g38710 PE=1 SV=1	1	---	----	0,467	0,56300	1595,80	60,30%
rev_Q9LNN0	reversed F8L10.9 protein OS=Arabidopsis thaliana GN=F8L10.9 PE=4 SV=1	1	---	----	0,209	0,56204	1593,08	60,30%

Q9SIT1	Leucine-rich repeat receptor-like protein kinase OS=Arabidopsis thaliana GN=LRR-RLK PE=2 SV=1	1	---	----	0,208	0,55804	1581,75	60,30%
Q8LAD0	Probable pyridoxal 5'-phosphate synthase subunit PDX2 OS=Arabidopsis thaliana GN=PDX2 PE=1 SV=1	2	---	----	0,146	0,56204	1593,08	60,30%
F4J8C0	HRF1 protein OS=Arabidopsis thaliana GN=HRF1 PE=2 SV=1	1	---	----	0,134	0,56004	1587,41	60,30%
Q9SGA6	40S ribosomal protein S19-1 OS=Arabidopsis thaliana GN=RPS19A PE=2 SV=1	2	---	----	0,1	0,56420	1599,21	60,30%
Q9FIB6	26S proteasome non-ATPase regulatory subunit 12 homolog A OS=Arabidopsis thaliana GN=RPN5A PE=1 SV=1	8	---	----	0,056	0,56260	1594,67	60,30%
Q9SUI5	Photosystem I reaction center subunit psaK, chloroplastic OS=Arabidopsis thaliana GN=PSAK PE=2 SV=2	2	---	----	-0,07	0,56004	1587,41	60,30%
Q9FK88	Alkaline/neutral invertase E, chloroplastic OS=Arabidopsis thaliana GN=INVE PE=1 SV=1	2	---	----	-0,128	0,56214	1593,37	60,30%
Q9SEL5	Vesicle transport v-SNARE 12 OS=Arabidopsis thaliana GN=VTI12 PE=1 SV=3	2	---	----	-0,132	0,56414	1599,03	60,30%
Q8LG92	LS1-like protein OS=Arabidopsis thaliana GN=At3g51660 PE=2 SV=1	1	---	----	-0,16	0,56004	1587,41	60,30%
Q9SUL1	AT4g16190/dl4135w OS=Arabidopsis thaliana GN=dl4135w PE=2 SV=1	2	---	----	-0,164	0,56414	1599,03	60,30%
Q9SD73	At3g47000 OS=Arabidopsis thaliana GN=F13I12.50 PE=2 SV=1	1	---	----	-0,189	0,56214	1593,37	60,30%
Q9C9P3	ADP-glucose pyrophosphorylase family protein OS=Arabidopsis thaliana GN=F9E10.24 PE=1 SV=1	1	RVSSFEALQPATR	Phospho S3	-0,366	0,56320	1596,37	60,30%
rev_Q9SI52	reversed Phosphatidylinositol 4-kinase gamma 7 OS=Arabidopsis thaliana GN=PI4KG7 PE=1 SV=2	1	---	----	0,234	0,56614	1604,70	60,40%
O64816	Casein kinase II subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=At2g23070 PE=2 SV=1	2	---	----	0,165	0,56400	1598,64	60,40%
P93654	Syntaxin-22 OS=Arabidopsis thaliana GN=SYP22 PE=1 SV=1	2	---	----	0,122	0,56414	1599,03	60,40%
F4K6X0	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g20935 PE=4 SV=1	1	---	----	-0,174	0,56414	1599,03	60,40%
Q8RWI4	Putative uncharacterized protein At3g01060 OS=Arabidopsis thaliana GN=At3g01060 PE=1 SV=1	2	---	----	-0,284	0,56614	1604,70	60,40%
Q9LKR3	Mediator of RNA polymerase II transcription subunit 37a OS=Arabidopsis thaliana GN=MED37A PE=1 SV=1	1	---	----	0,103	0,56814	1610,37	60,50%
Q9SUN5	Small nuclear ribonucleoprotein-associated protein OS=Arabidopsis thaliana GN=F9F13.90 PE=2 SV=1	2	---	----	-0,117	0,56581	1603,77	60,50%
Q9C5U0	Histidine kinase 4 OS=Arabidopsis thaliana GN=AHK4 PE=1 SV=1	1	---	----	-0,438	0,56604	1604,42	60,50%
rev_Q8VYM6	reversed Putative uncharacterized protein At4g26600 OS=Arabidopsis thaliana GN=At4g26600 PE=2 SV=1	1	---	----	0,173	0,56804	1610,09	60,60%
Q93ZV8	Putative uncharacterized protein At1g10510 OS=Arabidopsis thaliana GN=emb2004 PE=2 SV=1	2	---	----	0,161	0,56814	1610,37	60,60%
Q93XN8	Probable sucrose-phosphatase 3b OS=Arabidopsis thaliana GN=SPP3B PE=2 SV=1	2	---	----	0,137	0,57121	1619,08	60,60%
Q94JX5	LIM domain-containing protein WLIM1 OS=Arabidopsis thaliana GN=WLIM1 PE=1 SV=1	1	---	----	0,119	0,57621	1633,25	60,60%
Q9CAT7;Q9SMW7	Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=T18K17.10 PE=2 SV=1	1	---	----	0,105	0,57040	1616,78	60,60%
O65581;Q9LF98;Q9SJQ9	Fructose-bisphosphate aldolase OS=Arabidopsis thaliana GN=M3E9.40 PE=2 SV=1	3	---	----	0,068	0,56761	1608,87	60,60%
Q9SHI1	Translation initiation factor IF-2, chloroplastic OS=Arabidopsis thaliana GN=At1g17220 PE=2 SV=2	9	---	----	0,06	0,57014	1616,04	60,60%
Q9LXV0	UDP-glycosyltransferase 92A1 OS=Arabidopsis thaliana GN=UGT92A1 PE=2 SV=1	3	---	----	-0,11	0,57060	1617,35	60,60%
Q94AG6	S-adenosylmethionine carrier 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=SAMC1 PE=1 SV=1	1	---	----	-0,12	0,57214	1621,71	60,60%
rev_Q9M667	reversed Disease resistance protein RPP13 OS=Arabidopsis thaliana GN=RPP13 PE=2 SV=2	1	---	----	-0,175	0,57080	1617,91	60,60%
Q8LGI2	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410 OS=Arabidopsis thaliana GN=At5g	1	---	----	-0,204	0,56860	1611,68	60,60%
O49299;Q9SGC1	Probable phosphoglucomutase, cytoplasmic 1 OS=Arabidopsis thaliana GN=At1g23190 PE=2 SV=2	1	AFILTASHNPGGPTED	Phospho S10	-0,269	0,57014	1616,04	60,60%
Q9SXC8	Ubiquitin-fold modifier-conjugating enzyme 1 OS=Arabidopsis thaliana GN=At1g27530 PE=2 SV=1	1	---	----	0,202	0,57161	1620,21	60,70%
O82204;Q9M0E2	60S ribosomal protein L28-1 OS=Arabidopsis thaliana GN=RPL28A PE=2 SV=1	1	---	----	0,146	0,56961	1614,54	60,70%
Q8LF21	Dynamin-related protein 1C OS=Arabidopsis thaliana GN=DRP1C PE=1 SV=2	3	---	----	0,145	0,57014	1616,04	60,70%
P53799	Squalene synthase OS=Arabidopsis thaliana GN=SQS1 PE=1 SV=1	1	---	----	0,123	0,57414	1627,38	60,70%
P49689	40S ribosomal protein S30 OS=Arabidopsis thaliana GN=RPS30A PE=3 SV=3	1	---	----	0,102	0,57621	1633,25	60,70%
Q949X7;Q94A94	Diaminopimelate decarboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=LYSA1 PE=2 SV=1	3	---	----	0,087	0,57004	1615,76	60,70%
Q9FYR6	At5g52520 OS=Arabidopsis thaliana GN=OVA6 PE=2 SV=1	8	---	----	0,061	0,57204	1621,42	60,70%
Q9C9P3	ADP-glucose pyrophosphorylase family protein OS=Arabidopsis thaliana GN=F9E10.24 PE=1 SV=1	9	---	----	-0,048	0,57614	1633,04	60,70%
Q9SXJ6	ATP-dependent Clp protease proteolytic subunit 3, chloroplastic OS=Arabidopsis thaliana GN=CLPP3 PE=1 SV=1	3	---	----	-0,071	0,57614	1633,04	60,70%
P0CAN7;Q39258	V-type proton ATPase subunit E3 OS=Arabidopsis thaliana GN=VHA-E3 PE=2 SV=1	1	---	----	-0,086	0,57414	1627,38	60,70%
Q8VY84	Probable UMP-CMP kinase 1 OS=Arabidopsis thaliana GN=UMK1 PE=2 SV=1	1	---	----	-0,179	0,57614	1633,04	60,70%
P0CJ48	Chlorophyll a-b binding protein 2, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.1 PE=1 SV=1	1	---	----	-0,201	0,57204	1621,42	60,70%
Q8LFD1	Putative lipid phosphate phosphatase 3, chloroplastic OS=Arabidopsis thaliana GN=LPP3 PE=2 SV=1	1	---	----	0,339	0,57604	1632,76	60,80%
Q9FI78	Shikimate O-hydroxycinnamoyltransferase OS=Arabidopsis thaliana GN=HST PE=2 SV=1	1	---	----	0,174	0,57404	1627,09	60,80%
Q93WI0	Rhodanese-like/PpiC domain-containing protein 12 OS=Arabidopsis thaliana GN=At5g19370 PE=2 SV=1	2	---	----	0,142	0,57920	1641,72	60,80%
O82240	Adenine nucleotide alpha hydrolases-like protein OS=Arabidopsis thaliana GN=At2g47710 PE=2 SV=1	1	---	----	0,128	0,57404	1627,09	60,80%
Q41188	Cold shock protein 2 OS=Arabidopsis thaliana GN=CSP2 PE=1 SV=1	1	---	----	0,107	0,57614	1633,04	60,80%
Q39227	24-methylenesterol C-methyltransferase 2 OS=Arabidopsis thaliana GN=SMT2 PE=1 SV=2	3	---	----	0,106	0,57881	1640,62	60,80%
O80476	Methylesterase 2 OS=Arabidopsis thaliana GN=MES2 PE=1 SV=1	4	---	----	0,087	0,57614	1633,04	60,80%
Q9LHT0	Tropinone reductase homolog At5g06060 OS=Arabidopsis thaliana GN=At5g06060 PE=2 SV=1	6	---	----	-0,057	0,57804	1638,43	60,80%
Q9FLP6	Small ubiquitin-related modifier 2 OS=Arabidopsis thaliana GN=SUMO2 PE=1 SV=1	3	---	----	-0,076	0,57414	1627,38	60,80%
Q9FM67	Protein TIC 20-v, chloroplastic OS=Arabidopsis thaliana GN=TIC20-V PE=2 SV=1	2	---	----	-0,109	0,57404	1627,09	60,80%
Q42134	Proteasome subunit alpha type-5-B OS=Arabidopsis thaliana GN=PAE2 PE=1 SV=2	2	---	----	-0,109	0,57814	1638,71	60,80%

O22244	Pectin methylesterase inhibitor 6 OS=Arabidopsis thaliana GN=At2g47670 PE=4 SV=1	1	---	----	-0,142	0,57604	1632,76	60,80%
Q93XY5	Tetraspanin-18 OS=Arabidopsis thaliana GN=TOM2AH2 PE=2 SV=1	2	---	----	-0,154	0,57614	1633,04	60,80%
O22826	At2g43770 OS=Arabidopsis thaliana GN=At2g43770 PE=2 SV=1	1	---	----	-0,176	0,57814	1638,71	60,80%
Q8W586	AT4g21800/F17L22_260 OS=Arabidopsis thaliana GN=QQT2 PE=2 SV=1	1	---	----	-0,24	0,57461	1628,71	60,80%
P28185;Q39222;Q96283;	Ras-related protein RABA1a OS=Arabidopsis thaliana GN=RABA1A PE=1 SV=1	1	---	----	0,166	0,58014	1644,38	60,90%
O80763	Probable nucleoredoxin 1 OS=Arabidopsis thaliana GN=At1g60420 PE=1 SV=1	2	---	----	0,095	0,58014	1644,38	60,90%
Q96291;Q9C5R8	2-Cys peroxiredoxin BAS1, chloroplastic OS=Arabidopsis thaliana GN=BAS1 PE=1 SV=2	6	---	----	0,042	0,57980	1643,42	60,90%
Q9FGC7	Zeaxanthin epoxidase, chloroplastic OS=Arabidopsis thaliana GN=ZEP PE=1 SV=1	13	---	----	-0,04	0,57581	1632,11	60,90%
Q9C9Z6	AT3g08600/F17O14_7 OS=Arabidopsis thaliana GN=F17O14.7 PE=2 SV=1	2	---	----	-0,124	0,57604	1632,76	60,90%
rev_Q6A333	reversed Protein ALWAYS EARLY 2 OS=Arabidopsis thaliana GN=ALY2 PE=1 SV=1	1	---	----	-0,165	0,58014	1644,38	60,90%
O81826	Probable histone H2A.3 OS=Arabidopsis thaliana GN=At4g27230 PE=1 SV=1	1	---	----	-0,17	0,58214	1650,05	61,00%
Q9MAK9	26S protease regulatory subunit S10B homolog B OS=Arabidopsis thaliana GN=RPT4B PE=1 SV=1	4	---	----	0,082	0,58414	1655,72	61,10%
Q9FKS5;Q9LK29	Cytochrome c1 2, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC12 PE=1 SV=1	3	---	----	0,076	0,58260	1651,36	61,10%
Q9ZPE7	Protein EXORDIUM OS=Arabidopsis thaliana GN=EXO PE=2 SV=1	1	---	----	-0,199	0,58320	1653,06	61,10%
Q9FJH0	Ras-related protein RABA1f OS=Arabidopsis thaliana GN=RABA1F PE=2 SV=1	3	---	----	0,106	0,58414	1655,72	61,20%
Q84K25	Conserved oligomeric Golgi complex component-related protein OS=Arabidopsis thaliana GN=At5g11980 PE=2 SV=1	1	---	----	-0,204	0,58414	1655,72	61,20%
O64732	UDP-glycosyltransferase 87A1 OS=Arabidopsis thaliana GN=UGT87A1 PE=2 SV=1	1	---	----	-0,211	0,58814	1667,05	61,20%
Q9FY54	Probable sucrose-phosphate synthase 2 OS=Arabidopsis thaliana GN=SPS2 PE=1 SV=1	1	---	----	0,199	0,58804	1666,77	61,30%
Q84L30	Ubiquitin receptor RAD23d OS=Arabidopsis thaliana GN=RAD23D PE=1 SV=2	2	---	----	0,176	0,58814	1667,05	61,30%
O49668	Protein PAM68, chloroplastic OS=Arabidopsis thaliana GN=PAM68 PE=1 SV=1	1	---	----	0,167	0,58614	1661,39	61,30%
Q8H151	Malonate--CoA ligase OS=Arabidopsis thaliana GN=AAE13 PE=1 SV=1	2	---	----	0,12	0,58814	1667,05	61,30%
O49460;Q9ZNT7	Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1	1	---	----	0,112	0,58814	1667,05	61,30%
Q5XEP2;Q9LNB6;Q9STH1	Hsp70-Hsp90 organizing protein 2 OS=Arabidopsis thaliana GN=HOP2 PE=1 SV=1	2	---	----	0,11	0,58814	1667,05	61,30%
Q9MAC4	At3g01130 OS=Arabidopsis thaliana GN=T4P13.18 PE=2 SV=1	2	---	----	0,098	0,59014	1672,72	61,30%
Q9LU64	Superoxide dismutase [Fe] 2, chloroplastic OS=Arabidopsis thaliana GN=FSD2 PE=1 SV=1	3	---	----	0,082	0,59014	1672,72	61,30%
Q949R9	Mitochondrial pyruvate carrier 1 OS=Arabidopsis thaliana GN=MPC1 PE=3 SV=1	2	---	----	0,076	0,58614	1661,39	61,30%
Q8W1B3	At4g21445 OS=Arabidopsis thaliana GN=PRIP PE=2 SV=1	2	---	----	-0,086	0,59040	1673,47	61,30%
Q9LYP2	IQ-domain 24 protein OS=Arabidopsis thaliana GN=T28J14_180 PE=2 SV=1	1	---	----	-0,166	0,58880	1668,93	61,30%
Q9LS02;Q9LS03	Allene oxide cyclase 2, chloroplastic OS=Arabidopsis thaliana GN=AOC2 PE=1 SV=1	1	---	----	0,087	0,59214	1678,39	61,40%
Q8RWP0	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At3g20790 PE=2 SV=1	3	---	----	0,085	0,58801	1666,69	61,40%
Q9S9P1	40S ribosomal protein S12-1 OS=Arabidopsis thaliana GN=RPS12A PE=2 SV=1	2	---	----	0,083	0,58804	1666,77	61,40%
Q9LER7	50S ribosomal protein 5, chloroplastic OS=Arabidopsis thaliana GN=PSRP5 PE=2 SV=1	2	---	----	0,083	0,59204	1678,11	61,40%
Q8LCW9	60S acidic ribosomal protein P1-1 OS=Arabidopsis thaliana GN=RPP1A PE=2 SV=2	2	---	----	0,05	0,58681	1663,29	61,40%
O82230	At2g24020/T29E15.22 OS=Arabidopsis thaliana GN=At2g24020 PE=2 SV=2	4	---	----	-0,052	0,58804	1666,77	61,40%
Q0WN54	Molecular chaperone Hsp40/DnaJ-like protein OS=Arabidopsis thaliana GN=At1g80030 PE=2 SV=1	4	---	----	-0,07	0,59004	1672,44	61,40%
O65570;O81645	Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1	1	---	----	-0,11	0,59214	1678,39	61,40%
Q9ZW19	Tropinone reductase homolog At2g29360 OS=Arabidopsis thaliana GN=SDR PE=1 SV=1	1	---	----	-0,136	0,58804	1666,77	61,40%
Q8LKS5	Long chain acyl-CoA synthetase 7, peroxisomal OS=Arabidopsis thaliana GN=LACS7 PE=1 SV=2	1	---	----	-0,171	0,59004	1672,44	61,40%
Q940S3	UDP-N-acetylglucosamine diphosphorylase 1 OS=Arabidopsis thaliana GN=GLCNAC1PUT1 PE=1 SV=1	1	---	----	-0,195	0,58761	1665,56	61,40%
Q9C6S7	Probable methyltransferase PMT20 OS=Arabidopsis thaliana GN=At1g31850 PE=2 SV=1	1	---	----	-0,284	0,59014	1672,72	61,40%
Q9M1J1	Mitochondrial fission 1 protein A OS=Arabidopsis thaliana GN=FIS1A PE=1 SV=1	3	---	----	-0,073	0,59414	1684,06	61,50%
Q9LT75	Protein phosphatase and tensin homolog deleted on chromosome ten 2A OS=Arabidopsis thaliana GN=PEN2 PE=1 SV=	1	---	----	-0,161	0,59414	1684,06	61,50%
Q9LKU2	Sec-independent protein translocase protein TATA, chloroplastic OS=Arabidopsis thaliana GN=TATA PE=1 SV=1	1	---	----	-0,165	0,59204	1678,11	61,50%
F4IBL0	Putative glutathione S-transferase OS=Arabidopsis thaliana GN=At1g65820 PE=4 SV=1	1	---	----	0,169	0,59404	1683,78	61,60%
Q93ZC5	Allene oxide cyclase 4, chloroplastic OS=Arabidopsis thaliana GN=AOC4 PE=2 SV=1	3	---	----	0,08	0,59414	1684,06	61,60%
O82790	AT2G45990 protein OS=Arabidopsis thaliana GN=At2g45990 PE=1 SV=1	7	---	----	-0,054	0,59404	1683,78	61,60%
Q8VY57	ADP-RIBOSYLATION FACTOR-like protein OS=Arabidopsis thaliana GN=ARLA1C PE=2 SV=1	2	---	----	-0,141	0,59614	1689,73	61,60%
Q8H0T4	E3 ubiquitin-protein ligase UPL2 OS=Arabidopsis thaliana GN=UPL2 PE=1 SV=3	1	---	----	0,167	0,59814	1695,40	61,70%
rev_F4JSP7	reversed Uncharacterized protein OS=Arabidopsis thaliana GN=At4g31570 PE=4 SV=1	1	---	----	0,166	0,59841	1696,17	61,70%
P41376	Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	2	---	----	0,107	0,59604	1689,44	61,70%
Q93VP9	Putative uncharacterized protein At4g27585 OS=Arabidopsis thaliana GN=At4g27585 PE=1 SV=1	7	---	----	-0,064	0,59814	1695,40	61,70%
Q9C7V7	At1g64330 OS=Arabidopsis thaliana GN=F15H21.4 PE=2 SV=1	1	---	----	-0,378	0,59604	1689,44	61,70%
Q93Z55	AT3g58470/F14P22_60 OS=Arabidopsis thaliana GN=At3g58470 PE=2 SV=1	1	---	----	0,321	0,59804	1695,11	61,80%
Q944P7	Leucine aminopeptidase 3, chloroplastic OS=Arabidopsis thaliana GN=At4g30920 PE=2 SV=2	8	---	----	-0,045	0,59804	1695,11	61,80%
Q9LJE2	Lysine--tRNA ligase OS=Arabidopsis thaliana GN=OVA5 PE=2 SV=1	1	---	----	-0,183	0,59804	1695,11	61,80%

Q0WQB7	Putative uncharacterized protein At2g25800 OS=Arabidopsis thaliana GN=At2g25800 PE=2 SV=1	1	---	----	-0,399	0,59814	1695,40	61,80%
rev_Q9C5C7	reversed AAA-type ATPase family protein / ankyrin repeat family protein OS=Arabidopsis thaliana GN=At3g24530 PE=2	1	---	----	-0,167	0,60041	1701,84	61,90%
Q9LHA7	Peroxidase 31 OS=Arabidopsis thaliana GN=PER31 PE=2 SV=1	1	---	----	0,182	0,60214	1706,73	62,00%
Q9FFG6	AT5g05480/MOP10_2 OS=Arabidopsis thaliana GN=At5g05480 PE=2 SV=1	1	---	----	0,166	0,60204	1706,45	62,00%
Q9LJW6	60S ribosomal protein L34-3 OS=Arabidopsis thaliana GN=RPL34C PE=2 SV=1	1	---	----	0,165	0,60181	1705,81	62,00%
Q9LNB6	Hsp70-Hsp90 organizing protein 1 OS=Arabidopsis thaliana GN=HOP1 PE=2 SV=1	2	---	----	0,121	0,60201	1706,38	62,00%
F4JWS8;Q9SUU5	Cytochrome b-c1 complex subunit 7-2 OS=Arabidopsis thaliana GN=QCR7-2 PE=1 SV=1	1	---	----	0,095	0,60414	1712,40	62,00%
O65370	At1g12080 OS=Arabidopsis thaliana GN=F12F1.4 PE=2 SV=1	4	---	----	0,086	0,60261	1708,08	62,00%
Q9FL87	Chlororespiratory reduction 7 OS=Arabidopsis thaliana GN=CRR7 PE=2 SV=1	1	---	----	-0,128	0,60214	1706,73	62,00%
Q944H0;Q9FR44	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2	1	---	----	-0,131	0,60204	1706,45	62,00%
Q9SUM2	Probable small nuclear ribonucleoprotein F OS=Arabidopsis thaliana GN=At4g30220 PE=2 SV=1	1	---	----	-0,355	0,60414	1712,40	62,00%
O04951	Serine/threonine-protein phosphatase PP2A-5 catalytic subunit OS=Arabidopsis thaliana GN=PP2A5 PE=1 SV=1	1	---	----	0,197	0,60614	1718,07	62,10%
Q9ZNV8	Histidine-containing phosphotransfer protein 2 OS=Arabidopsis thaliana GN=AHP2 PE=1 SV=1	1	---	----	0,184	0,60404	1712,12	62,10%
Q84MD7	At1g72880 OS=Arabidopsis thaliana GN=At1g72880 PE=2 SV=1	1	---	----	0,169	0,60404	1712,12	62,10%
Q8LA96	Putative RRM-containing protein OS=Arabidopsis thaliana GN=At4g17720 PE=1 SV=1	2	---	----	0,114	0,60681	1719,98	62,10%
O04922	Probable glutathione peroxidase 2 OS=Arabidopsis thaliana GN=GPX2 PE=1 SV=1	7	---	----	-0,046	0,60614	1718,07	62,10%
Q39041;Q43348	Acid beta-fructofuranosidase 4, vacuolar OS=Arabidopsis thaliana GN=BFRUCT4 PE=2 SV=2	2	---	----	-0,084	0,60614	1718,07	62,10%
Q1ACB3	Homogentisate solanesyltransferase, chloroplastic OS=Arabidopsis thaliana GN=HST PE=1 SV=1	1	---	----	-0,107	0,60404	1712,12	62,10%
F4I3I1	FAD/NAD(P)-binding oxidoreductase domain-containing protein OS=Arabidopsis thaliana GN=At1g55980 PE=4 SV=1	1	---	----	0,16	0,60614	1718,07	62,20%
Q9LYL4	Putative uncharacterized protein At3g56290 OS=Arabidopsis thaliana GN=F18O21_250 PE=2 SV=1	1	---	----	0,119	0,60580	1717,12	62,20%
Q9SZE4	Vacuolar protein sorting-associated protein 32 homolog 2 OS=Arabidopsis thaliana GN=VPS32.2 PE=1 SV=1	2	---	----	0,104	0,60814	1723,74	62,20%
Q9LIM9;Q9SUQ9;Q9SUR	Major latex protein-like OS=Arabidopsis thaliana GN=At3g26460 PE=4 SV=1	1	---	----	0,093	0,60614	1718,07	62,20%
Q9LVV5	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic OS=Arabidopsis thaliana GN=At5g52970 PE=1 SV=2	3	---	----	0,086	0,60804	1723,45	62,20%
Q9SIP1	At2g31670 OS=Arabidopsis thaliana GN=At2g31670 PE=2 SV=1	6	---	----	0,039	0,60804	1723,45	62,20%
P42643;P46077;Q01525	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	---	----	0,106	0,60921	1726,78	62,30%
Q9ZS97	UPF0051 protein ABCI8, chloroplastic OS=Arabidopsis thaliana GN=ABCI8 PE=2 SV=1	5	---	----	0,079	0,61014	1729,41	62,30%
Q8S4Y1	Acetyl-CoA acetyltransferase, cytosolic 1 OS=Arabidopsis thaliana GN=AAT1 PE=2 SV=1	8	---	----	-0,053	0,61001	1729,05	62,30%
Q9ZSJ6	Glycine-rich protein 3 short isoform OS=Arabidopsis thaliana GN=GRP3S PE=1 SV=2	2	---	----	-0,11	0,61021	1729,62	62,30%
A3KPE8	Small RNA degrading nuclease 1 OS=Arabidopsis thaliana GN=SDN1 PE=2 SV=1	1	---	----	-0,115	0,61214	1735,07	62,30%
O81770	Monogalactosyldiacylglycerol synthase 1, chloroplastic OS=Arabidopsis thaliana GN=MGD1 PE=1 SV=1	1	---	----	-0,157	0,61004	1729,12	62,30%
Q8GTR4	Pullulanase 1, chloroplastic OS=Arabidopsis thaliana GN=PU1 PE=2 SV=2	1	---	----	-0,17	0,60981	1728,48	62,30%
Q9LMR1	At1g15730/F7H2_7 OS=Arabidopsis thaliana GN=F7H2.7 PE=2 SV=1	1	---	----	-0,21	0,61041	1730,18	62,30%
Q9LJG3	GDSL esterase/lipase ESM1 OS=Arabidopsis thaliana GN=ESM1 PE=1 SV=1	1	---	----	0,19	0,61204	1734,79	62,40%
Q9SI54	Sm-like protein LSM7 OS=Arabidopsis thaliana GN=LSM7 PE=1 SV=1	1	---	----	0,15	0,61214	1735,07	62,40%
Q9LFQ9	E2F transcription factor-like E2FD OS=Arabidopsis thaliana GN=E2FD PE=1 SV=1	1	---	----	0,141	0,61214	1735,07	62,40%
O80386	COP1-Interacting Protein 7 (CIP7) OS=Arabidopsis thaliana GN=CIP7 PE=1 SV=1	1	---	----	-0,194	0,61141	1733,02	62,40%
P52901	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=E1 ALPHA PE=2 S	9	---	----	0,044	0,61414	1740,74	62,50%
F4K452	SOUL heme-binding protein OS=Arabidopsis thaliana GN=At5g20140 PE=4 SV=1	2	---	----	-0,167	0,61414	1740,74	62,50%
Q94BR2	Aluminum induced protein with YGL and LRDR motifs OS=Arabidopsis thaliana GN=AILP1 PE=2 SV=1	4	---	----	0,071	0,61621	1746,62	62,60%
O05000	NADH-ubiquinone oxidoreductase chain 2 OS=Arabidopsis thaliana GN=ND2 PE=2 SV=2	1	---	----	-0,115	0,61604	1746,13	62,60%
O65784	Cytochrome P450 71B5 OS=Arabidopsis thaliana GN=CYP71B5 PE=2 SV=1	1	---	----	0,149	0,61814	1752,08	62,70%
Q8L773	THO complex subunit 4A OS=Arabidopsis thaliana GN=ALY1 PE=1 SV=1	2	---	----	0,102	0,62014	1757,75	62,70%
Q94CC6	Prolyl carboxypeptidase like protein OS=Arabidopsis thaliana GN=At4g36195 PE=2 SV=1	5	---	----	-0,073	0,62014	1757,75	62,70%
Q8W496	Protochlorophyllide-dependent translocon component 52, chloroplastic OS=Arabidopsis thaliana GN=PTC52 PE=2 SV=1	3	---	----	-0,09	0,61604	1746,13	62,70%
Q9SZ54	Putative glutathione peroxidase 7, chloroplastic OS=Arabidopsis thaliana GN=GPX7 PE=3 SV=2	2	---	----	-0,094	0,61721	1749,46	62,70%
Q9SBJ1	[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial OS=Arabidopsis thaliana GN=PDK PE=1 SV=1	2	---	----	-0,12	0,61604	1746,13	62,70%
Q6NLQ7	Monofunctional riboflavin biosynthesis protein RIBA 2, chloroplastic OS=Arabidopsis thaliana GN=RIBA2 PE=1 SV=1	1	---	----	0,202	0,62014	1757,75	62,80%
Q9FMX0	Superoxide dismutase [Fe] 3, chloroplastic OS=Arabidopsis thaliana GN=FSD3 PE=1 SV=1	2	---	----	0,127	0,62014	1757,75	62,80%
Q93Z53;Q9FLW9	Plastidial pyruvate kinase 3, chloroplastic OS=Arabidopsis thaliana GN=PKP3 PE=1 SV=1	1	---	----	0,106	0,61814	1752,08	62,80%
O82628	V-type proton ATPase subunit G1 OS=Arabidopsis thaliana GN=VHA-G1 PE=2 SV=1	8	---	----	0,043	0,62014	1757,75	62,80%
Q8L7S6	Beta-hexosaminidase 3 OS=Arabidopsis thaliana GN=HEXO3 PE=1 SV=1	6	---	----	-0,066	0,61901	1754,56	62,80%
Q9FN03	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana GN=UVR8 PE=1 SV=1	3	---	----	-0,092	0,62004	1757,46	62,80%
Q8VZ55	50S ribosomal protein L35 OS=Arabidopsis thaliana GN=At2g24090 PE=2 SV=1	1	---	----	-0,095	0,62014	1757,75	62,80%
Q8S944	Dynamin-related protein 3A OS=Arabidopsis thaliana GN=DRP3A PE=1 SV=2	2	---	----	-0,128	0,61800	1751,70	62,80%
O82656	Protein-tyrosine-phosphatase PTP1 OS=Arabidopsis thaliana GN=PTP1 PE=1 SV=1	1	---	----	0,147	0,62004	1757,46	62,90%

P56772	ATP-dependent Clp protease proteolytic subunit 1 OS=Arabidopsis thaliana GN=clpP1 PE=1 SV=2	3	---	----	-0,073	0,62214	1763,41	62,90%
Q9FXD4	Signal recognition particle subunit SRP72 OS=Arabidopsis thaliana GN=At1g67680 PE=2 SV=1	1	---	----	-0,185	0,62241	1764,20	62,90%
Q8GUP3	Putative uncharacterized protein At4g31880 OS=Arabidopsis thaliana GN=At4g31880 PE=1 SV=1	1	---	----	-0,227	0,62004	1757,46	62,90%
Q56Y85	Methionine aminopeptidase 2B OS=Arabidopsis thaliana GN=MAP2B PE=2 SV=2	1	---	----	0,145	0,62614	1774,75	63,00%
Q9LF33	UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1	2	---	----	0,113	0,62320	1766,44	63,00%
Q94BQ2	26S protease regulatory subunit 8 homolog B OS=Arabidopsis thaliana GN=RPT6B PE=1 SV=1	4	---	----	0,08	0,62814	1780,42	63,00%
Q9XI10	DPP6 N-terminal domain-like protein OS=Arabidopsis thaliana GN=F8K7.10 PE=2 SV=1	7	---	----	0,062	0,62461	1770,43	63,00%
Q8S9L5	Trigger factor-like protein TIG, Chloroplastic OS=Arabidopsis thaliana GN=TIG PE=2 SV=1	25	---	----	0,026	0,62401	1768,73	63,00%
Q8GUN2	HIS triad family protein 3 OS=Arabidopsis thaliana GN=HIT3 PE=1 SV=1	6	---	----	-0,05	0,62614	1774,75	63,00%
Q9SA23	Syntaxin-51 OS=Arabidopsis thaliana GN=SYP51 PE=1 SV=1	1	---	----	-0,214	0,62380	1768,14	63,00%
O80916	Putative uncharacterized protein At2g38350 OS=Arabidopsis thaliana GN=At2g38350 PE=4 SV=1	1	---	----	0,167	0,62804	1780,14	63,10%
Q9LME4	Probable protein phosphatase 2C 9 OS=Arabidopsis thaliana GN=At1g22280 PE=1 SV=1	1	---	----	0,165	0,62614	1774,75	63,10%
P29514;P29516	Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1	1	---	----	0,153	0,62814	1780,42	63,10%
Q8GYA6;Q8RWF0	26S proteasome non-ATPase regulatory subunit 13 homolog B OS=Arabidopsis thaliana GN=RPN9B PE=1 SV=1	3	---	----	0,105	0,62581	1773,83	63,10%
Q9SZE1	Probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial OS=Arabidopsis thaliana GN=At4g29120 PE=2 SV=	3	---	----	0,103	0,62741	1778,37	63,10%
Q94BZ7	DNA gyrase subunit B, mitochondrial OS=Arabidopsis thaliana GN=GYRBM PE=2 SV=1	1	---	----	0,101	0,62814	1780,42	63,10%
P29513	Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1	6	---	----	-0,042	0,62614	1774,75	63,10%
Q9SVD1	Aspartyl protease family protein OS=Arabidopsis thaliana GN=F22O6_120 PE=2 SV=1	5	---	----	-0,051	0,62604	1774,47	63,10%
rev_Q9SQY0	reversed F18K10.6 protein OS=Arabidopsis thaliana GN=F13M14.23 PE=4 SV=1	1	---	----	-0,119	0,62614	1774,75	63,10%
Q8LDC9	GroES-like protein OS=Arabidopsis thaliana GN=At1g23100 PE=2 SV=1	1	---	----	-0,156	0,62804	1780,14	63,10%
Q6DYE4	Uncharacterized protein At1g26090, chloroplastic OS=Arabidopsis thaliana GN=At1g26090 PE=2 SV=1	1	---	----	-0,223	0,63014	1786,09	63,10%
F4J912	60S ribosomal protein L5-1 OS=Arabidopsis thaliana GN=ATL5 PE=4 SV=1	1	---	----	-0,329	0,62814	1780,42	63,10%
Q9SLN5	Methionine aminopeptidase 1A OS=Arabidopsis thaliana GN=MAP1A PE=1 SV=1	1	---	----	0,183	0,63014	1786,09	63,20%
Q9ZVD0	Serrate RNA effector molecule OS=Arabidopsis thaliana GN=SE PE=1 SV=2	1	---	----	0,182	0,63004	1785,80	63,20%
F4I7X1	SKU5 similar 6 OS=Arabidopsis thaliana GN=SKS6 PE=4 SV=1	1	---	----	0,15	0,63004	1785,80	63,20%
P50318;Q9LD57;Q9SAJ4	Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=2 SV=3	2	---	----	-0,037	0,62801	1780,07	63,20%
F4K3A9	HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase OS=Arabidopsis thaliana GN=At5g48960 PE=4 SV=1	4	---	----	-0,09	0,63014	1786,09	63,20%
F4I3C3	Uncharacterized protein OS=Arabidopsis thaliana GN=NQR PE=4 SV=1	5	---	----	0,068	0,63204	1791,47	63,30%
Q9SSK5	MLP-like protein 43 OS=Arabidopsis thaliana GN=MLP43 PE=1 SV=1	7	---	----	0,05	0,63414	1797,42	63,30%
Q9ZR03	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic OS=Arabidopsis thaliana GN=petC PE=1 SV=1	4	---	----	0,034	0,63414	1797,42	63,30%
Q9LJI5	V-type proton ATPase subunit d1 OS=Arabidopsis thaliana GN=VHA-d1 PE=2 SV=1	9	---	----	-0,038	0,63214	1791,76	63,30%
Q8LBP4	Inner membrane protein ALBINO3, chloroplastic OS=Arabidopsis thaliana GN=ALB3 PE=1 SV=2	2	---	----	-0,08	0,63404	1797,14	63,30%
Q8L3S7	Expressed protein OS=Arabidopsis thaliana GN=At3g57785 PE=2 SV=1	1	---	----	-0,192	0,63214	1791,76	63,30%
F4HWL4	Probably tyrosine-tRNA synthetase OS=Arabidopsis thaliana GN=At1g28350 PE=1 SV=1	1	---	----	0,266	0,63681	1805,01	63,40%
O22898	Long chain acyl-CoA synthetase 1 OS=Arabidopsis thaliana GN=LACS1 PE=2 SV=1	1	---	----	0,238	0,63404	1797,14	63,40%
Q9SKM7	At2g28430/T1B3.5 OS=Arabidopsis thaliana GN=At2g28430 PE=2 SV=1	1	---	----	0,182	0,63340	1795,35	63,40%
F4IE14	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g19140 PE=4 SV=1	3	---	----	0,102	0,63400	1797,05	63,40%
Q9LK47	AT3g23700/MYM9_3 OS=Arabidopsis thaliana GN=At3g23700 PE=2 SV=1	6	---	----	-0,051	0,63614	1803,09	63,40%
Q9S7Z3	Glutathione gamma-glutamylcysteinyltransferase 1 OS=Arabidopsis thaliana GN=PCS1 PE=1 SV=1	5	---	----	-0,073	0,63614	1803,09	63,40%
Q9LZV4	Serine/threonine-protein kinase STN8, chloroplastic OS=Arabidopsis thaliana GN=STN8 PE=2 SV=1	1	---	----	-0,141	0,63614	1803,09	63,40%
F4K692	RPM1-interacting protein 4 (RIN4) family protein OS=Arabidopsis thaliana GN=NOI PE=1 SV=1	1	---	----	-0,154	0,63614	1803,09	63,40%
Q8GRX2	Eukaryotic translation initiation factor 3 subunit J OS=Arabidopsis thaliana GN=At5g37475 PE=2 SV=1	2	---	----	-0,167	0,63361	1795,94	63,40%
Q8W207	COP9 signalosome complex subunit 2 OS=Arabidopsis thaliana GN=CSN2 PE=1 SV=1	1	---	----	0,177	0,63804	1808,48	63,50%
Q9SF53	60S ribosomal protein L35-1 OS=Arabidopsis thaliana GN=RPL35A PE=2 SV=1	1	---	----	0,152	0,64004	1814,15	63,50%
Q9FKV6	Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=At5g44320 PE=2 SV=1	1	---	----	0,144	0,63604	1802,81	63,50%
Q8W4D0	Peptidyl-prolyl cis-trans isomerase CYP71 OS=Arabidopsis thaliana GN=CYP71 PE=1 SV=1	1	---	----	0,134	0,64014	1814,43	63,50%
Q9M8T0	Probable inactive receptor kinase At3g02880 OS=Arabidopsis thaliana GN=At3g02880 PE=1 SV=1	3	---	----	0,094	0,63814	1808,76	63,50%
Q8LPJ5;Q9SRZ6	Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At5g14590 PE=2 SV=1	3	---	----	0,064	0,63821	1808,98	63,50%
Q94II5	Dessication responsive protein OS=Arabidopsis thaliana GN=RD2 PE=2 SV=1	4	---	----	0,052	0,63814	1808,76	63,50%
Q9SAU2	D-ribulose-5-phosphate-3-epimerase OS=Arabidopsis thaliana GN=RPE PE=2 SV=1	6	---	----	-0,035	0,63601	1802,75	63,50%
B9DHK3	AT5G14540 protein OS=Arabidopsis thaliana GN=At5g14540 PE=1 SV=1	2	---	----	-0,129	0,64014	1814,43	63,50%
Q38906	Translocase of chloroplast 34, chloroplastic OS=Arabidopsis thaliana GN=TOC34 PE=1 SV=2	1	---	----	-0,151	0,64014	1814,43	63,50%
F4IIM1	Cellulose synthase-interactive protein 1 OS=Arabidopsis thaliana GN=At2g22125 PE=4 SV=1	1	---	----	-0,278	0,63781	1807,85	63,50%
Q9FIJ4	At5g47870 OS=Arabidopsis thaliana GN=At5g47870 PE=2 SV=1	2	---	----	0,108	0,64121	1817,48	63,60%
O82258	At2g47910 OS=Arabidopsis thaliana GN=CRR6 PE=2 SV=1	4	---	----	0,082	0,64004	1814,15	63,60%

Q9LKR8	Rubisco accumulation factor 1, chloroplastic OS=Arabidopsis thaliana GN=RAF1 PE=2 SV=1	4	---	----	0,074	0,64001	1814,08	63,60%
O81235	Superoxide dismutase [Mn] 1, mitochondrial OS=Arabidopsis thaliana GN=MSD1 PE=1 SV=2	7	---	----	0,041	0,64214	1820,10	63,60%
Q9SQR4	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=T11I18.9 PE=3 SV=1	2	---	----	-0,083	0,64214	1820,10	63,60%
Q9LM71	Peptidyl-prolyl cis-trans isomerase FKBP18, chloroplastic OS=Arabidopsis thaliana GN=FKBP18 PE=1 SV=2	2	---	----	-0,09	0,64141	1818,05	63,60%
Q940G5	Aldose 1-epimerase family protein OS=Arabidopsis thaliana GN=F14M19.180 PE=2 SV=1	1	---	----	-0,135	0,64004	1814,15	63,60%
O23342	Preprotein translocase subunit SECE1 OS=Arabidopsis thaliana GN=SECE1 PE=1 SV=1	1	---	----	-0,145	0,64414	1825,77	63,60%
Q9SD45	AT3g51000/F24M12_40 OS=Arabidopsis thaliana GN=F24M12.40 PE=2 SV=1	1	---	----	0,174	0,64404	1825,48	63,70%
Q8L3X8	Serine/arginine-rich SC35-like splicing factor SCL30 OS=Arabidopsis thaliana GN=SCL30 PE=1 SV=1	1	---	----	0,141	0,64614	1831,43	63,70%
Q93W05	At1g10590/F20B24_1 OS=Arabidopsis thaliana GN=At1g10590 PE=2 SV=1	2	---	----	0,1	0,64501	1828,26	63,70%
P49243	3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic OS=Arabidopsis thaliana GN=At1g62640 PE=2 SV=2	4	---	----	0,062	0,64614	1831,43	63,70%
Q9LKA3;Q9ZP06	Malate dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=At3g15020 PE=2 SV=1	7	---	----	0,036	0,64414	1825,77	63,70%
O82413	Histidyl-tRNA synthetase OS=Arabidopsis thaliana GN=F12M12_70 PE=2 SV=1	2	---	----	-0,088	0,64414	1825,77	63,70%
Q9FNK4	Ornithine aminotransferase, mitochondrial OS=Arabidopsis thaliana GN=DELTA-OAT PE=1 SV=1	2	---	----	-0,091	0,64414	1825,77	63,70%
Q5XEP2	Hsp70-Hsp90 organizing protein 2 OS=Arabidopsis thaliana GN=HOP2 PE=1 SV=1	2	---	----	-0,095	0,64621	1831,66	63,70%
Q9FE38	Potassium transporter 3 OS=Arabidopsis thaliana GN=POT3 PE=1 SV=1	1	---	----	-0,138	0,64414	1825,77	63,70%
Q9LE16	Genomic DNA, chromosome 3, P1 clone: MJK13 OS=Arabidopsis thaliana GN=MJK13.12 PE=2 SV=1	1	---	----	0,403	0,64814	1837,10	63,80%
Q9S7W4	AT3g07720/F17A17_6 OS=Arabidopsis thaliana GN=F17A17.6 PE=2 SV=1	4	---	----	0,093	0,64814	1837,10	63,80%
Q9FPT1	Ubiquitin carboxyl-terminal hydrolase 12 OS=Arabidopsis thaliana GN=UBP12 PE=1 SV=2	3	---	----	0,092	0,64814	1837,10	63,80%
O23654	V-type proton ATPase catalytic subunit A OS=Arabidopsis thaliana GN=VHA-A PE=1 SV=1	31	---	----	-0,018	0,64404	1825,48	63,80%
Q8H0Y1	Outer envelope pore protein 24B, chloroplastic OS=Arabidopsis thaliana GN=OEP24B PE=2 SV=1	4	---	----	-0,054	0,64604	1831,15	63,80%
Q9SU27	At4g12590 OS=Arabidopsis thaliana GN=At4g12590 PE=2 SV=1	1	---	----	-0,237	0,64814	1837,10	63,80%
Q9STW1	At4g24330 OS=Arabidopsis thaliana GN=T22A6.160 PE=2 SV=1	1	---	----	-0,266	0,64604	1831,15	63,80%
P94014;Q9FZ27;Q9M263	Germin-like protein subfamily 2 member 1 OS=Arabidopsis thaliana GN=GLP4 PE=2 SV=2	1	---	----	0,133	0,65020	1842,97	63,90%
Q24JL3	Thiosulfate/3-mercaptopyruvate sulfurtransferase 2 OS=Arabidopsis thaliana GN=STR2 PE=1 SV=1	3	---	----	0,085	0,65013	1842,77	63,90%
Q9LV11	ATPase 11, plasma membrane-type OS=Arabidopsis thaliana GN=AHA11 PE=1 SV=1	5	---	----	0,08	0,64814	1837,10	63,90%
O04482	Ubiquitin carboxyl-terminal hydrolase OS=Arabidopsis thaliana GN=F5I14.18 PE=1 SV=1	2	---	----	-0,091	0,64804	1836,82	63,90%
Q9FFF4	Acetolactate synthase small subunit 1, chloroplastic OS=Arabidopsis thaliana GN=VAT1 PE=1 SV=1	1	---	----	-0,152	0,65003	1842,49	63,90%
Q93XX5	PI-PLC X domain-containing protein At5g67130 OS=Arabidopsis thaliana GN=At5g67130 PE=1 SV=1	1	---	----	0,139	0,65203	1848,16	64,00%
P49077	Aspartate carbamoyltransferase, chloroplastic OS=Arabidopsis thaliana GN=PYRB PE=2 SV=2	6	---	----	-0,049	0,65213	1848,44	64,00%
Q9FKM2	Mitochondrial outer membrane protein porin 4 OS=Arabidopsis thaliana GN=VDAC4 PE=1 SV=1	2	---	----	-0,089	0,65181	1847,53	64,00%
Q9FIF9	Ras-related protein RABA2d OS=Arabidopsis thaliana GN=RABA2D PE=2 SV=1	1	---	----	-0,307	0,65213	1848,44	64,00%
P31168	Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2	1	SNSSSSSSSDEEGEEK	Phospho S6	-0,361	0,65203	1848,16	64,00%
Q7X659	Vacuolar protein sorting-associated protein 35A OS=Arabidopsis thaliana GN=VPS35A PE=1 SV=1	2	---	----	0,156	0,65403	1853,82	64,10%
O82768	Histidine biosynthesis bifunctional protein hisIE, chloroplastic OS=Arabidopsis thaliana GN=HISN2 PE=1 SV=1	2	---	----	0,128	0,65413	1854,11	64,10%
Q8GWP5	Riboflavin biosynthesis protein PYRD, chloroplastic OS=Arabidopsis thaliana GN=PYRD PE=1 SV=1	1	---	----	0,115	0,65413	1854,11	64,10%
Q9CAD1	At1g63660 OS=Arabidopsis thaliana GN=F24D7.15 PE=2 SV=1	5	---	----	0,058	0,65413	1854,11	64,10%
F4HY32	Calcium-binding EF-hand-containing protein OS=Arabidopsis thaliana GN=At1g21630 PE=1 SV=1	1	---	----	0,11	0,65613	1859,78	64,20%
O80840	Phosphomannomutase OS=Arabidopsis thaliana GN=PMM PE=1 SV=1	3	---	----	0,084	0,65501	1856,60	64,20%
Q93Y22	Coatomer subunit delta OS=Arabidopsis thaliana GN=At5g05010 PE=1 SV=2	5	---	----	0,063	0,65621	1860,00	64,20%
P92947	Monodehydroascorbate reductase, chloroplastic OS=Arabidopsis thaliana GN=At1g63940 PE=2 SV=3	17	---	----	-0,024	0,65541	1857,73	64,20%
Q9SCV4	Beta-galactosidase 8 OS=Arabidopsis thaliana GN=BGAL8 PE=2 SV=2	3	---	----	-0,082	0,65613	1859,78	64,20%
Q9C535	Metallo-beta-lactamase domain-containing protein OS=Arabidopsis thaliana GN=F15D2.25 PE=2 SV=1	4	---	----	-0,083	0,65681	1861,70	64,20%
O22527	Chlorophyllase-1 OS=Arabidopsis thaliana GN=CLH1 PE=1 SV=1	1	---	----	0,293	0,66013	1871,11	64,30%
Q8LB02;Q8LBZ7	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial OS=Arabidopsis thaliana GN=SDH2-2 PE=1	1	---	----	0,143	0,65813	1865,44	64,30%
Q9XH75	Sec-independent protein translocase protein TATB, chloroplastic OS=Arabidopsis thaliana GN=TATB PE=1 SV=1	3	---	----	-0,066	0,66020	1871,31	64,30%
Q9SIV9	Purple acid phosphatase 10 OS=Arabidopsis thaliana GN=PAP10 PE=2 SV=1	1	---	----	-0,105	0,65813	1865,44	64,30%
P11832	Nitrate reductase [NADH] 1 OS=Arabidopsis thaliana GN=NIA1 PE=1 SV=3	1	---	----	0,127	0,66013	1871,11	64,40%
Q9FPJ4;Q9ZRE2	Ras-related protein RABD2b OS=Arabidopsis thaliana GN=RABD2B PE=2 SV=1	1	---	----	0,085	0,66413	1882,45	64,40%
Q9SZV4	AT4g30010/F6G3_40 OS=Arabidopsis thaliana GN=F6G3.40 PE=2 SV=1	3	---	----	0,075	0,66013	1871,11	64,40%
Q9FNN5	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Arabidopsis thaliana GN=At5g08530 PE=2 SV=1	6	---	----	0,059	0,66213	1876,78	64,40%
Q940P8	T-complex protein 1 subunit beta OS=Arabidopsis thaliana GN=CCT2 PE=1 SV=1	5	---	----	-0,055	0,66281	1878,71	64,40%
Q0WV90;Q94AI7	Topless-related protein 1 OS=Arabidopsis thaliana GN=TPR1 PE=1 SV=3	4	---	----	-0,062	0,66203	1876,50	64,40%
Q9FM77	Putative uncharacterized protein At5g55610 OS=Arabidopsis thaliana GN=At5g55610 PE=2 SV=1	3	---	----	-0,07	0,66413	1882,45	64,40%
O82251	Protein TIC 20-II, chloroplastic OS=Arabidopsis thaliana GN=TIC20-II PE=2 SV=1	3	---	----	-0,091	0,66213	1876,78	64,40%
Q9C6P3	Calcium-dependent protein kinase 33 OS=Arabidopsis thaliana GN=CPK33 PE=2 SV=1	1	---	----	-0,1	0,66013	1871,11	64,40%

Q39189	DEAD-box ATP-dependent RNA helicase 7 OS=Arabidopsis thaliana GN=RH7 PE=1 SV=2	1	---	----	-0,137	0,66013	1871,11	64,40%
Q9C6C8	Glutathione S-transferase F14 OS=Arabidopsis thaliana GN=GSTF14 PE=2 SV=1	1	---	----	-0,251	0,66413	1882,45	64,40%
Q9LDK9	Beta-adaptin-like protein A OS=Arabidopsis thaliana GN=BETAA-AD PE=1 SV=1	1	---	----	0,24	0,66613	1888,12	64,50%
Q8L4S3	AT5g09390/T5E8_190 OS=Arabidopsis thaliana GN=At5g09390 PE=1 SV=1	1	---	----	0,133	0,67013	1899,45	64,50%
Q9FFP6	Pyruvate kinase OS=Arabidopsis thaliana GN=At5g63680 PE=3 SV=1	2	---	----	0,097	0,66413	1882,45	64,50%
Q9SE96	GEM-like protein 1 OS=Arabidopsis thaliana GN=FIP1 PE=1 SV=1	2	---	----	0,097	0,66813	1893,79	64,50%
Q5M731	Thiamine biosynthetic bifunctional enzyme TH1, chloroplastic OS=Arabidopsis thaliana GN=TH1 PE=1 SV=1	2	---	----	0,078	0,66413	1882,45	64,50%
O49453	Uncharacterized protein At4g28440 OS=Arabidopsis thaliana GN=At4g28440 PE=1 SV=1	3	---	----	0,073	0,66541	1886,08	64,50%
P48349	14-3-3-like protein GF14 lambda OS=Arabidopsis thaliana GN=GRF6 PE=1 SV=1	3	---	----	0,051	0,66813	1893,79	64,50%
Q9LW52	Genomic DNA, chromosome 3, P1 clone: MLM24 OS=Arabidopsis thaliana GN=At3g23450 PE=4 SV=1	4	---	----	0,05	0,66203	1876,50	64,50%
Q39161	Ferredoxin--nitrite reductase, chloroplastic OS=Arabidopsis thaliana GN=NIR1 PE=1 SV=1	22	---	----	-0,021	0,66821	1894,01	64,50%
Q94B60	ATP-dependent Clp protease proteolytic subunit 4, chloroplastic OS=Arabidopsis thaliana GN=CLPP4 PE=1 SV=1	7	---	----	-0,039	0,67013	1899,45	64,50%
Q9SX22	30S ribosomal protein 3-1, chloroplastic OS=Arabidopsis thaliana GN=At1g68590 PE=2 SV=1	2	---	----	-0,071	0,67013	1899,45	64,50%
Q8LBB2	SNF1-related protein kinase regulatory subunit gamma-1 OS=Arabidopsis thaliana GN=KING1 PE=1 SV=2	2	---	----	-0,078	0,66813	1893,79	64,50%
O65719;Q9LHA8	Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	1	---	----	-0,088	0,66413	1882,45	64,50%
Q9S7T8	Serpin-ZX OS=Arabidopsis thaliana GN=At1g47710 PE=1 SV=1	2	---	----	-0,091	0,66013	1871,11	64,50%
P46637	Arginase 1, mitochondrial OS=Arabidopsis thaliana GN=ARGAH1 PE=2 SV=1	2	---	----	-0,093	0,67013	1899,45	64,50%
Q8L4N1	AT4g27320/M4I22_130 OS=Arabidopsis thaliana GN=PHOS34 PE=2 SV=1	2	---	----	-0,094	0,66413	1882,45	64,50%
F4K4A6	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein OS=Arabidopsis thaliana GN=At5g27390	2	---	----	-0,096	0,66641	1888,91	64,50%
Q9LZP9	Calvin cycle protein CP12-2, chloroplastic OS=Arabidopsis thaliana GN=CP12-2 PE=1 SV=1	1	---	----	-0,098	0,66003	1870,83	64,50%
F4JAF4	Uncharacterized protein OS=Arabidopsis thaliana GN=At3g53470 PE=4 SV=1	1	---	----	-0,098	0,66203	1876,50	64,50%
Q9FWT4	ATP-dependent protease La domain-containing protein OS=Arabidopsis thaliana GN=F1B16.1 PE=2 SV=1	2	---	----	-0,102	0,66603	1887,83	64,50%
Q9C942	Caffeoylshikimate esterase OS=Arabidopsis thaliana GN=CSE PE=1 SV=1	2	---	----	-0,11	0,67013	1899,45	64,50%
P92558	NADH-ubiquinone oxidoreductase chain 1 OS=Arabidopsis thaliana GN=ND1 PE=2 SV=4	1	---	----	-0,12	0,66603	1887,83	64,50%
Q8LEU3	Chlorophyll(ide) b reductase NOL, chloroplastic OS=Arabidopsis thaliana GN=NOL PE=1 SV=1	1	---	----	-0,134	0,66521	1885,51	64,50%
Q9FE38	Potassium transporter 3 OS=Arabidopsis thaliana GN=POT3 PE=1 SV=1	1	SISEANIAGSSR	Phospho S3	-0,272	0,66561	1886,64	64,50%
O65570	Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1	1	SPAFNALAATFESQN	Phospho S3	-0,298	0,66813	1893,79	64,50%
Q39099;Q9XIW1	Xyloglucan endotransglucosylase/hydrolase protein 4 OS=Arabidopsis thaliana GN=XTH4 PE=1 SV=1	1	---	----	0,135	0,66813	1893,79	64,60%
Q9ZW34	Cytosolic enolase 3 OS=Arabidopsis thaliana GN=ENO3 PE=1 SV=1	1	---	----	0,134	0,67213	1905,12	64,60%
Q93Y40	Oxysterol-binding protein-related protein 3C OS=Arabidopsis thaliana GN=ORP3C PE=2 SV=1	1	---	----	0,13	0,66803	1893,50	64,60%
P56795	50S ribosomal protein L22, chloroplastic OS=Arabidopsis thaliana GN=rpl22 PE=3 SV=1	5	---	----	0,042	0,67213	1905,12	64,60%
Q8L7S1	At1g45200 OS=Arabidopsis thaliana GN=TLL1 PE=2 SV=1	9	---	----	0,04	0,66941	1897,41	64,60%
O65570	Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1	4	---	----	-0,054	0,67203	1904,84	64,60%
O65660;Q9SIE7	AT4g39730/T19P19_120 OS=Arabidopsis thaliana GN=At4g39730 PE=2 SV=1	1	---	----	-0,079	0,66961	1897,98	64,60%
Q84XU2	Serine/threonine-protein phosphatase 5 OS=Arabidopsis thaliana GN=PAPP5 PE=1 SV=1	1	---	----	-0,131	0,66413	1882,45	64,60%
Q9ZUA0	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1B OS=Arabidopsis thaliana GN=OST1B PE=2 S	1	---	----	-0,134	0,67003	1899,17	64,60%
Q94BU1	Uncharacterized aarF domain-containing protein kinase At1g71810, chloroplastic OS=Arabidopsis thaliana GN=At1g71	1	---	----	-0,141	0,66803	1893,50	64,60%
Q8H101	AT1G10660 protein OS=Arabidopsis thaliana GN=At1g10660 PE=2 SV=1	1	---	----	-0,167	0,67003	1899,17	64,60%
O64481	Subtilisin-like protease SBT2.5 OS=Arabidopsis thaliana GN=SBT2.5 PE=2 SV=1	1	---	----	0,195	0,67460	1912,13	64,70%
P31582	Ras-related protein RABF2a OS=Arabidopsis thaliana GN=RABF2A PE=1 SV=1	1	---	----	0,097	0,67413	1910,79	64,70%
Q9LF46	2-hydroxyacyl-CoA lyase OS=Arabidopsis thaliana GN=HACL PE=1 SV=1	8	---	----	0,048	0,67413	1910,79	64,70%
P42760	Glutathione S-transferase F6 OS=Arabidopsis thaliana GN=GSTF6 PE=2 SV=2	7	---	----	-0,054	0,67381	1909,89	64,70%
Q8H1H9	Primary amine oxidase OS=Arabidopsis thaliana GN=At1g62810 PE=2 SV=1	1	---	----	0,138	0,67603	1916,18	64,80%
F4I3J0	Obg-like ATPase 1 OS=Arabidopsis thaliana GN=At1g56050 PE=3 SV=1	11	---	----	0,032	0,67613	1916,46	64,80%
rev_Q9LZQ3	reversed Heme binding protein OS=Arabidopsis thaliana GN=T12C14_70 PE=2 SV=1	1	---	----	-0,127	0,67603	1916,18	64,80%
Q9LMM0	Glycerol-3-phosphate 2-O-acyltransferase 4 OS=Arabidopsis thaliana GN=GPAT4 PE=1 SV=1	1	---	----	-0,332	0,67613	1916,46	64,80%
Q9M292	Nicalin OS=Arabidopsis thaliana GN=T22K7_10 PE=2 SV=1	2	---	----	0,103	0,67813	1922,13	64,90%
O23710;Q7DLS1	Proteasome subunit beta type-7-A OS=Arabidopsis thaliana GN=PBB1 PE=1 SV=2	3	---	----	0,081	0,67813	1922,13	64,90%
Q9FZA2	Non-classical arabinogalactan protein 31 OS=Arabidopsis thaliana GN=AGP31 PE=1 SV=1	4	---	----	0,055	0,67741	1920,09	64,90%
Q41969	Eukaryotic translation initiation factor 2 subunit beta OS=Arabidopsis thaliana GN=EMB1401 PE=1 SV=3	4	---	----	0,045	0,67813	1922,13	64,90%
Q42545	Cell division protein FtsZ homolog 1, chloroplastic OS=Arabidopsis thaliana GN=FTSZ1 PE=1 SV=2	8	---	----	0,04	0,67760	1920,63	64,90%
O65655	Putative uncharacterized protein AT4g39680 OS=Arabidopsis thaliana GN=At4g39680 PE=1 SV=1	1	SDSSVSEDGPK	Phospho S3	0,239	0,68081	1929,73	65,00%
Q9LZG0	Adenosine kinase 2 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	2	---	----	0,077	0,68013	1927,80	65,00%
Q5M729;Q8RWN9	Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial OS=Ar	2	---	----	0,072	0,68003	1927,51	65,00%
Q9SRH5	Mitochondrial outer membrane protein porin 1 OS=Arabidopsis thaliana GN=VDAC1 PE=1 SV=3	10	---	----	0,032	0,68061	1929,16	65,00%

Q9ZST4	Nitrogen regulatory protein P-II homolog OS=Arabidopsis thaliana GN=GLB1 PE=1 SV=1	6	---	----	-0,043	0,67941	1925,76	65,00%
Q42418	Profilin-2 OS=Arabidopsis thaliana GN=PRO2 PE=2 SV=1	3	---	----	-0,051	0,68013	1927,80	65,00%
Q9SE83	Dynamin-2A OS=Arabidopsis thaliana GN=DRP2A PE=1 SV=2	1	---	----	-0,112	0,68213	1933,46	65,00%
Q9XIP8	Protein CDI OS=Arabidopsis thaliana GN=CDI PE=2 SV=1	1	---	----	-0,112	0,68213	1933,46	65,00%
Q8VZJ2	AT4g16260/dl4170c OS=Arabidopsis thaliana GN=At4g16260 PE=2 SV=1	1	---	----	-0,145	0,68013	1927,80	65,00%
Q93W28	Uncharacterized protein At4g15545 OS=Arabidopsis thaliana GN=At4g15545 PE=1 SV=1	1	.TPPGSPPILSASGTPI	Phospho S6	-0,283	0,68220	1933,67	65,00%
Q9ZQY6	Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B' delta isoform OS=Arabidopsis thaliana GN=B'DE	1	---	----	0,254	0,68403	1938,85	65,10%
Q949W6	Protein KAKU4 OS=Arabidopsis thaliana GN=KAKU4 PE=1 SV=1	1	---	----	0,13	0,68461	1940,50	65,10%
Q8GXU7	At4g13612 OS=Arabidopsis thaliana GN=At4g13615 PE=2 SV=1	1	---	----	0,109	0,68213	1933,46	65,10%
Q9FY64	40S ribosomal protein S15-4 OS=Arabidopsis thaliana GN=RPS15D PE=2 SV=1	1	---	----	0,103	0,68413	1939,13	65,10%
O23680	Translocase of chloroplast 33, chloroplastic OS=Arabidopsis thaliana GN=TOC33 PE=1 SV=1	2	---	----	0,079	0,68413	1939,13	65,10%
Q9LV66	Uncharacterized protein At5g48480 OS=Arabidopsis thaliana GN=At5g48480 PE=1 SV=1	6	---	----	-0,051	0,68481	1941,06	65,10%
Q9SHH6;Q9ZRW8	Glutathione S-transferase U24 OS=Arabidopsis thaliana GN=GSTU24 PE=2 SV=1	2	---	----	-0,057	0,68413	1939,13	65,10%
Q9SX85	Exocyst complex component SEC3A OS=Arabidopsis thaliana GN=SEC3A PE=1 SV=1	2	---	----	-0,11	0,68413	1939,13	65,10%
F4JRN0	Rho termination factor OS=Arabidopsis thaliana GN=At4g18740 PE=4 SV=1	1	---	----	-0,15	0,68201	1933,13	65,10%
Q5E924	Glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic OS=Arabidopsis thaliana GN=GAPCP2 PE=2 SV=1	3	---	----	0,067	0,68613	1944,80	65,20%
Q93VB0	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=At2g40660 PE=2 SV=1	4	---	----	0,061	0,68813	1950,47	65,20%
Q8GY96	Phosphoglycerate mutase-like protein OS=Arabidopsis thaliana GN=PGM PE=2 SV=1	1	---	----	-0,09	0,68803	1950,19	65,20%
O49711	Pentatricopeptide repeat-containing protein At4g21880, mitochondrial OS=Arabidopsis thaliana GN=At4g21880 PE=3 S	1	---	----	-0,161	0,68613	1944,80	65,20%
F4JPA3	Ribosomal L25/TL5/CTC N-terminal 5S rRNA binding domain-containing protein OS=Arabidopsis thaliana GN=At4g2362	1	---	----	0,334	0,69013	1956,14	65,30%
A2RVS4	AIG2-like protein OS=Arabidopsis thaliana GN=At4g31310 PE=1 SV=1	1	---	----	0,131	0,69013	1956,14	65,30%
Q9LFS0	At5g16040 OS=Arabidopsis thaliana GN=F1N13_180 PE=2 SV=1	1	---	----	0,123	0,68860	1951,81	65,30%
Q9FFE0	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 OS=Arabidopsis thaliana GN=At5g16450 PE=1 SV=1	2	---	----	0,091	0,68803	1950,19	65,30%
P19366;Q9C5A9	ATP synthase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=atpB PE=1 SV=2	1	---	----	-0,032	0,68803	1950,19	65,30%
Q9LKA3;Q9SN86;Q9ZP06	Malate dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=At3g15020 PE=2 SV=1	1	---	----	-0,091	0,68803	1950,19	65,30%
Q84VQ1	SNF1-related protein kinase regulatory subunit beta-1 OS=Arabidopsis thaliana GN=KINB1 PE=1 SV=1	1	---	----	-0,211	0,69013	1956,14	65,30%
F4JHV8	Small nuclear ribonucleoprotein family protein OS=Arabidopsis thaliana GN=At4g02840 PE=4 SV=1	1	---	----	-0,359	0,68803	1950,19	65,30%
Q9FNC4;Q9ZWC4	HAD superfamily, subfamily IIIB acid phosphatase OS=Arabidopsis thaliana GN=At5g44020 PE=2 SV=1	1	---	----	0,146	0,69213	1961,81	65,40%
Q9SVI9	At4g39040 OS=Arabidopsis thaliana GN=F19H22.140 PE=1 SV=1	1	---	----	0,115	0,69203	1961,52	65,40%
O23710	Proteasome subunit beta type-7-A OS=Arabidopsis thaliana GN=PBB1 PE=1 SV=2	1	---	----	0,091	0,69213	1961,81	65,40%
Q9SXP7	Octanoyltransferase OS=Arabidopsis thaliana GN=LIP2 PE=2 SV=1	2	---	----	-0,091	0,69013	1956,14	65,40%
Q9FMD7;Q9M8T0	Probable inactive receptor kinase At5g16590 OS=Arabidopsis thaliana GN=At5g16590 PE=1 SV=1	1	---	----	-0,116	0,69003	1955,85	65,40%
P11829	Acyl carrier protein 1, chloroplastic OS=Arabidopsis thaliana GN=ACP1 PE=1 SV=1	1	---	----	0,186	0,69403	1967,19	65,50%
Q8LGU1	ABC transporter C family member 8 OS=Arabidopsis thaliana GN=ABCC8 PE=2 SV=3	1	---	----	0,171	0,69413	1967,47	65,50%
P93834	Hexokinase-2 OS=Arabidopsis thaliana GN=HXK2 PE=1 SV=1	1	---	----	0,129	0,69400	1967,11	65,50%
F4JUM1	Sec23/sec24-like transport protein OS=Arabidopsis thaliana GN=At4g14160 PE=4 SV=1	1	---	----	0,093	0,69413	1967,47	65,50%
Q9ZW33	Mitochondrial import inner membrane translocase subunit TIM10 OS=Arabidopsis thaliana GN=TIM10 PE=1 SV=1	1	---	----	0,083	0,69341	1965,44	65,50%
Q9SGE9	Probable phenylalanine--tRNA ligase beta subunit OS=Arabidopsis thaliana GN=At1g72550 PE=2 SV=1	7	---	----	0,048	0,69421	1967,71	65,50%
Q9FI53	Fumarate hydratase 2, chloroplastic OS=Arabidopsis thaliana GN=FUM2 PE=2 SV=1	1	---	----	-0,325	0,69403	1967,19	65,50%
Q9LSU9	AT3g25550/MWL2_17 OS=Arabidopsis thaliana GN=At3g25545 PE=2 SV=1	1	---	----	0,121	0,69603	1972,86	65,60%
A8MSC5	AT2G47470 protein OS=Arabidopsis thaliana GN=UNE5 PE=2 SV=1	1	---	----	0,4	0,69813	1978,81	65,70%
Q9SRL6	Outer membrane OMP85-like protein OS=Arabidopsis thaliana GN=F9F8.12 PE=2 SV=1	1	---	----	0,124	0,69813	1978,81	65,70%
Q9FGF0	Phosphoglycerate mutase-like protein 1 OS=Arabidopsis thaliana GN=At5g64460 PE=2 SV=1	2	---	----	-0,132	0,69813	1978,81	65,70%
Q8GUG7	DEAD-box ATP-dependent RNA helicase 50 OS=Arabidopsis thaliana GN=RH50 PE=2 SV=2	1	---	----	0,19	0,70013	1984,48	65,80%
O49482;P48523	Cinnamyl alcohol dehydrogenase 5 OS=Arabidopsis thaliana GN=CAD5 PE=1 SV=1	1	---	----	0,089	0,70013	1984,48	65,80%
Q8RWG8	Ran-binding protein 1 homolog b OS=Arabidopsis thaliana GN=RANBP1B PE=1 SV=2	2	---	----	0,077	0,70413	1995,82	65,80%
F4IUJ0	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g26340 PE=4 SV=1	4	---	----	0,063	0,70213	1990,15	65,80%
F4I9J7	Exon junction complex protein OS=Arabidopsis thaliana GN=Y14 PE=1 SV=1	3	---	----	0,055	0,70213	1990,15	65,80%
Q9FLN4	50S ribosomal protein L27, chloroplastic OS=Arabidopsis thaliana GN=RPL27 PE=2 SV=1	3	---	----	0,046	0,69813	1978,81	65,80%
Q9FN41	Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 OS=Arabidopsis thaliana	6	---	----	0,043	0,70013	1984,48	65,80%
Q39085	Delta(24)-sterol reductase OS=Arabidopsis thaliana GN=DIM PE=1 SV=2	9	---	----	0,03	0,70213	1990,15	65,80%
rev_F4IN78	reversed HUA2-like protein 3 OS=Arabidopsis thaliana GN=At2g48160 PE=2 SV=2	1	---	----	-0,12	0,70013	1984,48	65,80%
Q9C718	DEAD-box ATP-dependent RNA helicase 20 OS=Arabidopsis thaliana GN=RH20 PE=2 SV=1	1	---	----	-0,121	0,69813	1978,81	65,80%
Q38854	1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=DXS PE=1 SV=2	1	---	----	0,113	0,70413	1995,82	65,90%
Q93VK9	Kinetochore Spc25 domain-containing protein OS=Arabidopsis thaliana GN=At3g48210 PE=2 SV=1	1	---	----	0,111	0,70413	1995,82	65,90%

P52420	Phosphoribosylamine--glycine ligase, chloroplastic OS=Arabidopsis thaliana GN=PUR2 PE=2 SV=2	1	---	----	0,085	0,70413	1995,82	65,90%
O81149	Proteasome subunit alpha type-5-A OS=Arabidopsis thaliana GN=PAE1 PE=1 SV=1	2	---	----	0,057	0,70413	1995,82	65,90%
Q8LGG8	Universal stress protein A-like protein OS=Arabidopsis thaliana GN=At3g01520 PE=1 SV=2	2	---	----	-0,07	0,70213	1990,15	65,90%
F4I6B2	SIT4 phosphatase-associated family protein OS=Arabidopsis thaliana GN=At1g30470 PE=1 SV=1	2	---	----	-0,071	0,70203	1989,86	65,90%
Q9XFH9	Thioredoxin F2, chloroplastic OS=Arabidopsis thaliana GN=At5g16400 PE=2 SV=1	1	---	----	-0,072	0,70121	1987,55	65,90%
Q8L493	D-amino-acid transaminase, chloroplastic OS=Arabidopsis thaliana GN=DAAT PE=1 SV=1	2	---	----	-0,08	0,70013	1984,48	65,90%
Q8GWS0	Glutaredoxin-C5, chloroplastic OS=Arabidopsis thaliana GN=GRXC5 PE=1 SV=1	1	---	----	-0,118	0,70203	1989,86	65,90%
Q84J75	At4g26580 OS=Arabidopsis thaliana GN=RGTB1 PE=2 SV=1	1	---	----	-0,152	0,70203	1989,86	65,90%
Q94KD0	Transcription initiation factor TFIID subunit 15b OS=Arabidopsis thaliana GN=TAF15B PE=1 SV=1	1	---	----	0,139	0,70580	2000,56	66,00%
Q9LD60	Spliceosomal associated protein 130A OS=Arabidopsis thaliana GN=T26I12.100 PE=4 SV=1	1	---	----	0,09	0,70413	1995,82	66,00%
Q9SMN0	Probable carboxylesterase 12 OS=Arabidopsis thaliana GN=CXE12 PE=1 SV=1	4	---	----	0,049	0,70813	2007,15	66,00%
Q9SGZ5	Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2	7	---	----	0,045	0,70661	2002,86	66,00%
P19456;P20431;P20649	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	5	---	----	-0,045	0,70613	2001,48	66,00%
Q9C5E8	Succinate dehydrogenase subunit 7A, mitochondrial OS=Arabidopsis thaliana GN=SDH7A PE=1 SV=1	1	---	----	-0,111	0,70613	2001,48	66,00%
Q948K8	Ras-related protein RABG3a OS=Arabidopsis thaliana GN=RABG3A PE=2 SV=1	6	---	----	-0,046	0,70813	2007,15	66,10%
Q9ASX5	Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic OS=Arabidopsis thaliana GN=At5g052	3	---	----	-0,057	0,70813	2007,15	66,10%
O23193	CBS domain-containing protein CBSX1, chloroplastic OS=Arabidopsis thaliana GN=CBSX1 PE=1 SV=2	2	---	----	-0,107	0,71013	2012,82	66,10%
P92966	Serine/arginine-rich splicing factor RS41 OS=Arabidopsis thaliana GN=RS41 PE=1 SV=2	1	GASPVAHK	Phospho S3	-0,13	0,71013	2012,82	66,10%
Q8VYC9	Putative uncharacterized protein At1g16210 OS=Arabidopsis thaliana GN=At1g16210 PE=2 SV=1	1	---	----	-0,134	0,70803	2006,87	66,10%
Q93ZV7	La protein 1 OS=Arabidopsis thaliana GN=LA1 PE=1 SV=1	2	---	----	0,088	0,71013	2012,82	66,20%
Q9CAI1	Developmentally-regulated G-protein 2 OS=Arabidopsis thaliana GN=DRG2 PE=2 SV=1	3	---	----	0,072	0,71013	2012,82	66,20%
Q9M2V1	AT3g54360/T12E18_50 OS=Arabidopsis thaliana GN=T12E18_50 PE=2 SV=1	2	---	----	0,071	0,71003	2012,54	66,20%
F4J355	Protein-tyrosine phosphatase OS=Arabidopsis thaliana GN=At3g44620 PE=4 SV=1	1	---	----	-0,084	0,71213	2018,49	66,20%
Q9FPJ2	AT3g62110 OS=Arabidopsis thaliana GN=At3g62110 PE=2 SV=1	1	---	----	-0,194	0,71213	2018,49	66,20%
O22785	Pre-mRNA-processing factor 19 homolog 2 OS=Arabidopsis thaliana GN=PRP19B PE=1 SV=3	3	---	----	0,069	0,71413	2024,16	66,30%
F4JLK2	Probable sucrose-phosphate synthase 4 OS=Arabidopsis thaliana GN=SPS4 PE=1 SV=1	1	---	----	-0,088	0,71213	2018,49	66,30%
Q93VI4	Polyadenylate-binding protein 1 OS=Arabidopsis thaliana GN=PABN1 PE=1 SV=1	1	---	----	-0,101	0,71203	2018,21	66,30%
P51407	60S acidic ribosomal protein P2-1 OS=Arabidopsis thaliana GN=RPP2A PE=2 SV=2	3	---	----	0,041	0,71413	2024,16	66,40%
P46416	Glutathione synthetase, chloroplastic OS=Arabidopsis thaliana GN=GSH2 PE=2 SV=3	8	---	----	0,039	0,71481	2026,10	66,40%
Q9C891	Dirigent protein 20 OS=Arabidopsis thaliana GN=DIR20 PE=2 SV=1	3	---	----	-0,052	0,71413	2024,16	66,40%
F4IJD7	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g15860 PE=1 SV=1	1	LENSVQQGSSPR	Phospho S10	-0,193	0,71613	2029,83	66,40%
Q8VYN9	Putative uncharacterized protein At5g54430 OS=Arabidopsis thaliana GN=PHOS32 PE=2 SV=1	4	---	----	0,061	0,71603	2029,54	66,50%
Q941A6	Succinate dehydrogenase subunit 6, mitochondrial OS=Arabidopsis thaliana GN=SDH6 PE=1 SV=1	2	---	----	-0,104	0,71603	2029,54	66,50%
Q9C524	Probable fructokinase-6, chloroplastic OS=Arabidopsis thaliana GN=At1g66430 PE=2 SV=1	7	---	----	0,037	0,71813	2035,49	66,60%
Q08AA8	At5g27290 OS=Arabidopsis thaliana GN=At5g27290 PE=2 SV=1	1	---	----	-0,116	0,71803	2035,21	66,60%
Q944A6	Sucrose nonfermenting 4-like protein OS=Arabidopsis thaliana GN=SNF4 PE=1 SV=1	1	---	----	-0,199	0,71813	2035,49	66,60%
Q9LSX7	Peroxisome biogenesis protein 22 OS=Arabidopsis thaliana GN=PEX22 PE=1 SV=1	1	---	----	0,154	0,72013	2041,16	66,70%
Q66GR6;Q9M9S3	Single-stranded DNA-binding protein WHY3, chloroplastic OS=Arabidopsis thaliana GN=WHY3 PE=1 SV=1	1	---	----	0,122	0,72013	2041,16	66,70%
O04316;Q9SDM9	Nitrile-specifier protein 4 OS=Arabidopsis thaliana GN=NSP4 PE=2 SV=1	6	---	----	0,038	0,72120	2044,21	66,70%
Q9FX45	At1g73530 OS=Arabidopsis thaliana GN=T9L24.48 PE=2 SV=1	1	---	----	-0,065	0,72003	2040,88	66,70%
Q9C5Y0	Phospholipase D delta OS=Arabidopsis thaliana GN=PLDDELTA PE=1 SV=2	3	---	----	-0,083	0,72013	2041,16	66,70%
Q9SL48	SEC1 family transport protein SLY1 OS=Arabidopsis thaliana GN=SLY1 PE=1 SV=1	1	---	----	0,118	0,72613	2058,17	66,80%
Q9LVI8	Glutamine synthetase cytosolic isozyme 1-3 OS=Arabidopsis thaliana GN=GLN1-3 PE=1 SV=1	2	---	----	0,08	0,72421	2052,74	66,80%
F4HYF3	Bifunctional D-cysteine desulfhydrase/1-aminocyclopropane-1-carboxylate deaminase, mitochondrial OS=Arabidopsis t	3	---	----	0,063	0,72413	2052,50	66,80%
Q9M1X8	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=F24G16.250 PE=2 SV=1	4	---	----	-0,064	0,72213	2046,83	66,80%
Q9M060	Eukaryotic translation initiation factor 6-2 OS=Arabidopsis thaliana GN=EIF6-2 PE=2 SV=1	1	---	----	-0,096	0,72203	2046,55	66,80%
rev_Q9M7Z1	reversed Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochonc	1	---	----	-0,126	0,72413	2052,50	66,80%
O04036	Sugar transporter ERD6 OS=Arabidopsis thaliana GN=ERD6 PE=1 SV=3	1	---	----	0,306	0,72603	2057,88	66,90%
Q9FH05	Serine carboxypeptidase-like 42 OS=Arabidopsis thaliana GN=SCPL42 PE=2 SV=1	3	---	----	0,074	0,72613	2058,17	66,90%
Q9FN05	Probable glucan 1,3-alpha-glucosidase OS=Arabidopsis thaliana GN=PSL5 PE=1 SV=1	4	---	----	0,071	0,72413	2052,50	66,90%
P11035;P11832	Nitrate reductase [NADH] 2 OS=Arabidopsis thaliana GN=NIA2 PE=1 SV=1	1	---	----	0,068	0,72403	2052,22	66,90%
Q9SCT5	AT3g51730/T18N14_110 OS=Arabidopsis thaliana GN=T18N14.110 PE=2 SV=1	2	---	----	0,068	0,72803	2063,55	66,90%
Q9ZVJ6	Annexin D4 OS=Arabidopsis thaliana GN=ANN4 PE=2 SV=1	4	---	----	0,039	0,72921	2066,91	66,90%
Q9S7B5	Threonine synthase 1, chloroplastic OS=Arabidopsis thaliana GN=TS1 PE=1 SV=1	8	---	----	0,029	0,72341	2050,47	66,90%
P21240;Q9LJE4	Chaperonin 60 subunit beta 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60B1 PE=1 SV=3	10	---	----	0,018	0,72741	2061,81	66,90%

Q9FN48	Calcium sensing receptor, chloroplastic OS=Arabidopsis thaliana GN=CAS PE=1 SV=1	15	---	----	-0,017	0,72741	2061,81	66,90%
Q9C969	At1g80360 OS=Arabidopsis thaliana GN=F5I6.11 PE=2 SV=1	5	---	----	-0,044	0,72613	2058,17	66,90%
B9DHQ0	Tubulin alpha-5 chain OS=Arabidopsis thaliana GN=TUBA5 PE=1 SV=2	4	---	----	-0,051	0,72813	2063,84	66,90%
Q9XI84	[Fructose-bisphosphate aldolase]-lysine N-methyltransferase, chloroplastic OS=Arabidopsis thaliana GN=LSMT-L PE=1 S	3	---	----	-0,075	0,72613	2058,17	66,90%
Q940U6	Protein FLUORESCENT IN BLUE LIGHT, chloroplastic OS=Arabidopsis thaliana GN=FLU PE=1 SV=1	2	---	----	-0,087	0,72413	2052,50	66,90%
O80480	Importin subunit alpha-4 OS=Arabidopsis thaliana GN=IMPA4 PE=1 SV=1	2	---	----	-0,097	0,72813	2063,84	66,90%
Q8H0U4	Transportin-1 OS=Arabidopsis thaliana GN=TRN1 PE=1 SV=1	3	---	----	-0,101	0,72413	2052,50	66,90%
Q94AG1	AT3g07470/F21O3_18 OS=Arabidopsis thaliana GN=At3g07470 PE=2 SV=1	1	---	----	-0,101	0,72813	2063,84	66,90%
Q9M903	Protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic OS=Arabidopsis thaliana GN=TGD4 PE=1 SV=1	1	---	----	-0,116	0,72603	2057,88	66,90%
F4JS86	RING/U-box domain-containing protein OS=Arabidopsis thaliana GN=At4g13100 PE=4 SV=1	1	---	----	-0,148	0,72803	2063,55	66,90%
Q9ZPF5	Arginase 2, mitochondrial OS=Arabidopsis thaliana GN=ARGAH2 PE=2 SV=1	5	---	----	-0,041	0,72800	2063,48	67,00%
F4HS99	Tetratricopeptide repeat-containing protein OS=Arabidopsis thaliana GN=At1g01320 PE=1 SV=1	10	---	----	0,041	0,73203	2074,89	67,10%
O81645	Villin-3 OS=Arabidopsis thaliana GN=VLN3 PE=1 SV=2	9	---	----	-0,031	0,73213	2075,17	67,10%
Q9C685	At1g51100 OS=Arabidopsis thaliana GN=F23H24.6 PE=2 SV=1	5	---	----	-0,044	0,73213	2075,17	67,10%
P69834	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic OS=Arabidopsis thaliana GN=ISPD PE=1 SV=1	5	---	----	-0,051	0,73213	2075,17	67,10%
Q8VZ34	Ankyrin repeat family protein OS=Arabidopsis thaliana GN=At2g26210 PE=2 SV=1	2	---	----	0,075	0,73403	2080,56	67,20%
O23714;O24633	Proteasome subunit beta type-2-A OS=Arabidopsis thaliana GN=PBD1 PE=1 SV=1	4	---	----	0,043	0,73403	2080,56	67,20%
O80983;Q8W585	ATP-dependent zinc metalloprotease FTSH 4, mitochondrial OS=Arabidopsis thaliana GN=FTSH4 PE=1 SV=2	1	---	----	-0,049	0,73613	2086,51	67,20%
O80574	4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic OS=Arabidopsis thaliana GN=DAPB1 PE=2 SV=2	2	---	----	-0,084	0,73203	2074,89	67,20%
O04848;Q9S9K7	Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1	2	---	----	-0,092	0,73413	2080,84	67,20%
Q9SJH9	Expressed protein OS=Arabidopsis thaliana GN=At2g42770 PE=2 SV=2	1	---	----	0,12	0,73613	2086,51	67,30%
P93732	Proline iminopeptidase OS=Arabidopsis thaliana GN=PIP PE=2 SV=3	5	---	----	0,04	0,73613	2086,51	67,30%
Q9ZNT7	Prohibitin-2, mitochondrial OS=Arabidopsis thaliana GN=PHB2 PE=1 SV=1	4	---	----	0,036	0,73603	2086,23	67,30%
O24616;P30186	Proteasome subunit alpha type-7-B OS=Arabidopsis thaliana GN=PAD2 PE=1 SV=2	6	---	----	-0,034	0,73613	2086,51	67,30%
Q9LJR2	Lectin-like protein LEC OS=Arabidopsis thaliana GN=LEC PE=1 SV=1	5	---	----	-0,043	0,73613	2086,51	67,30%
Q9SS48	Glycerol-3-phosphate dehydrogenase SDP6, mitochondrial OS=Arabidopsis thaliana GN=SDP6 PE=1 SV=1	3	---	----	-0,062	0,73541	2084,49	67,30%
rev_Q8VZA0	reversed Protein SIEL OS=Arabidopsis thaliana GN=SIEL PE=1 SV=1	1	---	----	0,121	0,74613	2114,85	67,40%
Q9SRK5	Phosphoglucan phosphatase LSF2, chloroplastic OS=Arabidopsis thaliana GN=LSF2 PE=1 SV=1	2	---	----	0,087	0,73803	2091,89	67,40%
Q8GYA6	26S proteasome non-ATPase regulatory subunit 13 homolog B OS=Arabidopsis thaliana GN=RPN9B PE=1 SV=1	1	---	----	0,078	0,74013	2097,85	67,40%
Q38954	Inorganic phosphate transporter 2-1, chloroplastic OS=Arabidopsis thaliana GN=PHT2-1 PE=1 SV=1	3	---	----	0,063	0,73813	2092,18	67,40%
P51412	50S ribosomal protein L21, chloroplastic OS=Arabidopsis thaliana GN=RPL21 PE=2 SV=1	5	---	----	-0,036	0,74013	2097,85	67,40%
F4HXZ1	Endosomal targeting BRO1-like domain-containing protein OS=Arabidopsis thaliana GN=At1g15130 PE=1 SV=1	5	---	----	-0,05	0,74013	2097,85	67,40%
P92985;Q9LMK7	Ran-binding protein 1 homolog c OS=Arabidopsis thaliana GN=RANBP1C PE=2 SV=1	2	---	----	-0,057	0,74613	2114,85	67,40%
Q949Q7	Serine carboxypeptidase-like 29 OS=Arabidopsis thaliana GN=SCPL29 PE=2 SV=1	1	---	----	-0,082	0,74041	2098,66	67,40%
rev_Q9FK30	reversed At5g50420 OS=Arabidopsis thaliana GN=At5g50420 PE=2 SV=1	1	---	----	-0,095	0,73880	2094,09	67,40%
O23404	Pyruvate, phosphate dikinase 1, chloroplastic OS=Arabidopsis thaliana GN=PPDK PE=1 SV=2	1	GGMTSHAAVVAR	Phospho S5	0,209	0,74413	2109,18	67,50%
Q9MA55	Acyl-CoA-binding domain-containing protein 4 OS=Arabidopsis thaliana GN=ACBP4 PE=1 SV=1	1	---	----	0,115	0,74281	2105,46	67,50%
Q9SUR9	Protein SGT1 homolog A OS=Arabidopsis thaliana GN=SGT1A PE=1 SV=1	1	---	----	0,097	0,74213	2103,51	67,50%
Q9LT68	Genomic DNA, chromosome 3, P1 clone: MLD14 OS=Arabidopsis thaliana GN=NHD1 PE=2 SV=1	1	---	----	0,093	0,74603	2114,57	67,50%
Q9ZV34	At2g28790 OS=Arabidopsis thaliana GN=CBP1 PE=2 SV=1	1	---	----	0,083	0,74013	2097,85	67,50%
P93009	Protein CutA, chloroplastic OS=Arabidopsis thaliana GN=CUTA PE=1 SV=1	1	---	----	0,072	0,74003	2097,56	67,50%
P11139	Tubulin alpha-1 chain OS=Arabidopsis thaliana GN=TUBA1 PE=2 SV=1	3	---	----	0,057	0,74461	2110,56	67,50%
Q9ZVA2	At1g78830/F9K20_12 OS=Arabidopsis thaliana GN=F9K20.12 PE=2 SV=1	6	---	----	-0,025	0,73961	2096,39	67,50%
Q29Q26	Ankyrin repeat-containing 2B OS=Arabidopsis thaliana GN=AKR2B PE=2 SV=1	4	---	----	-0,034	0,74413	2109,18	67,50%
Q9FNM5	Translation factor GUF1 homolog, chloroplastic OS=Arabidopsis thaliana GN=At5g08650 PE=2 SV=2	6	---	----	-0,034	0,74613	2114,85	67,50%
Q9M385	50S ribosomal protein L17, chloroplastic OS=Arabidopsis thaliana GN=RPL17 PE=2 SV=1	5	---	----	-0,039	0,74413	2109,18	67,50%
Q8RX79	Peptide chain release factor APG3, chloroplastic OS=Arabidopsis thaliana GN=APG3 PE=2 SV=1	5	---	----	-0,043	0,74213	2103,51	67,50%
Q9FN42	ATP-dependent Clp protease proteolytic subunit 2, mitochondrial OS=Arabidopsis thaliana GN=CLPP2 PE=1 SV=1	3	---	----	-0,06	0,74613	2114,85	67,50%
Q96321	Importin subunit alpha-1 OS=Arabidopsis thaliana GN=IMPA1 PE=1 SV=2	2	---	----	-0,067	0,74003	2097,56	67,50%
Q67Y83	Serine carboxypeptidase-like 51 OS=Arabidopsis thaliana GN=SCPL51 PE=2 SV=2	2	---	----	-0,091	0,74440	2109,97	67,50%
Q940P0	AT5g03660/F17C15_80 OS=Arabidopsis thaliana GN=At5g03660 PE=2 SV=1	1	---	----	-0,097	0,74613	2114,85	67,50%
Q39097	Eukaryotic peptide chain release factor subunit 1-1 OS=Arabidopsis thaliana GN=ERF1-1 PE=1 SV=2	1	---	----	-0,106	0,74541	2112,83	67,50%
F4KF14	AAA-type ATPase family protein OS=Arabidopsis thaliana GN=At5g64580 PE=4 SV=1	2	---	----	-0,115	0,74603	2114,57	67,50%
Q38821	Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Arabidopsis thaliana GN=PP2A	1	---	----	-0,184	0,74213	2103,51	67,50%
B9DHQ0;P11139	Tubulin alpha-5 chain OS=Arabidopsis thaliana GN=TUBA5 PE=1 SV=2	1	---	----	0,243	0,74403	2108,90	67,60%

Q56ZN6	Pyrophosphate-energized membrane proton pump 2 OS=Arabidopsis thaliana GN=AVPL1 PE=1 SV=2	1	---	----	0,105	0,74603	2114,57	67,60%
O04193	LIM domain-containing protein WLIM2a OS=Arabidopsis thaliana GN=WLIN2A PE=1 SV=1	1	---	----	0,099	0,74813	2120,52	67,60%
Q9FKH6	Cytochrome b561 and DOMON domain-containing protein At5g35735 OS=Arabidopsis thaliana GN=At5g35735 PE=2 SV	1	---	----	0,092	0,74413	2109,18	67,60%
Q9FHB8	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g52420 PE=4 SV=1	2	---	----	0,062	0,74413	2109,18	67,60%
Q38900	Peptidyl-prolyl cis-trans isomerase CYP19-1 OS=Arabidopsis thaliana GN=CYP19-1 PE=1 SV=1	3	---	----	0,032	0,74803	2120,24	67,60%
Q94JQ4	Reactive Intermediate Deaminase A, chloroplastic OS=Arabidopsis thaliana GN=RIDA PE=1 SV=1	8	---	----	-0,022	0,74581	2113,96	67,60%
Q9SJ81	Fasciclin-like arabinogalactan protein 7 OS=Arabidopsis thaliana GN=FLA7 PE=1 SV=1	3	---	----	-0,057	0,74413	2109,18	67,60%
O64760	At2g34970 OS=Arabidopsis thaliana GN=At2g34970 PE=1 SV=1	1	---	----	-0,126	0,75021	2126,44	67,60%
Q6NQL4;Q9AV97	2-dehydro-3-deoxyphosphooctonate aldolase 2 OS=Arabidopsis thaliana GN=KDSA2 PE=1 SV=1	1	---	----	-0,268	0,75012	2126,19	67,60%
Q9SIP0	Ras-related protein RABA5d OS=Arabidopsis thaliana GN=RABA5D PE=1 SV=1	2	---	----	0,075	0,75002	2125,90	67,70%
O23523	AT4g16830/dl4440w OS=Arabidopsis thaliana GN=dl4440w PE=2 SV=1	4	---	----	-0,04	0,75012	2126,19	67,70%
O22682	Probable S-sulfocysteine synthase, chloroplastic OS=Arabidopsis thaliana GN=At3g03630 PE=1 SV=1	1	---	----	-0,101	0,75012	2126,19	67,70%
Q9SGW3	26S proteasome non-ATPase regulatory subunit 8 homolog A OS=Arabidopsis thaliana GN=RPN12A PE=1 SV=1	3	---	----	0,062	0,75212	2131,86	67,80%
Q9SU63	Aldehyde dehydrogenase family 2 member B4, mitochondrial OS=Arabidopsis thaliana GN=ALDH2B4 PE=2 SV=1	16	---	----	0,022	0,75212	2131,86	67,80%
Q9FPJ8	Polyadenylate-binding protein RBP45A OS=Arabidopsis thaliana GN=RBP45A PE=2 SV=1	3	---	----	0,068	0,75341	2135,51	67,90%
Q9XFH8	Thioredoxin F1, chloroplastic OS=Arabidopsis thaliana GN=At3g02730 PE=1 SV=2	2	---	----	-0,036	0,75412	2137,52	67,90%
Q9FVV7	Organellar dna-binding protein OS=Arabidopsis thaliana GN=F3I17.4 PE=2 SV=1	1	---	----	-0,082	0,75412	2137,52	67,90%
Q39253	Vacuolar cation/proton exchanger 1 OS=Arabidopsis thaliana GN=CAX1 PE=1 SV=3	1	---	----	-0,198	0,75412	2137,52	67,90%
O23166	Thioredoxin-like protein HCF164, chloroplastic OS=Arabidopsis thaliana GN=HCF164 PE=2 SV=2	2	---	----	0,114	0,75612	2143,19	68,00%
Q9SZN1	V-type proton ATPase subunit B2 OS=Arabidopsis thaliana GN=VHA-B2 PE=1 SV=1	3	---	----	0,036	0,75641	2144,01	68,00%
F4KIH8	WD40 domain-containing protein OS=Arabidopsis thaliana GN=At5g24710 PE=4 SV=1	2	---	----	-0,065	0,75612	2143,19	68,00%
Q5XEV6	At4g24090 OS=Arabidopsis thaliana GN=At4g24090 PE=2 SV=1	1	---	----	-0,11	0,75612	2143,19	68,00%
rev_Q0WUG6	reversed Subtilisin-like protease SBT6.1 OS=Arabidopsis thaliana GN=SBT6.1 PE=1 SV=1	1	---	----	-0,21	0,75612	2143,19	68,00%
Q9LQI9	Oligouridylate-binding protein 1B OS=Arabidopsis thaliana GN=UBP1B PE=1 SV=1	1	---	----	0,11	0,76012	2154,53	68,10%
P46283	Sedoheptulose-1,7-bisphosphatase, chloroplastic OS=Arabidopsis thaliana GN=At3g55800 PE=2 SV=1	13	---	----	-0,016	0,75861	2150,24	68,10%
O82663	Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial OS=Arabidopsis thaliana GN=SDH1-1 PE=	6	---	----	-0,033	0,76012	2154,53	68,10%
F4KCR0	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g16280 PE=4 SV=1	1	---	----	-0,094	0,75812	2148,86	68,10%
rev_Q9SB63	reversed Protein MODIFIER OF SNC1 1 OS=Arabidopsis thaliana GN=MOS1 PE=1 SV=2	1	---	----	-0,133	0,76012	2154,53	68,10%
Q9FNA0	At5g59610 OS=Arabidopsis thaliana GN=At5g59610 PE=2 SV=1	1	---	----	0,196	0,76212	2160,20	68,20%
Q4PSZ5	Putative cinnamyl-alcohol dehydrogenase OS=Arabidopsis thaliana GN=At1g51410 PE=2 SV=1	1	---	----	0,1	0,76212	2160,20	68,20%
Q944H0;Q9C6B9	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2	1	---	----	0,099	0,76412	2165,87	68,20%
Q9FY49	Leukotriene A-4 hydrolase homolog OS=Arabidopsis thaliana GN=LKHA4 PE=2 SV=1	2	---	----	0,089	0,76000	2154,18	68,20%
O04147	Cyclic phosphodiesterase OS=Arabidopsis thaliana GN=At4g18930 PE=1 SV=1	2	---	----	0,066	0,76202	2159,91	68,20%
Q9SHU7	Protein TIC 21, chloroplastic OS=Arabidopsis thaliana GN=TIC21 PE=1 SV=1	1	---	----	0,058	0,76002	2154,25	68,20%
P46010	Nitrilase 3 OS=Arabidopsis thaliana GN=NIT3 PE=1 SV=1	2	---	----	0,048	0,76661	2172,92	68,20%
Q8L785	Glycine--tRNA ligase 2, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLYRS-2 PE=2 SV=1	7	---	----	0,038	0,76212	2160,20	68,20%
Q9LIM9;Q9LIN0	Major latex protein-like OS=Arabidopsis thaliana GN=At3g26460 PE=4 SV=1	3	---	----	0,032	0,76002	2154,25	68,20%
P46421	Glutathione S-transferase U5 OS=Arabidopsis thaliana GN=GSTU5 PE=2 SV=1	8	---	----	0,023	0,76001	2154,21	68,20%
P11035	Nitrate reductase [NADH] 2 OS=Arabidopsis thaliana GN=NIA2 PE=1 SV=1	8	---	----	-0,04	0,76612	2171,53	68,20%
Q67Y99	Putative uncharacterized protein At2g03390 OS=Arabidopsis thaliana GN=At2g03390 PE=2 SV=1	3	---	----	-0,051	0,76212	2160,20	68,20%
P57742	Probable prefoldin subunit 5 OS=Arabidopsis thaliana GN=At5g23290 PE=2 SV=1	2	---	----	-0,07	0,76412	2165,87	68,20%
P32746	Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Arabidopsis thaliana GN=PYRD PE=1 SV=2	1	---	----	-0,116	0,76612	2171,53	68,20%
Q9SI77	At1g62730 OS=Arabidopsis thaliana GN=At1g62730 PE=2 SV=1	1	---	----	0,19	0,76612	2171,53	68,30%
F4KE93	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g23700 PE=4 SV=1	1	---	----	0,105	0,76612	2171,53	68,30%
P93828	F19P19.27 protein OS=Arabidopsis thaliana GN=F19P19.27 PE=2 SV=1	1	---	----	0,099	0,76812	2177,20	68,30%
Q9LML6	UDP-glycosyltransferase 71C4 OS=Arabidopsis thaliana GN=UGT71C4 PE=2 SV=2	1	---	----	0,09	0,76402	2165,58	68,30%
Q9ZRT5	Glutathione S-transferase T1 OS=Arabidopsis thaliana GN=GSTT1 PE=2 SV=1	2	---	----	0,051	0,76812	2177,20	68,30%
Q9ZUB3	Spermidine synthase 1 OS=Arabidopsis thaliana GN=SPDSYN1 PE=1 SV=1	4	---	----	0,04	0,76612	2171,53	68,30%
P34795	Glucose-6-phosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=PGIC PE=1 SV=1	8	---	----	0,031	0,76612	2171,53	68,30%
Q94AM1	Organellar oligopeptidase A, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OOP PE=1 SV=1	8	---	----	0,026	0,76412	2165,87	68,30%
O04983	Biotin carboxylase, chloroplastic OS=Arabidopsis thaliana GN=CAC2 PE=1 SV=1	14	---	----	-0,021	0,76701	2174,05	68,30%
Q9M099	Serine carboxypeptidase 24 OS=Arabidopsis thaliana GN=SCPL24 PE=1 SV=1	2	---	----	-0,076	0,76400	2165,52	68,30%
Q9C8I1	Putative uncharacterized protein At1g51730 OS=Arabidopsis thaliana GN=F19C24.6 PE=2 SV=1	1	---	----	-0,142	0,76402	2165,58	68,30%
Q9C8W7	At1g71950 OS=Arabidopsis thaliana GN=F17M19.10 PE=2 SV=1	1	---	----	0,08	0,77012	2182,87	68,40%
O04023	At1g09070/F7G19_6 OS=Arabidopsis thaliana GN=F7G19.6 PE=2 SV=1	3	---	----	0,046	0,76602	2171,25	68,40%

P48348	14-3-3-like protein GF14 kappa OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=2	3	---	----	0,041	0,76612	2171,53	68,40%
Q84WU2;Q9FPT1	Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana GN=UBP13 PE=1 SV=1	5	---	----	-0,039	0,77012	2182,87	68,40%
Q9FKE9	Protein ROOT HAIR DEFECTIVE 3 homolog 2 OS=Arabidopsis thaliana GN=At5g45160 PE=2 SV=1	1	---	----	0,202	0,77612	2199,88	68,50%
Q9SHC8	Vesicle-associated protein 1-2 OS=Arabidopsis thaliana GN=PVA12 PE=1 SV=1	1	---	----	0,158	0,77212	2188,54	68,50%
Q8LPK7	Putative myosin heavy chain OS=Arabidopsis thaliana GN=At1g24560 PE=2 SV=1	1	---	----	0,156	0,77212	2188,54	68,50%
Q93V72	PLASMODESMATA CALLOSE-BINDING PROTEIN 4 OS=Arabidopsis thaliana GN=PDCB4 PE=1 SV=1	1	---	----	0,095	0,77012	2182,87	68,50%
Q9C958;Q9FFP9	Serine/threonine-protein kinase SRK2B OS=Arabidopsis thaliana GN=SRK2B PE=1 SV=1	1	---	----	0,084	0,77212	2188,54	68,50%
Q9SAH1	At1g80890 OS=Arabidopsis thaliana GN=F23A5.25 PE=2 SV=1	2	---	----	0,058	0,77412	2194,21	68,50%
O82796	Phosphoserine phosphatase, chloroplastic OS=Arabidopsis thaliana GN=PSP PE=1 SV=2	3	---	----	0,045	0,77221	2188,79	68,50%
Q9M876	Tyrosine--tRNA ligase OS=Arabidopsis thaliana GN=F16B3.29 PE=2 SV=1	3	---	----	0,044	0,77612	2199,88	68,50%
P48523	Cinnamyl alcohol dehydrogenase 4 OS=Arabidopsis thaliana GN=CAD4 PE=1 SV=1	6	---	----	0,03	0,77141	2186,53	68,50%
Q9SGC1	Probable phosphoglucomutase, cytoplasmic 2 OS=Arabidopsis thaliana GN=At1g70730 PE=2 SV=1	16	---	----	0,016	0,77812	2205,54	68,50%
Q8RWN5	Glycine-rich RNA-binding protein RZ1C OS=Arabidopsis thaliana GN=RZ1C PE=1 SV=1	5	---	----	-0,039	0,77412	2194,21	68,50%
Q9ZPY7	Exportin-2 OS=Arabidopsis thaliana GN=CAS PE=2 SV=1	5	---	----	-0,043	0,77012	2182,87	68,50%
Q9LZ26	Aspartyl aminopeptidase OS=Arabidopsis thaliana GN=T1E3_70 PE=3 SV=1	2	---	----	-0,08	0,77412	2194,21	68,50%
rev_Q8H1D7	reversed Transcription factor GTE5, chloroplastic OS=Arabidopsis thaliana GN=GTE5 PE=1 SV=1	1	---	----	-0,086	0,77412	2194,21	68,50%
P52901;Q8H1Y0	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=E1 ALPHA PE=2 S	1	YHGHSMSDPGSTYR	Phospho S5	-0,314	0,77212	2188,54	68,50%
Q0WPK4	AT1G79090 protein OS=Arabidopsis thaliana GN=At1g79090 PE=1 SV=1	1	---	----	0,193	0,78412	2222,55	68,60%
Q8H104;Q9M084	Asx tRNA synthetase (AspRS/AsnRS) class II core domain-contating protein OS=Arabidopsis thaliana GN=At4g26870 PE=	1	---	----	0,093	0,77612	2199,88	68,60%
Q9FKI4	Peptide alpha-N-acetyltransferase OS=Arabidopsis thaliana GN=MXE10.5 PE=2 SV=1	2	---	----	0,091	0,78212	2216,88	68,60%
Q93YP9	Sugar transporter ERD6-like 4 OS=Arabidopsis thaliana GN=At1g19450 PE=2 SV=1	1	---	----	0,087	0,78412	2222,55	68,60%
Q9M8Z8	Probable pectate lyase 8 OS=Arabidopsis thaliana GN=At3g07010 PE=2 SV=1	1	---	----	0,083	0,77402	2193,92	68,60%
rev_Q84VV0	reversed At3g58830 OS=Arabidopsis thaliana GN=At3g58830 PE=2 SV=1	1	---	----	0,08	0,78012	2211,21	68,60%
Q6NQL4	2-dehydro-3-deoxyphosphooctonate aldolase 2 OS=Arabidopsis thaliana GN=KDSA2 PE=1 SV=1	1	---	----	0,069	0,78101	2213,74	68,60%
P32826	Serine carboxypeptidase-like 49 OS=Arabidopsis thaliana GN=SCPL49 PE=2 SV=2	2	---	----	0,051	0,77581	2199,00	68,60%
O80575	6,7-dimethyl-8-ribityllumazine synthase, chloroplastic OS=Arabidopsis thaliana GN=At2g44050 PE=2 SV=1	3	---	----	0,05	0,78061	2212,60	68,60%
Q9LS94;Q9XI98	Ras-related protein RABG3f OS=Arabidopsis thaliana GN=RABG3F PE=2 SV=1	4	---	----	0,048	0,77602	2199,59	68,60%
P93306	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2 OS=Arabidopsis thaliana GN=NAD7 PE=2 SV=2	5	---	----	0,045	0,77402	2193,92	68,60%
Q9FGI6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial OS=Arabidopsis thaliana GN=EMB1467 PE=1 S	12	---	----	0,023	0,77781	2204,67	68,60%
P59259	Histone H4 OS=Arabidopsis thaliana GN=At1g07660 PE=1 SV=2	5	---	----	-0,021	0,78412	2222,55	68,60%
Q9LVW7	Carbamoyl-phosphate synthase small chain, chloroplastic OS=Arabidopsis thaliana GN=CARA PE=1 SV=1	8	---	----	-0,025	0,77612	2199,88	68,60%
Q06588	1-aminocyclopropane-1-carboxylate oxidase 4 OS=Arabidopsis thaliana GN=ACO4 PE=1 SV=2	5	---	----	-0,034	0,77801	2205,23	68,60%
O64883	Beta-glucosidase 26, peroxisomal OS=Arabidopsis thaliana GN=BGLU26 PE=1 SV=1	3	---	----	-0,048	0,78412	2222,55	68,60%
Q9C9C4	Enolase 1, chloroplastic OS=Arabidopsis thaliana GN=ENO1 PE=1 SV=1	5	---	----	-0,049	0,78012	2211,21	68,60%
Q9XGZ3	Early nodulin-related protein OS=Arabidopsis thaliana GN=T1N24.3 PE=2 SV=1	2	---	----	-0,051	0,77802	2205,26	68,60%
Q9FUS6	Glutathione S-transferase U13 OS=Arabidopsis thaliana GN=GSTU13 PE=2 SV=1	1	---	----	-0,054	0,78012	2211,21	68,60%
B9DHD3	Histidinol-phosphate aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN6A PE=2 SV=1	2	---	----	-0,063	0,77612	2199,88	68,60%
Q94BR1	MA3 domain-containing protein OS=Arabidopsis thaliana GN=At5g63190 PE=2 SV=1	3	---	----	-0,066	0,77381	2193,33	68,60%
Q9LVM1	ABC transporter B family member 25, mitochondrial OS=Arabidopsis thaliana GN=ABCB25 PE=1 SV=1	2	---	----	-0,067	0,78212	2216,88	68,60%
Q9M088	Glucan endo-1,3-beta-glucosidase 5 OS=Arabidopsis thaliana GN=At4g31140 PE=1 SV=1	2	---	----	-0,073	0,78212	2216,88	68,60%
Q9LX99	Kinesin-like protein KCA1 OS=Arabidopsis thaliana GN=KCA1 PE=1 SV=1	1	LNLEEGSSPIPNPSTA	none	-0,096	0,77802	2205,26	68,60%
Q9XIE2	ABC transporter G family member 36 OS=Arabidopsis thaliana GN=ABCG36 PE=1 SV=1	1	SLSTADGNR	Phospho S3	-0,199	0,77812	2205,54	68,60%
Q9FEF9	At2g20820 OS=Arabidopsis thaliana GN=At2g20820 PE=2 SV=1	1	---	----	-0,229	0,77812	2205,54	68,60%
Q9SHS7	Serine/threonine-protein phosphatase BSL3 OS=Arabidopsis thaliana GN=BSL3 PE=1 SV=2	1	QLSIDQFENEGR	Phospho S3	-0,229	0,78012	2211,21	68,60%
Q9XF87	At3g27700 OS=Arabidopsis thaliana GN=Lhcb2:4 PE=2 SV=1	1	---	----	0,257	0,78612	2228,22	68,70%
Q56Y19	Putative uncharacterized protein At2g43240 OS=Arabidopsis thaliana GN=At2g43235 PE=2 SV=1	1	---	----	0,14	0,79212	2245,22	68,70%
Q9SR00	Pentatricopeptide repeat-containing protein At3g04760, chloroplastic OS=Arabidopsis thaliana GN=At3g04760 PE=2 S	1	---	----	0,099	0,78612	2228,22	68,70%
Q9XIW1	Probable xyloglucan endotransglucosylase/hydrolase protein 5 OS=Arabidopsis thaliana GN=XTH5 PE=2 SV=1	1	---	----	0,095	0,79012	2239,55	68,70%
Q9C907	Glycerophosphodiester phosphodiesterase GDPD5 OS=Arabidopsis thaliana GN=GDPD5 PE=2 SV=1	1	---	----	0,085	0,78012	2211,21	68,70%
Q9M1Y7	Putative uncharacterized protein F24G16.140 OS=Arabidopsis thaliana GN=F24G16.140 PE=4 SV=1	2	---	----	0,063	0,78212	2216,88	68,70%
O49485;Q9LT69	D-3-phosphoglycerate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=PGDH1 PE=1 SV=1	1	---	----	0,06	0,79061	2240,95	68,70%
F4JTN1	Patched family protein OS=Arabidopsis thaliana GN=At4g38350 PE=4 SV=1	4	---	----	0,052	0,78401	2222,24	68,70%
Q42560;Q94A28;Q9SIB9	Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2	1	---	----	0,046	0,78812	2233,89	68,70%
P24636;P29517;Q56YW9	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	1	---	----	0,041	0,78212	2216,88	68,70%
P47999	Cysteine synthase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=OASB PE=1 SV=2	15	---	----	0,017	0,78402	2222,27	68,70%

Q94A65	Rhodanese-like domain-containing protein 14, chloroplastic OS=Arabidopsis thaliana GN=At4g27700 PE=2 SV=1	5	---	----	-0,03	0,78812	2233,89	68,70%
Q8GWE1	Ubiquitin carboxyl-terminal hydrolase OS=Arabidopsis thaliana GN=UCH3 PE=2 SV=1	2	---	----	-0,054	0,78412	2222,55	68,70%
Q9FG81	Aluminium induced protein with YGL and LRDR motifs OS=Arabidopsis thaliana GN=At5g43830 PE=1 SV=1	2	---	----	-0,068	0,78412	2222,55	68,70%
Q9SFB3	F17A17.35 protein OS=Arabidopsis thaliana GN=F17A17.35 PE=2 SV=1	1	---	----	-0,081	0,78012	2211,21	68,70%
Q9SVD7	Ubiquitin-conjugating enzyme E2 variant 1D OS=Arabidopsis thaliana GN=UEV1D PE=1 SV=1	1	---	----	-0,138	0,78612	2228,22	68,70%
Q9SBA5	Inositol-tetrakisphosphate 1-kinase 1 OS=Arabidopsis thaliana GN=ITPK1 PE=1 SV=1	1	---	----	-0,147	0,78412	2222,55	68,70%
Q8W4C8	ADP-ribosylation factor-like A1A OS=Arabidopsis thaliana GN=K12B20.15 PE=2 SV=1	1	---	----	-0,185	0,78212	2216,88	68,70%
F4IP13	Protein SHOOT GRAVITROPISM 6 OS=Arabidopsis thaliana GN=SGR6 PE=2 SV=1	1	---	----	0,205	0,79412	2250,89	68,80%
F4ICZ7	At1g59520 OS=Arabidopsis thaliana GN=CW7 PE=4 SV=1	1	---	----	0,16	0,78741	2231,88	68,80%
Q8LG77	Isocitrate dehydrogenase [NAD] catalytic subunit 6, mitochondrial OS=Arabidopsis thaliana GN=IDH6 PE=2 SV=2	1	---	----	0,133	0,79212	2245,22	68,80%
rev_P92943	reversed Chloride channel protein CLC-d OS=Arabidopsis thaliana GN=CLC-D PE=1 SV=2	1	---	----	0,091	0,79402	2250,61	68,80%
Q8GXE7	At5g15320 OS=Arabidopsis thaliana GN=At5g15320 PE=2 SV=1	1	---	----	0,09	0,79612	2256,56	68,80%
rev_F4KFV7	reversed ATP-dependent RNA helicase SUV3L, mitochondrial OS=Arabidopsis thaliana GN=At5g39840 PE=3 SV=1	1	---	----	0,08	0,79212	2245,22	68,80%
Q67XD6	At2g32500 OS=Arabidopsis thaliana GN=At2g32500 PE=2 SV=1	1	---	----	0,08	0,79612	2256,56	68,80%
Q9LSY8	UDP-glycosyltransferase 71B2 OS=Arabidopsis thaliana GN=UGT71B2 PE=1 SV=1	2	---	----	0,07	0,79012	2239,55	68,80%
Q9SW43	AT4g34920/F11I11_160 OS=Arabidopsis thaliana GN=T11I11.160 PE=2 SV=1	4	---	----	0,044	0,79412	2250,89	68,80%
Q9LFL3	AT5g16880/F2K13_30 OS=Arabidopsis thaliana GN=F2K13_30 PE=2 SV=1	6	---	----	0,038	0,79012	2239,55	68,80%
Q8LCE1;Q9LVI8	Glutamine synthetase cytosolic isozyme 1-2 OS=Arabidopsis thaliana GN=GLN1-2 PE=1 SV=2	3	---	----	0,03	0,79061	2240,95	68,80%
Q9C8X4	GrpE protein homolog OS=Arabidopsis thaliana GN=F7F23.11 PE=2 SV=1	4	---	----	0,03	0,79612	2256,56	68,80%
P25873	50S ribosomal protein L15, chloroplastic OS=Arabidopsis thaliana GN=RPL15 PE=2 SV=2	8	---	----	0,022	0,78802	2233,60	68,80%
Q9STE8	Protein TOC75-3, chloroplastic OS=Arabidopsis thaliana GN=TOC75-3 PE=1 SV=1	16	---	----	-0,02	0,78721	2231,31	68,80%
Q9FIZ7	5-oxoprolinase OS=Arabidopsis thaliana GN=OXP1 PE=2 SV=1	10	---	----	-0,03	0,79012	2239,55	68,80%
Q94JQ3	Serine hydroxymethyltransferase 3, chloroplastic OS=Arabidopsis thaliana GN=SHM3 PE=1 SV=2	7	---	----	-0,031	0,79412	2250,89	68,80%
Q9LMR1;Q9M8L6	At1g15730/F7H2_7 OS=Arabidopsis thaliana GN=F7H2.7 PE=2 SV=1	2	---	----	-0,036	0,78802	2233,60	68,80%
Q8LG77;Q945K7	Isocitrate dehydrogenase [NAD] catalytic subunit 6, mitochondrial OS=Arabidopsis thaliana GN=IDH6 PE=2 SV=2	3	---	----	-0,046	0,79412	2250,89	68,80%
O23227	Hydrolase, alpha/beta fold family protein OS=Arabidopsis thaliana GN=C7A10.830 PE=2 SV=2	3	---	----	-0,049	0,79141	2243,21	68,80%
Q9SCZ4	Receptor-like protein kinase FERONIA OS=Arabidopsis thaliana GN=FER PE=1 SV=1	2	---	----	-0,059	0,79141	2243,21	68,80%
Q9ZUT8	ABC transporter G family member 33 OS=Arabidopsis thaliana GN=ABCG33 PE=2 SV=1	1	---	----	-0,062	0,78812	2233,89	68,80%
F4JLK2;Q94BT0;Q9FY54	Probable sucrose-phosphate synthase 4 OS=Arabidopsis thaliana GN=SPS4 PE=1 SV=1	1	---	----	-0,064	0,79002	2239,27	68,80%
Q8GZ99	At5g49760 OS=Arabidopsis thaliana GN=LRR-RLK PE=1 SV=1	2	---	----	-0,064	0,79212	2245,22	68,80%
Q9M5J9	Polygalacturonase inhibitor 1 OS=Arabidopsis thaliana GN=PGIP1 PE=2 SV=1	1	---	----	-0,083	0,79281	2247,18	68,80%
Q9LD90	H/ACA ribonucleoprotein complex subunit 4 OS=Arabidopsis thaliana GN=CBF5 PE=1 SV=1	1	---	----	-0,099	0,79012	2239,55	68,80%
Q8W4Q1	At4g35360/F23E12_80 OS=Arabidopsis thaliana GN=At4g35360 PE=2 SV=1	1	---	----	-0,102	0,78941	2237,54	68,80%
Q9FEA2	Glutamate--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At5g64050 PE=2 SV=1	6	---	----	0,029	0,79612	2256,56	68,90%
Q9LYA9	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic OS=Arabidopsis thaliana GN=CSP41A PE=1 SV=1	17	---	----	0,011	0,79401	2250,58	68,90%
Q9LXT3	Multiprotein-bridging factor 1b OS=Arabidopsis thaliana GN=MBF1B PE=2 SV=1	5	---	----	-0,025	0,79612	2256,56	68,90%
O49460;Q9SIL6;Q9ZNT7	Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1	1	---	----	-0,051	0,79612	2256,56	68,90%
Q689D6	Protein ROOT PRIMORDIUM DEFECTIVE 1 OS=Arabidopsis thaliana GN=RPD1 PE=1 SV=1	1	---	----	-0,078	0,79612	2256,56	68,90%
Q56X72	Reticulon-like protein B21 OS=Arabidopsis thaliana GN=RTNLB21 PE=2 SV=2	1	---	----	-0,104	0,79812	2262,23	68,90%
Q9SIV2	26S proteasome non-ATPase regulatory subunit 2 homolog A OS=Arabidopsis thaliana GN=RPN1A PE=1 SV=2	6	---	----	0,031	0,79900	2264,73	69,00%
P56820	Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=TIF3D1 PE=1 SV=1	1	---	----	-0,082	0,80012	2267,90	69,00%
Q8LDV3	Uncharacterized protein At4g13200, chloroplastic OS=Arabidopsis thaliana GN=At4g13200 PE=2 SV=2	5	---	----	-0,03	0,80012	2267,90	69,10%
Q93W03	AT3g56130/F18O21_90 OS=Arabidopsis thaliana GN=At3g56130 PE=2 SV=1	1	---	----	-0,122	0,80012	2267,90	69,10%
O23717	Proteasome subunit beta type-5-A OS=Arabidopsis thaliana GN=PBE1 PE=1 SV=1	5	---	----	0,032	0,80212	2273,56	69,20%
Q9SIE1	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase OS=Arabidopsis thalia	7	---	----	-0,025	0,80212	2273,56	69,20%
Q9CAA0	Coatomer subunit beta'-1 OS=Arabidopsis thaliana GN=At1g79990 PE=2 SV=2	1	---	----	0,078	0,80660	2286,27	69,30%
Q9FGM0	ATP-dependent zinc metalloprotease FTSH 11, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=FTSH11 PE=1 S	1	---	----	0,07	0,80402	2278,95	69,30%
Q9FHL4	At5g23440 OS=Arabidopsis thaliana GN=FTRA1 PE=2 SV=1	1	---	----	0,058	0,80612	2284,90	69,30%
Q8H0W4	AT3G11560 protein OS=Arabidopsis thaliana GN=At3g11560 PE=2 SV=1	1	---	----	-0,053	0,80612	2284,90	69,30%
Q9LIG6	NifU-like protein 4, mitochondrial OS=Arabidopsis thaliana GN=NIFU4 PE=2 SV=1	1	---	----	-0,078	0,80612	2284,90	69,30%
Q9LSZ0	APO protein 4, mitochondrial OS=Arabidopsis thaliana GN=APO4 PE=2 SV=2	1	---	----	-0,107	0,80402	2278,95	69,30%
P92964	Serine/arginine-rich splicing factor RS31 OS=Arabidopsis thaliana GN=RS31 PE=1 SV=2	1	RPSPDYGR	Phospho S3	0,105	0,80602	2284,62	69,40%
O64700	Urease accessory protein G OS=Arabidopsis thaliana GN=UREG PE=2 SV=1	1	---	----	0,079	0,80802	2290,29	69,40%
Q9CAX6	40S ribosomal protein S14-2 OS=Arabidopsis thaliana GN=RPS14B PE=1 SV=1	1	---	----	-0,034	0,80600	2284,57	69,40%
Q9LVV6	At5g52960 OS=Arabidopsis thaliana GN=At5g52960 PE=1 SV=1	2	---	----	-0,04	0,80812	2290,57	69,40%

Q8GWC7	Putative uncharacterized protein At1g72165/T9N14_2 OS=Arabidopsis thaliana GN=At1g72165/T9N14_2 PE=2 SV=1	1	---	----	-0,055	0,80612	2284,90	69,40%
Q8H1G6	PTI1-like tyrosine-protein kinase 1 OS=Arabidopsis thaliana GN=PTI11 PE=1 SV=1	2	---	----	-0,061	0,80612	2284,90	69,40%
Q9XEA0	AT4g04350/T19B17_7 OS=Arabidopsis thaliana GN=T19B17.7 PE=2 SV=1	1	---	----	-0,078	0,80612	2284,90	69,40%
Q9FLH2	2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=At5g65750 PE=2 SV=1	1	---	----	0,084	0,81012	2296,24	69,50%
Q42344	High mobility group B protein 4 OS=Arabidopsis thaliana GN=HMGB4 PE=1 SV=1	1	---	----	0,121	0,81002	2295,95	69,60%
Q8VXZ7	Alpha-galactosidase 3 OS=Arabidopsis thaliana GN=AGAL3 PE=1 SV=1	2	---	----	-0,036	0,81212	2301,91	69,60%
Q9FND0	Gb|AAD20086.1 OS=Arabidopsis thaliana GN=At5g43960 PE=2 SV=1	2	---	----	-0,045	0,81212	2301,91	69,60%
F4JV80	Glutamyl-tRNA(Gln) amidotransferase subunit C, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GATC PE=2	1	---	----	-0,063	0,81212	2301,91	69,60%
O82266	Protein SLOW WALKER 1 OS=Arabidopsis thaliana GN=SWA1 PE=2 SV=1	1	---	----	-0,102	0,81212	2301,91	69,60%
Q9LHD9	UPF0496 protein At3g28270 OS=Arabidopsis thaliana GN=At3g28270 PE=2 SV=1	4	---	----	0,045	0,81412	2307,57	69,70%
Q9SVN5	Probable methionine--tRNA ligase OS=Arabidopsis thaliana GN=At4g13780 PE=2 SV=1	5	---	----	0,039	0,81212	2301,91	69,70%
Q9XJ35	ATP-dependent Clp protease proteolytic subunit-related protein 1, chloroplastic OS=Arabidopsis thaliana GN=CLPR1 PE	9	---	----	0,02	0,81461	2308,97	69,70%
Q8RWT8	Putative seryl-tRNA synthetase OS=Arabidopsis thaliana GN=SRS PE=2 SV=1	5	---	----	-0,03	0,81612	2313,24	69,70%
O82209;Q9M0D5	Copia-like retroelement pol polyprotein OS=Arabidopsis thaliana GN=At2g19680 PE=2 SV=1	1	---	----	-0,058	0,81202	2301,62	69,70%
F4KA19	Uncharacterized protein OS=Arabidopsis thaliana GN=At5g28830 PE=4 SV=1	1	---	----	-0,122	0,81402	2307,29	69,70%
Q9LPC5	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Arabidopsis thaliana GN=BIG3 PE=1 SV=1	2	---	----	0,059	0,81612	2313,24	69,80%
Q9SKC9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Arabidopsis thaliana GN=At2g02050 PE=3 SV=1	2	---	----	0,046	0,81540	2311,21	69,80%
Q9M0V6	Ferredoxin--NADP reductase, root isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=RFNR1 PE=2 SV=2	2	---	----	0,039	0,81701	2315,77	69,80%
P19456;P20649;Q9LV11	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	2	---	----	0,037	0,81601	2312,94	69,80%
O22607	WD-40 repeat-containing protein MSI4 OS=Arabidopsis thaliana GN=MSI4 PE=1 SV=3	4	---	----	0,031	0,81602	2312,96	69,80%
Q93VR3	GDP-mannose 3,5-epimerase OS=Arabidopsis thaliana GN=At5g28840 PE=1 SV=1	8	---	----	0,018	0,81521	2310,67	69,80%
P42643;P42644;P46077;C	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	---	----	0,1	0,82012	2324,58	70,00%
Q9ZPV8	Phosphopantetheine adenylyltransferase OS=Arabidopsis thaliana GN=COAD PE=1 SV=1	1	---	----	0,078	0,82012	2324,58	70,00%
Q93V88	Probable protein phosphatase 2C 62 OS=Arabidopsis thaliana GN=At4g33500 PE=2 SV=1	2	---	----	0,049	0,82002	2324,30	70,00%
P0CJ46;P53492	Actin-1 OS=Arabidopsis thaliana GN=ACT1 PE=1 SV=1	2	---	----	0,027	0,82212	2330,25	70,00%
Q9M1H3	ABC transporter F family member 4 OS=Arabidopsis thaliana GN=ABCF4 PE=2 SV=1	4	---	----	-0,041	0,82012	2324,58	70,00%
Q84W89	DEAD-box ATP-dependent RNA helicase 37 OS=Arabidopsis thaliana GN=RH37 PE=2 SV=2	2	---	----	-0,046	0,82012	2324,58	70,00%
F4IIU4	187-kDa microtubule-associated protein AIR9 OS=Arabidopsis thaliana GN=AIR9 PE=1 SV=1	1	---	----	0,097	0,82202	2329,96	70,10%
Q0WVL7	Golgin candidate 5 OS=Arabidopsis thaliana GN=GC5 PE=1 SV=1	1	---	----	0,085	0,82381	2335,05	70,10%
Q9SE50;Q9SR37	Beta-D-glucopyranosyl abscisate beta-glucosidase OS=Arabidopsis thaliana GN=BGLU18 PE=1 SV=2	1	---	----	0,083	0,82412	2335,92	70,10%
Q38932	Lycopene epsilon cyclase, chloroplastic OS=Arabidopsis thaliana GN=LUT2 PE=1 SV=2	1	---	----	0,063	0,82412	2335,92	70,10%
Q9FK35	Adenylate kinase 3 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	3	---	----	0,039	0,82361	2334,48	70,10%
Q8RXF8	Mitochondrial Rho GTPase 1 OS=Arabidopsis thaliana GN=MIRO1 PE=1 SV=1	6	---	----	-0,032	0,82212	2330,25	70,10%
F4J3Q8	P-loop containing nucleoside triphosphate hydrolases superfamily protein OS=Arabidopsis thaliana GN=At3g10350 PE=	2	---	----	-0,05	0,82161	2328,81	70,10%
Q8GWT4	Protein arginine N-methyltransferase 1.5 OS=Arabidopsis thaliana GN=PMRT15 PE=1 SV=2	1	---	----	-0,073	0,82412	2335,92	70,10%
Q9CAN8	Lysophospholipid acyltransferase 2 OS=Arabidopsis thaliana GN=LPLAT2 PE=1 SV=1	1	---	----	0,064	0,82612	2341,58	70,20%
Q8S948	Solanesyl diphosphate synthase 1 OS=Arabidopsis thaliana GN=SPS1 PE=1 SV=1	2	---	----	0,053	0,82612	2341,58	70,20%
P42762;Q9FI56;Q9SXJ7	Chaperone protein ClpD, chloroplastic OS=Arabidopsis thaliana GN=CLPD PE=1 SV=1	1	---	----	0,035	0,82812	2347,25	70,20%
Q0WQF7	Dihydrolipoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex, mitochondrial OS=Ara	6	---	----	0,028	0,82612	2341,58	70,20%
O82399	Probable malate dehydrogenase, glyoxysomal OS=Arabidopsis thaliana GN=At2g22780 PE=2 SV=1	7	---	----	0,025	0,82812	2347,25	70,20%
Q8LD27	Proteasome subunit beta type-6 OS=Arabidopsis thaliana GN=PBA1 PE=1 SV=2	5	---	----	-0,026	0,82612	2341,58	70,20%
F4JJT9	tRNA synthetase class II (D, K and N) family protein OS=Arabidopsis thaliana GN=At4g33760 PE=3 SV=1	6	---	----	-0,028	0,82602	2341,30	70,20%
F4HUX0	Regulator of Vps4 activity in the MVB pathway protein OS=Arabidopsis thaliana GN=At1g34220 PE=1 SV=1	1	---	----	-0,07	0,82812	2347,25	70,20%
Q5QIT3	Serine/threonine protein phosphatase 2A regulatory subunit B''beta OS=Arabidopsis thaliana GN=B''BETA PE=1 SV=1	1	---	----	0,105	0,82802	2346,97	70,30%
Q8GXU8	1-acyl-sn-glycerol-3-phosphate acyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=LPAT1 PE=2 SV=1	2	---	----	0,046	0,83012	2352,92	70,30%
P42645	14-3-3-like protein GF14 upsilon OS=Arabidopsis thaliana GN=GRF5 PE=1 SV=2	7	---	----	0,022	0,83012	2352,92	70,30%
Q9FFC7	Probable alanine--tRNA ligase, chloroplastic OS=Arabidopsis thaliana GN=EMB86 PE=1 SV=2	15	---	----	0,018	0,82812	2347,25	70,30%
Q76FS5	Solanesyl diphosphate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=SPS2 PE=1 SV=1	3	---	----	-0,029	0,82812	2347,25	70,30%
Q9LV60	Cysteine-rich repeat secretory protein 55 OS=Arabidopsis thaliana GN=CRRSP55 PE=2 SV=1	2	---	----	-0,053	0,82801	2346,95	70,30%
Q56XE2	At1g77122 OS=Arabidopsis thaliana GN=At1g77122 PE=2 SV=1	1	---	----	-0,06	0,83012	2352,92	70,30%
Q9SF45	FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=F11F8_15 PE=2 SV=1	1	---	----	-0,065	0,83012	2352,92	70,30%
Q94BY1	AT3g52150/F4F15_260 OS=Arabidopsis thaliana GN=At3g52155 PE=2 SV=1	1	---	----	0,15	0,83212	2358,59	70,40%
Q9LTR9	Glycylpeptide N-tetradecanoyltransferase 1 OS=Arabidopsis thaliana GN=NMT1 PE=1 SV=2	4	---	----	0,036	0,83212	2358,59	70,40%
P28186;Q9FJF1;Q9LZD4	Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	3	---	----	0,036	0,83812	2375,59	70,40%
Q93ZM7	Chaperonin CPN60-like 2, mitochondrial OS=Arabidopsis thaliana GN=At3g13860 PE=2 SV=2	6	---	----	0,03	0,83202	2358,31	70,40%

Q9FF88	At5g23920 OS=Arabidopsis thaliana GN=At5g23920 PE=2 SV=1	2	---	----	-0,057	0,83212	2358,59	70,40%
Q8LDD3	Protein CURVATURE THYLAKOID 1D, chloroplastic OS=Arabidopsis thaliana GN=CURT1D PE=1 SV=1	1	---	----	-0,058	0,83612	2369,93	70,40%
Q8L3X8	Serine/arginine-rich SC35-like splicing factor SCL30 OS=Arabidopsis thaliana GN=SCL30 PE=1 SV=1	1	GRSPPPPPPR	Phospho S3	0,096	0,83402	2363,97	70,50%
P58048	Cytochrome P450 71B8 OS=Arabidopsis thaliana GN=CYP71B8 PE=3 SV=1	1	---	----	0,08	0,83812	2375,59	70,50%
O80477	Methylesterase 3 OS=Arabidopsis thaliana GN=MES3 PE=2 SV=1	2	---	----	0,064	0,83612	2369,93	70,50%
Q94IB9	Acyl-CoA independent ceramide synthase OS=Arabidopsis thaliana GN=AtCES1 PE=2 SV=1	1	---	----	0,062	0,84012	2381,26	70,50%
Q41916	Cysteine proteinase inhibitor 5 OS=Arabidopsis thaliana GN=CYS5 PE=2 SV=2	1	---	----	0,06	0,83612	2369,93	70,50%
Q8GYN9	1,4-dihydroxy-2-naphthoyl-CoA synthase, peroxisomal OS=Arabidopsis thaliana GN=MENB PE=1 SV=2	2	---	----	0,056	0,84012	2381,26	70,50%
O23443	Fumarylacetoacetate hydrolase-like protein OS=Arabidopsis thaliana GN=dl4011w PE=4 SV=2	2	---	----	0,043	0,83641	2370,76	70,50%
Q38951	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A gamma isoform OS=Arabidopsis thaliana GN=PP	2	---	----	0,042	0,83612	2369,93	70,50%
Q8LA13	DEAD-box ATP-dependent RNA helicase 11 OS=Arabidopsis thaliana GN=RH11 PE=1 SV=1	2	---	----	0,04	0,83741	2373,60	70,50%
O23138	Cytochrome c-1 OS=Arabidopsis thaliana GN=CYTC-1 PE=1 SV=1	3	---	----	0,026	0,83781	2374,73	70,50%
Q96299;Q9S9Z8-2	14-3-3-like protein GF14 mu OS=Arabidopsis thaliana GN=GRF9 PE=1 SV=2	1	---	----	0,025	0,83801	2375,30	70,50%
P56793	50S ribosomal protein L16, chloroplastic OS=Arabidopsis thaliana GN=rpl16 PE=3 SV=1	4	---	----	-0,025	0,83501	2366,79	70,50%
Q9LV35	WD40 domain-containing protein OS=Arabidopsis thaliana GN=At3g18060 PE=2 SV=1	4	---	----	-0,03	0,83612	2369,93	70,50%
Q949X7	Diaminopimelate decarboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=LYSA1 PE=2 SV=1	1	---	----	-0,048	0,83761	2374,16	70,50%
Q9SR92	Rhodanese-like domain-containing protein 10 OS=Arabidopsis thaliana GN=STR10 PE=2 SV=1	2	---	----	-0,05	0,84012	2381,26	70,50%
O49313	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B OS=Arabidopsis thaliana GN=At2g33220 PE=2 SV	1	---	----	-0,051	0,83412	2364,26	70,50%
F4K5J1	Myosin-17 OS=Arabidopsis thaliana GN=XI-K PE=1 SV=2	1	---	----	-0,08	0,83812	2375,59	70,50%
Q9FJW0	AT5g67630/K9I9_20 OS=Arabidopsis thaliana GN=At5g67630 PE=2 SV=1	1	---	----	-0,081	0,83602	2369,64	70,50%
Q9SVW8	Plant intracellular Ras-group-related LRR protein 4 OS=Arabidopsis thaliana GN=PIRL4 PE=1 SV=1	1	---	----	-0,115	0,83812	2375,59	70,50%
Q9FNI2	Putative uncharacterized protein At5g06260 OS=Arabidopsis thaliana GN=At5g06260 PE=2 SV=1	1	---	----	-0,137	0,84012	2381,26	70,50%
A8MQW3	AT2G21270 protein OS=Arabidopsis thaliana GN=UFD1 PE=2 SV=1	1	---	----	0,06	0,83602	2369,64	70,60%
rev_Q9FZE0	reversed Beta-glucosidase 40 OS=Arabidopsis thaliana GN=BGLU40 PE=2 SV=1	1	---	----	0,038	0,83602	2369,64	70,60%
Q9M2E0	DEAD-box ATP-dependent RNA helicase 12 OS=Arabidopsis thaliana GN=RH12 PE=2 SV=1	2	---	----	0,037	0,84202	2386,65	70,60%
Q9LIK0	Plastidial pyruvate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=PKP1 PE=1 SV=1	10	---	----	0,017	0,84012	2381,26	70,60%
Q93VH5	AT5g10730/MAJ23_90 OS=Arabidopsis thaliana GN=At5g10730 PE=2 SV=1	2	---	----	-0,042	0,84141	2384,93	70,60%
Q9MAA1	GDSL esterase/lipase At3g05180 OS=Arabidopsis thaliana GN=At3g05180 PE=2 SV=1	2	---	----	-0,055	0,84412	2392,60	70,60%
F4JCI4	Melibiase family protein OS=Arabidopsis thaliana GN=At3g26380 PE=4 SV=1	2	---	----	-0,06	0,83602	2369,64	70,60%
Q9FE68	UDP-glycosyltransferase 71C5 OS=Arabidopsis thaliana GN=UGT71C5 PE=2 SV=1	1	---	----	-0,067	0,84212	2386,93	70,60%
Q8RXI0	AAA-type ATPase family protein OS=Arabidopsis thaliana GN=At5g16930 PE=2 SV=1	1	---	----	-0,071	0,84012	2381,26	70,60%
Q9SS96	F4P13.13 protein OS=Arabidopsis thaliana GN=F4P13.13 PE=2 SV=1	1	---	----	-0,122	0,84212	2386,93	70,60%
Q949Y0	Ubiquitin carboxyl-terminal hydrolase 6 OS=Arabidopsis thaliana GN=UBP6 PE=1 SV=1	1	---	----	0,067	0,84612	2398,27	70,70%
Q8LEQ0	60S acidic ribosomal protein P1-3 OS=Arabidopsis thaliana GN=RPP1C PE=1 SV=2	2	---	----	0,022	0,84621	2398,54	70,70%
Q9M8L6	At1g80480 OS=Arabidopsis thaliana GN=T21F11.27 PE=2 SV=1	3	---	----	-0,024	0,84612	2398,27	70,70%
P92939	Calcium-transporting ATPase 1, endoplasmic reticulum-type OS=Arabidopsis thaliana GN=ECA1 PE=1 SV=2	2	---	----	-0,043	0,84401	2392,30	70,70%
Q8GX78	Ascorbate transporter, chloroplastic OS=Arabidopsis thaliana GN=PHT4;4 PE=1 SV=1	2	---	----	-0,044	0,84412	2392,60	70,70%
Q9LSH2	Glutamate decarboxylase 5 OS=Arabidopsis thaliana GN=GAD5 PE=2 SV=1	1	---	----	-0,06	0,84402	2392,32	70,70%
Q9LDF8	At3g12950 OS=Arabidopsis thaliana GN=At3g12950 PE=1 SV=1	1	AIELQSPVGSLVGK	Phospho S6	0,136	0,84812	2403,94	70,80%
Q93VM8	Copper transporter 5 OS=Arabidopsis thaliana GN=COPT5 PE=1 SV=1	1	---	----	0,055	0,84812	2403,94	70,80%
Q9C522;Q9FGX1	ATP-citrate synthase beta chain protein 1 OS=Arabidopsis thaliana GN=ACLB-1 PE=2 SV=1	1	---	----	0,052	0,84612	2398,27	70,80%
Q7Y1W1	Protein TIC 56, chloroplastic OS=Arabidopsis thaliana GN=TIC56 PE=1 SV=1	2	---	----	0,035	0,84812	2403,94	70,80%
Q84M92	Actin-related protein 4 OS=Arabidopsis thaliana GN=ARP4 PE=1 SV=1	2	---	----	-0,045	0,85011	2409,60	70,80%
Q9LHQ4	AT3g20680/F3H11_7 OS=Arabidopsis thaliana GN=At3g20680 PE=2 SV=1	1	---	----	-0,048	0,85011	2409,60	70,80%
F4K2J2	Auxin-responsive GH3 family protein OS=Arabidopsis thaliana GN=At5g13360 PE=4 SV=1	1	---	----	-0,051	0,84802	2403,65	70,80%
Q9STH1	Hsp70-Hsp90 organizing protein 3 OS=Arabidopsis thaliana GN=HOP3 PE=2 SV=1	1	---	----	-0,057	0,84602	2397,98	70,80%
Q9LKB2	Genomic DNA, chromosome 3, TAC clone:K15M2 OS=Arabidopsis thaliana GN=At3g14920 PE=4 SV=1	1	---	----	-0,057	0,84861	2405,34	70,80%
Q9FX21	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Arabidopsis thaliana GN=STT3B PE=	1	---	----	-0,067	0,84812	2403,94	70,80%
O49195	Vegetative storage protein 1 OS=Arabidopsis thaliana GN=VSP1 PE=1 SV=2	2	---	----	0,03	0,84981	2408,74	70,90%
Q9LK88	NADPH:quinone oxidoreductase OS=Arabidopsis thaliana GN=NQR PE=1 SV=1	3	---	----	-0,03	0,85011	2409,60	70,90%
C0LGP4	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana GN=At3g47570 PE=2 S	1	---	----	-0,067	0,85211	2415,27	70,90%
Q1KPV0	FZL OS=Arabidopsis thaliana GN=FZL PE=2 SV=1	2	---	----	0,064	0,85211	2415,27	71,00%
Q8VZ31	Carboxylate clamp-tetratricopeptide repeat protein OS=Arabidopsis thaliana GN=At1g04530 PE=1 SV=1	2	---	----	0,054	0,85411	2420,94	71,00%
Q9LPU3	DNAJ heat shock N-terminal domain-containing protein OS=Arabidopsis thaliana GN=T22I11.9 PE=2 SV=1	2	---	----	-0,039	0,85211	2415,27	71,00%
rev_Q9LTP6	reversed Putative sugar transporter ERD6-like 13 OS=Arabidopsis thaliana GN=At3g20460 PE=3 SV=2	1	---	----	-0,056	0,85411	2420,94	71,00%

Q42404	U1 small nuclear ribonucleoprotein 70 kDa OS=Arabidopsis thaliana GN=RNU1 PE=1 SV=1	1	TSQSEEPSRPR	none	0,1	0,85811	2432,28	71,10%
Q9LDB4	Non-specific lipid-transfer protein 6 OS=Arabidopsis thaliana GN=LTP6 PE=2 SV=1	1	---	----	0,073	0,85581	2425,75	71,10%
Q9M314	AT3g61540/F2A19_140 OS=Arabidopsis thaliana GN=F2A19.140 PE=2 SV=1	1	---	----	0,053	0,85611	2426,61	71,10%
Q9M0G7	Leucine-rich repeat receptor-like protein kinase PXL2 OS=Arabidopsis thaliana GN=PXL2 PE=2 SV=1	1	---	----	0,047	0,85411	2420,94	71,10%
Q9S720	PsbP domain-containing protein 3, chloroplastic OS=Arabidopsis thaliana GN=PPD3 PE=1 SV=2	2	---	----	0,038	0,85611	2426,61	71,10%
Q9C5C4	Acetylornithine deacetylase OS=Arabidopsis thaliana GN=At4g17830 PE=2 SV=1	5	---	----	0,024	0,85611	2426,61	71,10%
Q9SUU5	Cytochrome b-c1 complex subunit 7-1 OS=Arabidopsis thaliana GN=QCR7-1 PE=1 SV=1	3	---	----	-0,023	0,85601	2426,32	71,10%
Q42338	AT3G48140 protein OS=Arabidopsis thaliana GN=T24C20_20 PE=2 SV=1	2	---	----	-0,029	0,85411	2420,94	71,10%
Q8LB01	4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic OS=Arabidopsis thaliana GN=DAPB2 PE=2 SV=1	1	---	----	0,057	0,85811	2432,28	71,20%
Q9S829	NAD(P)H-quinone oxidoreductase subunit O, chloroplastic OS=Arabidopsis thaliana GN=ndhO PE=2 SV=1	3	---	----	0,03	0,85811	2432,28	71,20%
Q8W033	Aldehyde dehydrogenase family 3 member I1, chloroplastic OS=Arabidopsis thaliana GN=ALDH3I1 PE=1 SV=2	4	---	----	-0,023	0,85811	2432,28	71,20%
O82499	Translation initiation factor IF-1, chloroplastic OS=Arabidopsis thaliana GN=At4g11175 PE=2 SV=2	1	---	----	-0,037	0,85811	2432,28	71,20%
Q9LS02	Allene oxide cyclase 2, chloroplastic OS=Arabidopsis thaliana GN=AOC2 PE=1 SV=1	7	---	----	-0,019	0,86121	2441,06	71,30%
Q9LZX1	Protein LURP-one-related 15 OS=Arabidopsis thaliana GN=At5g01750 PE=1 SV=1	1	---	----	-0,044	0,86211	2443,61	71,30%
Q9FY99	Glucose-6-phosphate 1-dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=At5g13110 PE=2 SV=2	1	---	----	-0,053	0,86081	2439,92	71,30%
Q8GW20	Uncharacterized protein At5g03900, chloroplastic OS=Arabidopsis thaliana GN=At5g03900 PE=2 SV=2	1	---	----	-0,073	0,86011	2437,95	71,30%
Q9CAF4	Nuclear pore complex protein NUP1 OS=Arabidopsis thaliana GN=NUP1 PE=1 SV=1	1	---	----	0,091	0,86611	2454,95	71,40%
Q9SKS8	At2g20920/F5H14.11 OS=Arabidopsis thaliana GN=At2g20920 PE=2 SV=1	1	---	----	0,054	0,86411	2449,28	71,40%
Q9FQ03	5'-3' exoribonuclease 3 OS=Arabidopsis thaliana GN=XRN3 PE=2 SV=1	1	---	----	0,053	0,86740	2458,60	71,40%
Q9XI19	AT1G21600 protein OS=Arabidopsis thaliana GN=F8K7.1 PE=2 SV=1	1	---	----	0,046	0,86211	2443,61	71,40%
Q949P3	Uncharacterized protein At2g17340 OS=Arabidopsis thaliana GN=At2g17340 PE=1 SV=1	3	---	----	0,043	0,86411	2449,28	71,40%
P54887	Delta-1-pyrroline-5-carboxylate synthase A OS=Arabidopsis thaliana GN=P5CSA PE=1 SV=1	2	---	----	0,034	0,86211	2443,61	71,40%
O48782	Heme oxygenase 1, chloroplastic OS=Arabidopsis thaliana GN=HO1 PE=1 SV=2	6	---	----	0,025	0,86261	2445,02	71,40%
Q9LHL7	Aha1 domain-containing protein OS=Arabidopsis thaliana GN=T21B14.13 PE=1 SV=1	7	---	----	0,022	0,86611	2454,95	71,40%
Q8L7K9	NAD-dependent malic enzyme 2, mitochondrial OS=Arabidopsis thaliana GN=NAD-ME2 PE=1 SV=1	7	---	----	0,021	0,86380	2448,40	71,40%
P56799	30S ribosomal protein S4, chloroplastic OS=Arabidopsis thaliana GN=rps4 PE=3 SV=1	7	---	----	0,015	0,86411	2449,28	71,40%
Q8VYI4	Aspartate semialdehyde dehydrogenase OS=Arabidopsis thaliana GN=At1g14810 PE=2 SV=1	8	---	----	0,011	0,86611	2454,95	71,40%
P25851	Fructose-1,6-bisphosphatase, chloroplastic OS=Arabidopsis thaliana GN=FBP PE=2 SV=2	11	---	----	-0,01	0,86701	2457,50	71,40%
Q8LPK4	AP-2 complex subunit alpha-2 OS=Arabidopsis thaliana GN=ALPHAC-AD PE=1 SV=1	5	---	----	-0,031	0,86611	2454,95	71,40%
O65272;Q9ZTZ7	K(+) efflux antiporter 2, chloroplastic OS=Arabidopsis thaliana GN=KEA2 PE=1 SV=2	2	---	----	-0,033	0,86611	2454,95	71,40%
Q94AU7	Gamma carbonic anhydrase 3, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA3 PE=1 SV=1	2	---	----	-0,035	0,86811	2460,62	71,40%
A8MRX0	Flavin-containing monooxygenase FMO GS-OX5 OS=Arabidopsis thaliana GN=FMOGS-OX5 PE=2 SV=2	2	---	----	-0,036	0,86811	2460,62	71,40%
Q9LZD3	Exocyst complex component EXO70A1 OS=Arabidopsis thaliana GN=EXO70A1 PE=1 SV=1	1	---	----	-0,073	0,86400	2448,96	71,40%
Q9FMF5	Root phototropism protein 3 OS=Arabidopsis thaliana GN=RPT3 PE=1 SV=2	1	---	----	0,09	0,87011	2466,29	71,50%
Q8L706	Synaptotagmin-5 OS=Arabidopsis thaliana GN=SYT5 PE=2 SV=1	2	---	----	0,062	0,87001	2466,00	71,50%
Q8W4Q1;Q949P3	At4g35360/F23E12_80 OS=Arabidopsis thaliana GN=At4g35360 PE=2 SV=1	1	---	----	0,057	0,86611	2454,95	71,50%
Q9FV53	Peptide deformylase 1A, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=PDF1A PE=1 SV=3	2	---	----	0,034	0,87011	2466,29	71,50%
F4JQH3	Aminopeptidase P1 OS=Arabidopsis thaliana GN=APP1 PE=1 SV=1	6	---	----	-0,02	0,87011	2466,29	71,50%
Q9LMI0	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7 OS=Arabidopsis thaliana GN=TPS7 PE=1 SV=1	5	---	----	-0,025	0,86611	2454,95	71,50%
Q9ZUR7	Arginine biosynthesis bifunctional protein ArgJ, chloroplastic OS=Arabidopsis thaliana GN=At2g37500 PE=2 SV=2	3	---	----	-0,031	0,86611	2454,95	71,50%
P26569	Histone H1.2 OS=Arabidopsis thaliana GN=At2g30620 PE=1 SV=1	2	---	----	-0,035	0,86811	2460,62	71,50%
Q42440	N-(5'-phosphoribosyl)anthranilate isomerase 1, chloroplastic OS=Arabidopsis thaliana GN=PAI1 PE=2 SV=1	2	---	----	-0,036	0,86981	2465,43	71,50%
Q8L5Y8	Putative uncharacterized protein At5g65840 OS=Arabidopsis thaliana GN=At5g65840 PE=2 SV=1	2	---	----	-0,037	0,86611	2454,95	71,50%
Q9M2W3	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase 2 OS=Arabidopsis thaliana GN=PGPS2 PE=1 SV=1	1	---	----	0,066	0,87811	2488,96	71,60%
Q9M287	Late embryogenesis abundant hydroxyproline-rich glycoprotein OS=Arabidopsis thaliana GN=T22K7_60 PE=4 SV=1	1	---	----	0,055	0,87201	2471,67	71,60%
Q9LSM3	Putative uncharacterized protein At5g65520 OS=Arabidopsis thaliana GN=At5g65520 PE=2 SV=1	1	---	----	0,043	0,87211	2471,96	71,60%
Q8L770	ATP-dependent Clp protease proteolytic subunit-related protein 3, chloroplastic OS=Arabidopsis thaliana GN=CLPR3 PE	7	---	----	0,01	0,87211	2471,96	71,60%
Q8RWR9	Putative uncharacterized protein At5g42070 OS=Arabidopsis thaliana GN=At5g42070 PE=2 SV=1	3	---	----	-0,026	0,87211	2471,96	71,60%
P0CZ23	Acyl-coenzyme A oxidase 3, peroxisomal OS=Arabidopsis thaliana GN=ACX3 PE=1 SV=1	5	---	----	-0,028	0,87811	2488,96	71,60%
Q944Q6	Expressed protein OS=Arabidopsis thaliana GN=At2g14835 PE=1 SV=1	1	---	----	0,134	0,87611	2483,29	71,70%
Q76FS5;Q8S948	Solanesyl diphosphate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=SPS2 PE=1 SV=1	1	---	----	0,047	0,88011	2494,63	71,70%
Q8VZV6	Esterase/lipase/thioesterase family protein OS=Arabidopsis thaliana GN=At5g19290 PE=2 SV=1	1	---	----	0,041	0,87811	2488,96	71,70%
Q944L8	At1g11930/F12F1_20 OS=Arabidopsis thaliana GN=At1g11930 PE=2 SV=1	1	---	----	0,04	0,87811	2488,96	71,70%
Q9LP53	Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=F28N24.7 PE=2 SV=1	2	---	----	0,034	0,87461	2479,04	71,70%
Q9ASY8	Mitochondrial import receptor subunit TOM7-1 OS=Arabidopsis thaliana GN=TOM7-1 PE=1 SV=1	1	---	----	0,034	0,87721	2486,41	71,70%

Q9LIM9	Major latex protein-like OS=Arabidopsis thaliana GN=At3g26460 PE=4 SV=1	1	---	----	0,024	0,87811	2488,96	71,70%
Q8W463	50S ribosomal protein L19-1, chloroplastic OS=Arabidopsis thaliana GN=At4g17560 PE=2 SV=1	2	---	----	0,022	0,87811	2488,96	71,70%
Q84WW2	Probable 6-phosphogluconolactonase 5, chloroplastic OS=Arabidopsis thaliana GN=EMB2024 PE=2 SV=1	5	---	----	0,018	0,88211	2500,30	71,70%
Q8VZW6	Elongation factor EF-P OS=Arabidopsis thaliana GN=At3g08740 PE=1 SV=1	8	---	----	0,017	0,87611	2483,29	71,70%
Q9LR64	Photosystem II repair protein PSB27-H1, chloroplastic OS=Arabidopsis thaliana GN=PSB27-1 PE=1 SV=1	5	---	----	-0,01	0,87701	2485,84	71,70%
Q9S831	Photosystem I reaction center subunit IV A, chloroplastic OS=Arabidopsis thaliana GN=PSAE1 PE=1 SV=1	4	---	----	-0,01	0,87920	2492,05	71,70%
Q9LHN3	AT3g18860/MCB22_3 OS=Arabidopsis thaliana GN=At3g18860 PE=2 SV=1	9	---	----	-0,015	0,87611	2483,29	71,70%
Q9LZE4	Phosphoadenosine phosphosulfate (PAPS) reductase family protein OS=Arabidopsis thaliana GN=F12E4_190 PE=4 SV=1	1	---	----	-0,043	0,88211	2500,30	71,70%
Q9LXJ0	Cell division protein FtsZ homolog 2-2, chloroplastic OS=Arabidopsis thaliana GN=FTSZ2-2 PE=1 SV=1	1	---	----	-0,048	0,87781	2488,11	71,70%
Q9SSK7	MLP-like protein 34 OS=Arabidopsis thaliana GN=MLP34 PE=2 SV=1	1	---	----	-0,049	0,88081	2496,61	71,70%
Q9ZU35	ABC transporter G family member 7 OS=Arabidopsis thaliana GN=ABCG7 PE=2 SV=1	1	---	----	-0,05	0,88011	2494,63	71,70%
Q9CAR7	Hypersensitive-induced response protein 2 OS=Arabidopsis thaliana GN=HIR2 PE=1 SV=1	1	---	----	-0,053	0,87811	2488,96	71,70%
Q8VXZ0	Nudix hydrolase 20, chloroplastic OS=Arabidopsis thaliana GN=NUDT20 PE=2 SV=1	1	---	----	-0,057	0,87941	2492,64	71,70%
Q9SZU7	Probable esterase KAI2 OS=Arabidopsis thaliana GN=KAI2 PE=1 SV=1	1	---	----	-0,07	0,87611	2483,29	71,70%
Q93ZY3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Arabidopsis thaliana GN=STT3A PE=	1	---	----	-0,112	0,88011	2494,63	71,70%
F4I600	V-ATPase-related protein OS=Arabidopsis thaliana GN=At1g16820 PE=4 SV=1	1	---	----	-0,124	0,87411	2477,62	71,70%
Q9LM59	Serine hydroxymethyltransferase 6 OS=Arabidopsis thaliana GN=SHM6 PE=2 SV=1	1	---	----	0,111	0,88201	2500,01	71,80%
P34047	Imidazoleglycerol-phosphate dehydratase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN5A PE=1 SV=1	1	---	----	0,083	0,87601	2483,01	71,80%
Q9FHW7	SKP1-like protein 1B OS=Arabidopsis thaliana GN=SKP1B PE=1 SV=1	1	---	----	0,079	0,87611	2483,29	71,80%
Q5XEP2;Q9LNB6	Hsp70-Hsp90 organizing protein 2 OS=Arabidopsis thaliana GN=HOP2 PE=1 SV=1	1	---	----	0,054	0,87601	2483,01	71,80%
Q9FE63	Profilin-5 OS=Arabidopsis thaliana GN=PRO5 PE=2 SV=1	2	---	----	0,035	0,87601	2483,01	71,80%
Q9M812	Protein CURVATURE THYLAKOID 1C, chloroplastic OS=Arabidopsis thaliana GN=CURT1C PE=1 SV=1	2	---	----	0,029	0,87601	2483,01	71,80%
Q9FUP0	12-oxophytodienoate reductase 3 OS=Arabidopsis thaliana GN=OPR3 PE=1 SV=2	2	---	----	0,026	0,88211	2500,30	71,80%
Q9XIF8	Glutathione S-transferase U16 OS=Arabidopsis thaliana GN=GSTU16 PE=2 SV=1	3	---	----	0,022	0,88441	2506,81	71,80%
Q38799	Pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial OS=Arabidopsis thaliana GN=PDH2 PE=1 SV=2	9	---	----	0,009	0,88411	2505,97	71,80%
Q9SD79	Putative uncharacterized protein F13G24.250 OS=Arabidopsis thaliana GN=F13G24.250 PE=1 SV=1	3	---	----	-0,012	0,88611	2511,63	71,80%
O81148	Proteasome subunit alpha type-4-A OS=Arabidopsis thaliana GN=PAC1 PE=1 SV=1	7	---	----	-0,013	0,88411	2505,97	71,80%
Q41932;Q9XFT3-2	Oxygen-evolving enhancer protein 3-2, chloroplastic OS=Arabidopsis thaliana GN=PSBQ2 PE=1 SV=2	1	---	----	-0,017	0,88401	2505,68	71,80%
Q93ZB6	Uroporphyrinogen decarboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=HEME1 PE=2 SV=2	5	---	----	-0,019	0,88611	2511,63	71,80%
P42645;Q96300	14-3-3-like protein GF14 upsilon OS=Arabidopsis thaliana GN=GRF5 PE=1 SV=2	3	---	----	-0,021	0,88611	2511,63	71,80%
Q2HIQ2	At1g01170 OS=Arabidopsis thaliana GN=At1g01170 PE=2 SV=1	2	---	----	-0,031	0,88611	2511,63	71,80%
Q9SHE7	Ubiquitin-NEDD8-like protein RUB1 OS=Arabidopsis thaliana GN=RUB1 PE=1 SV=3	2	---	----	-0,036	0,88211	2500,30	71,80%
Q9SNB5	Putative uncharacterized protein At3g46630 OS=Arabidopsis thaliana GN=F12A12.150 PE=2 SV=1	1	---	----	-0,051	0,88611	2511,63	71,80%
Q94JY3	Dienelactone hydrolase-like protein OS=Arabidopsis thaliana GN=MDB19.5 PE=2 SV=1	1	---	----	-0,062	0,88411	2505,97	71,80%
Q66GQ3	Protein disulfide isomerase-like 1-6 OS=Arabidopsis thaliana GN=PDIL1-6 PE=2 SV=1	1	---	----	-0,078	0,88411	2505,97	71,80%
Q6NQE2	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 1 OS=Arabidopsis thaliana GN=At4g27270 PE=2 SV=1	1	---	----	0,098	0,89011	2522,97	71,90%
P59231	60S ribosomal protein L10a-3 OS=Arabidopsis thaliana GN=RPL10AC PE=1 SV=1	1	---	----	0,062	0,89421	2534,59	71,90%
Q84L31	Ubiquitin receptor RAD23c OS=Arabidopsis thaliana GN=RAD23C PE=1 SV=2	1	---	----	0,054	0,88811	2517,30	71,90%
P56752	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic OS=Arabidopsis thaliana GN=ndhF PE=3 SV=1	3	---	----	0,03	0,88811	2517,30	71,90%
Q9SMU8	Peroxidase 34 OS=Arabidopsis thaliana GN=PER34 PE=1 SV=1	3	---	----	0,021	0,89011	2522,97	71,90%
Q8GWP4	At2g21530 OS=Arabidopsis thaliana GN=At2g21530 PE=2 SV=1	5	---	----	0,013	0,89411	2534,31	71,90%
Q38882	Phospholipase D alpha 1 OS=Arabidopsis thaliana GN=PLDALPHA1 PE=1 SV=2	13	---	----	0,01	0,88611	2511,63	71,90%
O80842	Cell division protein FtsY homolog, chloroplastic OS=Arabidopsis thaliana GN=CPFTSY PE=1 SV=2	2	---	----	-0,028	0,89011	2522,97	71,90%
Q42600	Cytochrome P450 84A1 OS=Arabidopsis thaliana GN=CYP84A1 PE=1 SV=1	2	---	----	-0,03	0,89011	2522,97	71,90%
Q8L4B2	Nuclear transcription factor Y subunit C-9 OS=Arabidopsis thaliana GN=NFYC9 PE=2 SV=1	2	---	----	-0,033	0,89411	2534,31	71,90%
Q9STU1	Probable inactive poly [ADP-ribose] polymerase SRO4 OS=Arabidopsis thaliana GN=SRO4 PE=2 SV=2	1	---	----	-0,043	0,88611	2511,63	71,90%
Q9LRN0	ABC1 protein kinase 6 OS=Arabidopsis thaliana GN=At3g24190 PE=2 SV=1	3	---	----	-0,05	0,88401	2505,68	71,90%
Q9FGK3	Putative MO25-like protein At5g47540 OS=Arabidopsis thaliana GN=At5g47540 PE=2 SV=1	1	---	----	-0,05	0,88811	2517,30	71,90%
Q9SU14	Nudix hydrolase 7 OS=Arabidopsis thaliana GN=NUDT7 PE=1 SV=1	1	---	----	0,076	0,89220	2528,89	72,00%
Q9LU21	Photosynthetic NDH subunit of subcomplex B 3, chloroplastic OS=Arabidopsis thaliana GN=PNSB3 PE=2 SV=1	1	---	----	0,069	0,89641	2540,83	72,00%
P93832;Q9SA14	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1	1	---	----	0,066	0,89811	2545,64	72,00%
Q9ZVN2	Acyltransferase-like protein At1g54570, chloroplastic OS=Arabidopsis thaliana GN=At1g54570 PE=2 SV=1	1	---	----	0,065	0,89211	2528,64	72,00%
Q9LTT8	Enhancer of mRNA-decapping protein 4 OS=Arabidopsis thaliana GN=VCS PE=1 SV=1	2	---	----	0,052	0,89011	2522,97	72,00%
B9DFK5	AT2G37860 protein OS=Arabidopsis thaliana GN=LCD1 PE=2 SV=1	1	---	----	0,047	0,89611	2539,98	72,00%
P21216;Q93V56	Soluble inorganic pyrophosphatase 2 OS=Arabidopsis thaliana GN=PPA2 PE=2 SV=2	1	---	----	0,045	0,89011	2522,97	72,00%

Q9SKU8	At2g20690/F5H14.34 OS=Arabidopsis thaliana GN=At2g20690 PE=2 SV=2	2	---	----	0,027	0,89411	2534,31	72,00%
O22683	Cyanate hydratase OS=Arabidopsis thaliana GN=CYN PE=2 SV=1	3	---	----	0,023	0,89211	2528,64	72,00%
Q9FJD4	Importin subunit beta-1 OS=Arabidopsis thaliana GN=KPNB1 PE=1 SV=1	10	---	----	0,01	0,89741	2543,66	72,00%
Q93XM7	Mitochondrial carnitine/acylcarnitine carrier-like protein OS=Arabidopsis thaliana GN=BOU PE=2 SV=1	10	---	----	0,008	0,89811	2545,64	72,00%
Q8H0V3	Lactoylglutathione lyase OS=Arabidopsis thaliana GN=At1g08110 PE=2 SV=1	9	---	----	-0,01	0,89611	2539,98	72,00%
Q9SEI2	26S protease regulatory subunit 6A homolog A OS=Arabidopsis thaliana GN=RPT5A PE=1 SV=1	6	---	----	-0,019	0,89611	2539,98	72,00%
Q949W8	Putative xylulose kinase OS=Arabidopsis thaliana GN=XK-2 PE=2 SV=1	5	---	----	-0,02	0,89411	2534,31	72,00%
Q9LKA5	Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MORF8 PE=1 SV=1	2	---	----	-0,024	0,89811	2545,64	72,00%
Q96300	14-3-3-like protein GF14 nu OS=Arabidopsis thaliana GN=GRF7 PE=1 SV=1	3	---	----	-0,027	0,89211	2528,64	72,00%
Q94K75	Rho-N domain-containing protein 1, chloroplastic OS=Arabidopsis thaliana GN=RHON1 PE=1 SV=1	2	---	----	-0,03	0,89011	2522,97	72,00%
Q9XH48	Mitochondrial import inner membrane translocase subunit TIM13 OS=Arabidopsis thaliana GN=TIM13 PE=1 SV=2	1	---	----	-0,03	0,89411	2534,31	72,00%
Q94C69	Cold shock domain-containing protein 3 OS=Arabidopsis thaliana GN=CSP3 PE=1 SV=1	1	---	----	-0,042	0,89411	2534,31	72,00%
Q8RWC3	Putative uncharacterized protein At3g19340 OS=Arabidopsis thaliana GN=At3g19340 PE=2 SV=1	1	---	----	-0,056	0,89411	2534,31	72,00%
Q8VXZ9	Polyadenylate-binding protein RBP47B' OS=Arabidopsis thaliana GN=RBP47B' PE=2 SV=1	1	---	----	-0,078	0,89611	2539,98	72,00%
Q9SAJ3	ATP-dependent zinc metalloprotease FTSH 12, chloroplastic OS=Arabidopsis thaliana GN=FTSH12 PE=2 SV=2	1	---	----	0,114	0,89811	2545,64	72,10%
Q9LJX0	ABC transporter B family member 19 OS=Arabidopsis thaliana GN=ABCB19 PE=1 SV=1	1	---	----	0,068	0,89411	2534,31	72,10%
Q84VZ1	At1g79790 OS=Arabidopsis thaliana GN=At1g79790 PE=2 SV=1	1	---	----	0,041	0,89941	2549,33	72,10%
Q9SYB5	Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3B OS=Arabidopsis thaliana GN=OST3	1	---	----	0,04	0,90101	2553,87	72,10%
F4IN59	Resistance to phytophthora 1 protein OS=Arabidopsis thaliana GN=RPH1 PE=4 SV=1	1	---	----	0,038	0,89811	2545,64	72,10%
Q9SX53	At1g50380/F14I3_27 OS=Arabidopsis thaliana GN=F14I3.4 PE=2 SV=1	3	---	----	0,021	0,90011	2551,31	72,10%
Q8LPJ7	40S ribosomal protein S26-2 OS=Arabidopsis thaliana GN=RPS26B PE=2 SV=2	2	---	----	0,02	0,90211	2556,98	72,10%
P43333	U2 small nuclear ribonucleoprotein A' OS=Arabidopsis thaliana GN=At1g09760 PE=2 SV=2	4	---	----	-0,018	0,90141	2555,00	72,10%
Q9FFP6;Q9FM97;Q9FNN1	Pyruvate kinase OS=Arabidopsis thaliana GN=At5g63680 PE=3 SV=1	1	---	----	-0,023	0,89401	2534,02	72,10%
O82314	Probable transcriptional regulatory protein At2g25830 OS=Arabidopsis thaliana GN=At2g25830 PE=2 SV=2	4	---	----	-0,025	0,89411	2534,31	72,10%
Q8GXH2	Apoptosis inhibitory protein 5 OS=Arabidopsis thaliana GN=At1g29030 PE=2 SV=1	1	---	----	-0,035	0,90211	2556,98	72,10%
B9DFG3	DEAD-box ATP-dependent RNA helicase ISE2, chloroplastic OS=Arabidopsis thaliana GN=ISE2 PE=1 SV=2	1	---	----	-0,048	0,90011	2551,31	72,10%
Q9SJ36	40S ribosomal protein S17-2 OS=Arabidopsis thaliana GN=RPS17B PE=2 SV=3	1	---	----	-0,085	0,90011	2551,31	72,10%
Q944A2	Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g20220 PE=1 SV=1	1	---	----	0,084	0,90360	2561,21	72,20%
F4K658	FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=At5g49555 PE=4 SV=1	1	---	----	0,079	0,90811	2573,99	72,20%
Q9FLK2	Probable cytochrome c oxidase subunit 5C-3 OS=Arabidopsis thaliana GN=At5g61310 PE=2 SV=1	1	---	----	0,052	0,90411	2562,65	72,20%
Q9FIS0	Genomic DNA, chromosome 5, P1 clone:MTG10 OS=Arabidopsis thaliana GN=At5g62170 PE=4 SV=1	1	---	----	0,03	0,90611	2568,32	72,20%
P93285	Cytochrome c oxidase subunit 2 OS=Arabidopsis thaliana GN=COX2 PE=2 SV=2	2	---	----	0,028	0,90811	2573,99	72,20%
A8MS68;F4JLP5	Dihydrolipoyl dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=LPD1 PE=2 SV=1	6	---	----	0,01	0,90411	2562,65	72,20%
F4K000	Metal-dependent protein hydrolase OS=Arabidopsis thaliana GN=At5g41970 PE=1 SV=1	6	---	----	-0,015	0,90611	2568,32	72,20%
Q9STS7	Chloroplastic lipocalin OS=Arabidopsis thaliana GN=T23J7.190 PE=2 SV=1	2	---	----	-0,028	0,90611	2568,32	72,20%
P93834;Q42525	Hexokinase-2 OS=Arabidopsis thaliana GN=HXK2 PE=1 SV=1	1	---	----	-0,038	0,90211	2556,98	72,20%
O04209	Clathrin light chain 2 OS=Arabidopsis thaliana GN=CLC2 PE=1 SV=1	1	---	----	-0,041	0,90811	2573,99	72,20%
Q8GUI4	Uncharacterized GPI-anchored protein At1g61900 OS=Arabidopsis thaliana GN=At1g61900 PE=1 SV=1	1	---	----	-0,044	0,90411	2562,65	72,20%
O81127	Serine/arginine-rich splicing factor RSZ21 OS=Arabidopsis thaliana GN=RSZ21 PE=1 SV=1	1	SPDYGYAR	Phospho S1	-0,059	0,90611	2568,32	72,20%
P92964	Serine/arginine-rich splicing factor RS31 OS=Arabidopsis thaliana GN=RS31 PE=1 SV=2	1	---	----	-0,063	0,90411	2562,65	72,20%
Q9FGK0	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Arabidopsis thaliana GN=At5g475	1	---	----	0,036	0,90801	2573,70	72,30%
Q940M2	Alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial OS=Arabidopsis thaliana GN=AGT2 PE=2 SV=1	2	---	----	0,028	0,90611	2568,32	72,30%
Q9M098	AT4g30620/F17I23_40 OS=Arabidopsis thaliana GN=At4g30620 PE=2 SV=1	2	---	----	0,027	0,90601	2568,03	72,30%
Q9FFD2	Probable UDP-arabinopyranose mutase 5 OS=Arabidopsis thaliana GN=RGP5 PE=1 SV=1	2	---	----	0,024	0,90811	2573,99	72,30%
Q8LPS6	Pentatricopeptide repeat-containing protein At1g02150 OS=Arabidopsis thaliana GN=At1g02150 PE=2 SV=2	4	---	----	0,018	0,90761	2572,57	72,30%
Q9LPZ1	Multiple organellar RNA editing factor 9, chloroplastic OS=Arabidopsis thaliana GN=MORF9 PE=1 SV=1	5	---	----	0,014	0,91011	2579,65	72,30%
Q9LEU8	Argininosuccinate lyase, chloroplastic OS=Arabidopsis thaliana GN=At5g10920 PE=2 SV=1	6	---	----	0,014	0,91060	2581,05	72,30%
F4IYF8	Histidyl-tRNA synthetase OS=Arabidopsis thaliana GN=At3g02760 PE=3 SV=1	8	---	----	0,012	0,90581	2567,47	72,30%
Q8W1X2	Pyridoxal kinase OS=Arabidopsis thaliana GN=PK PE=1 SV=2	5	---	----	-0,015	0,90801	2573,70	72,30%
Q9FFC0	Histone H2B.10 OS=Arabidopsis thaliana GN=At5g22880 PE=1 SV=3	1	---	----	-0,019	0,91011	2579,65	72,30%
Q9SEL6	Vesicle transport v-SNARE 11 OS=Arabidopsis thaliana GN=VTI11 PE=1 SV=2	2	---	----	-0,023	0,90611	2568,32	72,30%
Q2HIU0	At3g15110 OS=Arabidopsis thaliana GN=At3g15110 PE=2 SV=1	1	---	----	0,044	0,91211	2585,32	72,40%
Q9SX65	1,4-dihydroxy-2-naphthoyl-CoA thioesterase 1 OS=Arabidopsis thaliana GN=DHNAT1 PE=1 SV=1	2	---	----	0,023	0,91211	2585,32	72,40%
P34066	Proteasome subunit alpha type-1-A OS=Arabidopsis thaliana GN=PAF1 PE=1 SV=3	8	---	----	0,009	0,91211	2585,32	72,40%
Q70DU8	Aldehyde dehydrogenase family 3 member H1 OS=Arabidopsis thaliana GN=ALDH3H1 PE=1 SV=2	4	---	----	-0,019	0,91300	2587,85	72,40%

F4K5J1	Myosin-17 OS=Arabidopsis thaliana GN=XI-K PE=1 SV=2	1	GSPQSAGLSFLNR	Phospho S9	-0,083	0,91211	2585,32	72,40%
Q8GYC7	PGR5-like protein 1B, chloroplastic OS=Arabidopsis thaliana GN=PGRL1B PE=1 SV=1	3	---	----	-0,016	0,91401	2590,71	72,50%
Q9SCZ8	AT3g51510/F26O13_150 OS=Arabidopsis thaliana GN=F26O13.150 PE=2 SV=1	2	---	----	-0,028	0,91411	2590,99	72,50%
O04130;O49485	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2	1	---	----	-0,029	0,91411	2590,99	72,50%
Q84VV6	At4g16566 OS=Arabidopsis thaliana GN=HINT4 PE=2 SV=1	1	---	----	0,061	0,91611	2596,66	72,60%
F4K4Q2	Isoleucyl-tRNA synthetase OS=Arabidopsis thaliana GN=OVA2 PE=3 SV=1	3	---	----	-0,019	0,91611	2596,66	72,60%
Q208N7	Alpha-crystallin domain 32.1 OS=Arabidopsis thaliana GN=ACD32.1 PE=2 SV=1	2	---	----	-0,032	0,91611	2596,66	72,60%
O49595	High mobility group B protein 1 OS=Arabidopsis thaliana GN=HMGB1 PE=1 SV=1	1	---	----	0,04	0,91811	2602,33	72,70%
O80948;O80950	Jacalin-related lectin 23 OS=Arabidopsis thaliana GN=JAL23 PE=1 SV=1	1	---	----	0,036	0,91811	2602,33	72,70%
Q66GP0	BTB/POZ domain-containing protein At5g67385 OS=Arabidopsis thaliana GN=At5g67385 PE=1 SV=2	1	---	----	-0,031	0,92011	2607,99	72,70%
F4J1H2	Putative eukaryotic LigT protein OS=Arabidopsis thaliana GN=At3g16230 PE=4 SV=1	1	---	----	-0,054	0,91811	2602,33	72,70%
O04834	GTP-binding protein SAR1A OS=Arabidopsis thaliana GN=SAR1A PE=2 SV=1	1	---	----	0,055	0,92011	2607,99	72,80%
Q9ZV06	Probable acetyltransferase NATA1-like OS=Arabidopsis thaliana GN=At2g39020 PE=2 SV=1	2	---	----	0,034	0,92211	2613,66	72,80%
Q9C7F5	Nuclear transport factor 2 OS=Arabidopsis thaliana GN=NTF2 PE=1 SV=1	5	---	----	0,01	0,92211	2613,66	72,80%
F4JLP5	Dihydrolipoyl dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=LPD2 PE=2 SV=2	7	---	----	0,01	0,92211	2613,66	72,80%
F4I116	ATP binding/leucine-tRNA ligases/aminoacyl-tRNA ligases OS=Arabidopsis thaliana GN=At1g09620 PE=1 SV=1	13	---	----	0,01	0,92261	2615,09	72,80%
Q8LE52	Glutathione S-transferase DHAR3, chloroplastic OS=Arabidopsis thaliana GN=DHAR3 PE=1 SV=1	13	---	----	0,007	0,92061	2609,42	72,80%
Q9SRY4	Protein LOW PSII ACCUMULATION 1, chloroplastic OS=Arabidopsis thaliana GN=LPA1 PE=1 SV=1	5	---	----	-0,011	0,92211	2613,66	72,80%
Q9S7Z8	Auxin efflux carrier component 3 OS=Arabidopsis thaliana GN=PIN3 PE=1 SV=1	1	---	----	-0,032	0,92011	2607,99	72,80%
Q9ZV42	Putative signal recognition particle receptor beta subunit OS=Arabidopsis thaliana GN=At2g18770 PE=2 SV=1	1	---	----	0,047	0,92201	2613,38	72,90%
Q9FHG3	RimM-like 16S rRNA processing protein OS=Arabidopsis thaliana GN=At5g46420 PE=3 SV=1	1	---	----	0,03	0,92611	2625,00	72,90%
Q8H0S3	At1g05520/T25N20_16 OS=Arabidopsis thaliana GN=At1g05520 PE=2 SV=1	1	---	----	0,024	0,92811	2630,67	72,90%
Q93WG3	Chloroplast J-like domain 1-containing protein OS=Arabidopsis thaliana GN=CJD1 PE=1 SV=1	3	---	----	0,021	0,93211	2642,00	72,90%
Q9LTR8	At5g57040 OS=Arabidopsis thaliana GN=At5g57040 PE=2 SV=1	1	---	----	0,016	0,92611	2625,00	72,90%
Q9C9C0	Serine protease SPPA, chloroplastic OS=Arabidopsis thaliana GN=SPPA PE=2 SV=1	4	---	----	0,014	0,92541	2623,03	72,90%
Q1EBV4	At3g13235 OS=Arabidopsis thaliana GN=At3g13235 PE=1 SV=1	5	---	----	0,012	0,92411	2619,33	72,90%
F4I7X1;Q9SGR6	SKU5 similar 6 OS=Arabidopsis thaliana GN=SKS6 PE=4 SV=1	4	---	----	0,011	0,92441	2620,19	72,90%
Q96266	Glutathione S-transferase F8, chloroplastic OS=Arabidopsis thaliana GN=GSTF8 PE=1 SV=3	10	---	----	-0,006	0,92700	2627,53	72,90%
Q9C7N4	GDSL esterase/lipase At1g29670 OS=Arabidopsis thaliana GN=At1g29670 PE=2 SV=1	6	---	----	-0,009	0,93101	2638,90	72,90%
Q9LU14	GDSL esterase/lipase APG OS=Arabidopsis thaliana GN=APG PE=1 SV=1	4	---	----	-0,017	0,92811	2630,67	72,90%
Q949M9	ATPase ASNA1 homolog OS=Arabidopsis thaliana GN=At1g01910 PE=1 SV=1	3	---	----	-0,017	0,93011	2636,34	72,90%
Q0WL80	UDP-glucose:glycoprotein glucosyltransferase OS=Arabidopsis thaliana GN=UGGT PE=1 SV=1	3	---	----	-0,018	0,92411	2619,33	72,90%
O23461	L-arabinokinase OS=Arabidopsis thaliana GN=ARA1 PE=1 SV=1	3	---	----	-0,019	0,92611	2625,00	72,90%
Q67YI9	Clathrin interactor EPSIN 2 OS=Arabidopsis thaliana GN=EPSIN2 PE=1 SV=1	2	---	----	-0,024	0,93011	2636,34	72,90%
A0JQ00	At5g02740 OS=Arabidopsis thaliana GN=At5g02740 PE=2 SV=1	1	---	----	-0,026	0,92411	2619,33	72,90%
Q9LKJ1	3-hydroxyisobutyryl-CoA hydrolase 1 OS=Arabidopsis thaliana GN=CHY1 PE=1 SV=1	4	---	----	-0,027	0,93011	2636,34	72,90%
Q9LYR2	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Arabidopsis thaliana GN=T22N19_90 PE=2 SV=1	2	---	----	-0,029	0,92611	2625,00	72,90%
Q07098	Serine/threonine-protein phosphatase PP2A-2 catalytic subunit OS=Arabidopsis thaliana GN=PP2A2 PE=1 SV=1	1	---	----	-0,029	0,92611	2625,00	72,90%
Q9SUI7	Photosystem I reaction center subunit VI-1, chloroplastic OS=Arabidopsis thaliana GN=PSAH1 PE=2 SV=1	2	---	----	-0,032	0,93011	2636,34	72,90%
Q9C952	Cleavage and polyadenylation specificity factor subunit 3-I OS=Arabidopsis thaliana GN=CPSF73-I PE=1 SV=1	1	---	----	0,08	0,93211	2642,00	73,00%
Q39024	Mitogen-activated protein kinase 4 OS=Arabidopsis thaliana GN=MPK4 PE=1 SV=2	1	---	----	0,037	0,93211	2642,00	73,00%
F4JC32	60S ribosomal protein L29-2 OS=Arabidopsis thaliana GN=At3g06680 PE=4 SV=1	1	---	----	0,028	0,92901	2633,23	73,00%
Q9SV71	Cytochrome b561 and DOMON domain-containing protein At4g12980 OS=Arabidopsis thaliana GN=At4g12980 PE=2 SV	1	---	----	0,027	0,93411	2647,67	73,00%
O49457	DNAJ heat shock protein OS=Arabidopsis thaliana GN=F20O9.160 PE=2 SV=1	1	---	----	0,023	0,93411	2647,67	73,00%
Q9ZVF1	Calcium-dependent lipid-binding domain-containing protein OS=Arabidopsis thaliana GN=At2g01540 PE=2 SV=1	1	---	----	0,021	0,93011	2636,34	73,00%
Q9SXS7	Bifunctional L-3-cyanoalanine synthase/cysteine synthase D2 OS=Arabidopsis thaliana GN=CYSD2 PE=1 SV=1	2	---	----	0,021	0,93611	2653,34	73,00%
Q43307	Glycerol-3-phosphate acyltransferase, chloroplastic OS=Arabidopsis thaliana GN=ATS1 PE=2 SV=2	6	---	----	-0,012	0,92811	2630,67	73,00%
Q8S8K0	Expressed protein OS=Arabidopsis thaliana GN=At2g17972 PE=2 SV=1	4	---	----	-0,015	0,93011	2636,34	73,00%
Q940J8;Q9FH82	Pectin acetylesterase 7 OS=Arabidopsis thaliana GN=PAE7 PE=2 SV=1	1	---	----	-0,016	0,93011	2636,34	73,00%
Q8LCQ4	At1g19150 OS=Arabidopsis thaliana GN=LHCA6 PE=2 SV=1	3	---	----	-0,018	0,92611	2625,00	73,00%
Q9ZQN9	CTF2A like oxidoreductase OS=Arabidopsis thaliana GN=CTF2A PE=4 SV=2	3	---	----	-0,02	0,92811	2630,67	73,00%
O24616	Proteasome subunit alpha type-7-B OS=Arabidopsis thaliana GN=PAD2 PE=1 SV=2	2	---	----	-0,022	0,93211	2642,00	73,00%
Q9SSS7	AT1G52730 protein OS=Arabidopsis thaliana GN=F6D8.2 PE=2 SV=1	1	---	----	-0,027	0,93461	2649,10	73,00%
Q9SR09	AT3g04650/F7O18_13 OS=Arabidopsis thaliana GN=F7O18.13 PE=2 SV=1	1	---	----	-0,098	0,93001	2636,05	73,00%
Q9LM40	AT1g18060/T10F20.23 OS=Arabidopsis thaliana GN=At1g18060 PE=2 SV=1	3	---	----	0,012	0,93611	2653,34	73,10%

F4IWV2;Q9FLH2	2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=At3g55410 PE=4 SV=1	4	---	----	-0,008	0,93411	2647,67	73,10%
Q8VZ68	Is a member of the PF|00364 Biotin-requiring enzymes family OS=Arabidopsis thaliana GN=At1g52670 PE=2 SV=1	2	---	----	-0,012	0,93611	2653,34	73,10%
B3H5S2	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=At5g38410 PE=3 SV=1	1	---	----	-0,013	0,93401	2647,39	73,10%
P93042	Protein ROOT HAIR DEFECTIVE 3 OS=Arabidopsis thaliana GN=RHD3 PE=1 SV=1	3	---	----	-0,017	0,93561	2651,94	73,10%
Q9XEE2	Annexin D2 OS=Arabidopsis thaliana GN=ANN2 PE=1 SV=1	2	---	----	-0,023	0,93611	2653,34	73,10%
Q9SSL1	Calcium-dependent lipid-binding (CaLB domain) family protein OS=Arabidopsis thaliana GN=F15H11.6 PE=2 SV=1	1	---	----	-0,026	0,93611	2653,34	73,10%
P46032	Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana GN=NPF8.3 PE=1 SV=1	1	---	----	0,038	0,93811	2659,01	73,20%
P0CAN7	V-type proton ATPase subunit E3 OS=Arabidopsis thaliana GN=VHA-E3 PE=2 SV=1	1	---	----	0,025	0,94011	2664,68	73,20%
Q9S9Z8-2	Isoform 2 of 14-3-3-like protein GF14 omicron OS=Arabidopsis thaliana GN=GRF11	1	---	----	0,023	0,94001	2664,41	73,20%
P30302	Aquaporin PIP2-3 OS=Arabidopsis thaliana GN=PIP2-3 PE=1 SV=1	2	---	----	0,014	0,94011	2664,68	73,20%
Q38946;Q43314	Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1	2	---	----	0,012	0,93960	2663,25	73,20%
Q9LK73	UDP-glycosyltransferase 88A1 OS=Arabidopsis thaliana GN=UGT88A1 PE=2 SV=1	3	---	----	-0,009	0,94211	2670,35	73,20%
Q9M8R4	Protein DJ-1 homolog D OS=Arabidopsis thaliana GN=DJ1D PE=1 SV=1	3	---	----	-0,014	0,93921	2662,14	73,20%
rev_O48789	reversed Alpha/beta-hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g26750 PE=2 SV=1	1	---	----	-0,035	0,93961	2663,27	73,20%
O23344	AT4g14890/dl3485w OS=Arabidopsis thaliana GN=dl3485w PE=2 SV=1	1	---	----	0,019	0,94411	2676,01	73,30%
Q9FDW8	Cytochrome b5 isoform A OS=Arabidopsis thaliana GN=CB5-A PE=1 SV=1	1	---	----	0,018	0,94211	2670,35	73,30%
Q9LSE4	At3g26710 OS=Arabidopsis thaliana GN=CCB1 PE=2 SV=1	2	---	----	0,013	0,94411	2676,01	73,30%
Q9LNC5	Elongation factor like protein OS=Arabidopsis thaliana GN=F9P14.8 PE=2 SV=1	5	---	----	0,011	0,94341	2674,04	73,30%
P20649	ATPase 1, plasma membrane-type OS=Arabidopsis thaliana GN=AHA1 PE=1 SV=3	9	---	----	0,006	0,94211	2670,35	73,30%
Q9FIQ0	Probable ADP-ribosylation factor GTPase-activating protein AGD9 OS=Arabidopsis thaliana GN=AGD9 PE=1 SV=1	4	---	----	-0,008	0,94211	2670,35	73,30%
Q949S7	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At5g15910 PE=2 SV=1	3	---	----	-0,012	0,94611	2681,68	73,30%
Q9SKC5	UDP-glycosyltransferase 74D1 OS=Arabidopsis thaliana GN=UGT74D1 PE=1 SV=1	2	---	----	-0,015	0,94211	2670,35	73,30%
Q42599	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial OS=Arabidopsis thaliana GN=At1g79010 PE=	3	---	----	-0,015	0,94211	2670,35	73,30%
Q9ZVZ9	Photosystem II D1 precursor processing protein PSB27-H2, chloroplastic OS=Arabidopsis thaliana GN=PSB27-2 PE=1 SV	1	---	----	-0,032	0,94411	2676,01	73,30%
Q8RWG2	At3g17040 OS=Arabidopsis thaliana GN=HCF107 PE=2 SV=1	1	---	----	-0,044	0,94411	2676,01	73,30%
F4IVY6	Radical SAM domain-containing protein OS=Arabidopsis thaliana GN=At2g39670 PE=3 SV=1	1	---	----	0,019	0,94611	2681,68	73,40%
Q943Z6	Signal recognition particle 19 kDa protein OS=Arabidopsis thaliana GN=SRP19 PE=1 SV=1	1	---	----	0,017	0,94811	2687,35	73,40%
Q94A82	Nudix hydrolase 19, chloroplastic OS=Arabidopsis thaliana GN=NUDT19 PE=1 SV=1	1	---	----	0,015	0,94411	2676,01	73,40%
Q8L7W8	Alpha-L-fucosidase 2 OS=Arabidopsis thaliana GN=FUC95A PE=1 SV=1	5	---	----	0,011	0,94611	2681,68	73,40%
Q9SVA6	Developmentally-regulated G-protein 3 OS=Arabidopsis thaliana GN=DRG3 PE=1 SV=1	3	---	----	0,011	0,94811	2687,35	73,40%
Q9STS1	Betaine aldehyde dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=ALDH10A9 PE=2 SV=1	5	---	----	0,009	0,94811	2687,35	73,40%
Q9LNU4	26S proteasome non-ATPase regulatory subunit 3 homolog A OS=Arabidopsis thaliana GN=RPN3A PE=1 SV=3	11	---	----	0,006	0,94611	2681,68	73,40%
Q42601	Carbamoyl-phosphate synthase large chain, chloroplastic OS=Arabidopsis thaliana GN=CARB PE=1 SV=1	21	---	----	-0,004	0,94611	2681,68	73,40%
P11490	Plastocyanin minor isoform, chloroplastic OS=Arabidopsis thaliana GN=PETE PE=1 SV=2	1	---	----	-0,009	0,94721	2684,82	73,40%
Q84WU2	Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana GN=UBP13 PE=1 SV=1	2	---	----	-0,021	0,94811	2687,35	73,40%
Q8VZP3	Putative uncharacterized protein At2g35810 OS=Arabidopsis thaliana GN=At2g35810 PE=2 SV=1	1	---	----	-0,062	0,94811	2687,35	73,40%
Q9SFU6	Callose synthase 9 OS=Arabidopsis thaliana GN=CALS9 PE=2 SV=2	1	---	----	0,021	0,95210	2698,69	73,50%
F4HYQ1	Uncharacterized protein OS=Arabidopsis thaliana GN=At1g55160 PE=4 SV=1	2	---	----	0,013	0,95210	2698,69	73,50%
Q9FV81	Glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GATB PE=2	9	---	----	0,009	0,95010	2693,02	73,50%
P62126	30S ribosomal protein S12, chloroplastic OS=Arabidopsis thaliana GN=rps12-A PE=2 SV=2	3	---	----	-0,008	0,95000	2692,74	73,50%
F4J2Z0	Uncharacterized protein OS=Arabidopsis thaliana GN=At3g29185 PE=4 SV=1	7	---	----	-0,009	0,95041	2693,89	73,50%
Q9LE82	RAN GTPase-activating protein 1 OS=Arabidopsis thaliana GN=RANGAP1 PE=1 SV=1	2	---	----	-0,01	0,95200	2698,40	73,50%
Q9FNJ9	Probable 2-carboxy-D-arabinitol-1-phosphatase OS=Arabidopsis thaliana GN=At5g22620 PE=1 SV=1	3	---	----	-0,012	0,95321	2701,82	73,50%
Q9LJX0;Q9M1Q9	ABC transporter B family member 19 OS=Arabidopsis thaliana GN=ABCB19 PE=1 SV=1	1	---	----	-0,017	0,95010	2693,02	73,50%
Q8L856	Transmembrane ascorbate ferrireductase 1 OS=Arabidopsis thaliana GN=CYB561A PE=1 SV=1	1	---	----	-0,02	0,95210	2698,69	73,50%
O04153	Calreticulin-3 OS=Arabidopsis thaliana GN=CRT3 PE=1 SV=2	1	---	----	-0,021	0,95210	2698,69	73,50%
Q9FKA5	Uncharacterized protein At5g39570 OS=Arabidopsis thaliana GN=At5g39570 PE=1 SV=1	1	SGSGDDEEGSYGR	Phospho S3	0,034	0,95410	2704,36	73,60%
Q9M2B9	AT3g43670/F23N14_50 OS=Arabidopsis thaliana GN=F23N14_50 PE=2 SV=1	1	---	----	0,02	0,95441	2705,22	73,60%
P92941	Chloride channel protein CLC-a OS=Arabidopsis thaliana GN=CLC-A PE=1 SV=2	1	TLSSTPLALVGAK	none	0,017	0,96010	2721,36	73,60%
Q9SHP0	Phosphoserine aminotransferase 2, chloroplastic OS=Arabidopsis thaliana GN=PSAT2 PE=2 SV=1	1	---	----	0,016	0,96021	2721,66	73,60%
Q9LVI6	Probable inactive receptor kinase RLK902 OS=Arabidopsis thaliana GN=RLK902 PE=1 SV=1	3	---	----	0,012	0,95841	2716,56	73,60%
Q9SMY7	Probable pectinesterase/pectinesterase inhibitor 44 OS=Arabidopsis thaliana GN=PME44 PE=2 SV=2	4	---	----	0,011	0,95610	2710,02	73,60%
O24653;Q96254	Guanosine nucleotide diphosphate dissociation inhibitor 2 OS=Arabidopsis thaliana GN=GDI2 PE=2 SV=1	3	---	----	0,009	0,95810	2715,69	73,60%
P56794	50S ribosomal protein L20, chloroplastic OS=Arabidopsis thaliana GN=rpl20 PE=3 SV=1	1	---	----	-0,011	0,95181	2697,85	73,60%
O49543	Cysteine desulfurase, mitochondrial OS=Arabidopsis thaliana GN=NIFS1 PE=1 SV=1	2	---	----	-0,019	0,96010	2721,36	73,60%

rev_Q9FRH7	reversed Tubby-like F-box protein 10 OS=Arabidopsis thaliana GN=TULP10 PE=1 SV=1	1	---	----	0,042	0,95610	2710,02	73,70%
Q9LF68	Protein BOLA4, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=BOLA4 PE=1 SV=1	1	---	----	0,024	0,96000	2721,08	73,70%
Q9FFG3	Outer membrane OMP85 family protein OS=Arabidopsis thaliana GN=MOP10.6 PE=2 SV=1	2	---	----	0,023	0,95610	2710,02	73,70%
Q1H5E3	At5g16870 OS=Arabidopsis thaliana GN=At5g16870 PE=2 SV=1	1	---	----	0,021	0,95681	2712,03	73,70%
Q9LZX4	Fasciclin-like arabinogalactan protein 10 OS=Arabidopsis thaliana GN=FLA10 PE=1 SV=1	1	---	----	0,019	0,95810	2715,69	73,70%
Q93VH1	Protein YIPF OS=Arabidopsis thaliana GN=At4g30260 PE=1 SV=1	2	---	----	0,017	0,95810	2715,69	73,70%
Q9ZSK4	Actin-depolymerizing factor 3 OS=Arabidopsis thaliana GN=ADF3 PE=1 SV=1	3	---	----	0,012	0,95810	2715,69	73,70%
Q94CE3	Beta carbonic anhydrase 5, chloroplastic OS=Arabidopsis thaliana GN=BCA5 PE=2 SV=1	2	---	----	0,012	0,96210	2727,03	73,70%
Q38842	AT0ZI1 protein OS=Arabidopsis thaliana GN=ATOZI1 PE=2 SV=1	3	---	----	0,009	0,95761	2714,29	73,70%
Q9ZQX4	V-type proton ATPase subunit F OS=Arabidopsis thaliana GN=VHA-F PE=2 SV=1	4	---	----	0,006	0,96010	2721,36	73,70%
Q93VK7	AT5g14910/F2G14_30 OS=Arabidopsis thaliana GN=At5g14910 PE=2 SV=1	4	---	----	0,004	0,95681	2712,03	73,70%
Q8VZ10	Haloacid dehalogenase-like hydrolase family protein OS=Arabidopsis thaliana GN=At1g56500 PE=2 SV=1	13	---	----	0,004	0,96010	2721,36	73,70%
Q9SKR2	Synaptotagmin-1 OS=Arabidopsis thaliana GN=SYT1 PE=1 SV=2	7	---	----	-0,008	0,95810	2715,69	73,70%
F4HYC8	Dienelactone hydrolase-like protein OS=Arabidopsis thaliana GN=At1g35420 PE=4 SV=1	2	---	----	-0,011	0,95610	2710,02	73,70%
Q9SIE7	Expressed protein OS=Arabidopsis thaliana GN=At2g22170 PE=2 SV=1	3	---	----	-0,011	0,96210	2727,03	73,70%
Q8L466	Anticodon-binding domain-containing protein OS=Arabidopsis thaliana GN=At1g24050 PE=2 SV=1	1	---	----	-0,017	0,96010	2721,36	73,70%
Q9MB58	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase OS=Arabidopsis thaliana GN=FKFBP PE=1 SV=1	1	SVETLSPFQQK	Phospho S6	-0,028	0,96210	2727,03	73,70%
Q9MB58	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase OS=Arabidopsis thaliana GN=FKFBP PE=1 SV=1	1	SLSASSFLIDTK	Phospho S5	-0,035	0,96010	2721,36	73,70%
O65369	At1g12090/T28K15.14 OS=Arabidopsis thaliana GN=F12F1.3 PE=2 SV=1	1	---	----	0,014	0,96410	2732,70	73,80%
Q9SJQ9;Q9SJU4	Fructose-bisphosphate aldolase OS=Arabidopsis thaliana GN=At2g36460 PE=2 SV=1	1	---	----	0,01	0,96410	2732,70	73,80%
Q9LVA0	BAG family molecular chaperone regulator 7 OS=Arabidopsis thaliana GN=BAG7 PE=1 SV=1	6	---	----	0,007	0,96410	2732,70	73,80%
Q84TI2	Phosphoribosylaminoimidazole carboxylase like protein OS=Arabidopsis thaliana GN=At2g37690 PE=2 SV=1	5	---	----	-0,006	0,96610	2738,37	73,80%
Q84L30;Q84L31	Ubiquitin receptor RAD23d OS=Arabidopsis thaliana GN=RAD23D PE=1 SV=2	2	---	----	-0,008	0,96521	2735,84	73,80%
Q9SJM0	Callose synthase 10 OS=Arabidopsis thaliana GN=CALS10 PE=2 SV=5	1	---	----	-0,02	0,96410	2732,70	73,80%
Q9FM47	RNA-binding (RRM/RBD/RNP motifs) family protein OS=Arabidopsis thaliana GN=At5g40490 PE=2 SV=1	3	---	----	0,009	0,96610	2738,37	73,90%
P43082	Hevein-like preproprotein OS=Arabidopsis thaliana GN=HEL PE=1 SV=1	2	---	----	0,009	0,96810	2744,03	73,90%
O81146	Proteasome subunit alpha type-6-A OS=Arabidopsis thaliana GN=PAA1 PE=1 SV=2	3	---	----	0,006	0,96610	2738,37	73,90%
Q9T0K5	Leucine-rich repeat extensin-like protein 3 OS=Arabidopsis thaliana GN=LRX3 PE=1 SV=1	3	---	----	0,004	0,97210	2755,37	73,90%
Q9S7M0	AT5g54270/MDK4_9 OS=Arabidopsis thaliana GN=LHCB3*1 PE=2 SV=1	7	---	----	0,003	0,96581	2737,54	73,90%
Q9ZUU2	Thioredoxin-like protein AAED1, chloroplastic OS=Arabidopsis thaliana GN=At2g37240 PE=2 SV=2	2	---	----	-0,004	0,97410	2761,04	73,90%
Q94AX4	D-lactate dehydrogenase [cytochrome], mitochondrial OS=Arabidopsis thaliana GN=DLD PE=1 SV=1	3	---	----	-0,006	0,96901	2746,61	73,90%
Q9FZ89	UPF0426 protein At1g28150, chloroplastic OS=Arabidopsis thaliana GN=At1g28150 PE=2 SV=1	1	---	----	-0,01	0,96810	2744,03	73,90%
F4HXV6	Nuclear pore complex protein NUP155 OS=Arabidopsis thaliana GN=NUP155 PE=1 SV=1	1	---	----	-0,012	0,96810	2744,03	73,90%
Q8LDN8	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 3 OS=Arabidopsis thaliana GN=UGE3 PE=1 SV=1	1	---	----	-0,012	0,96810	2744,03	73,90%
Q9M2D8	Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1	1	IALESESPAK	Phospho S7	0,026	0,97810	2772,38	74,00%
Q7X9V3	Acetyltransferase NSI OS=Arabidopsis thaliana GN=NSI PE=1 SV=1	1	---	----	0,012	0,97010	2749,70	74,00%
Q84W12	At4g16450 OS=Arabidopsis thaliana GN=At4g16450 PE=2 SV=1	1	---	----	0,01	0,97010	2749,70	74,00%
Q9T0P4	Ferredoxin-dependent glutamate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=GLU2 PE=1 SV=2	2	---	----	0,008	0,98010	2778,04	74,00%
O81644;O81645	Villin-2 OS=Arabidopsis thaliana GN=VLN2 PE=1 SV=2	2	---	----	0,007	0,97210	2755,37	74,00%
Q8H0U3	Armadillo/beta-catenin-like repeat-containing protein OS=Arabidopsis thaliana GN=At1g23180 PE=2 SV=1	3	---	----	0,006	0,97081	2751,71	74,00%
Q9M9M9	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Arabidopsis thaliana GN=At3g03100 F	1	---	----	0,006	0,97901	2774,95	74,00%
P10896	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RCA PE=1 SV=2	2	---	----	0,004	0,97210	2755,37	74,00%
P82715	PsbP domain-containing protein 5, chloroplastic OS=Arabidopsis thaliana GN=PPD5 PE=1 SV=3	3	---	----	0,004	0,97610	2766,71	74,00%
Q9LR75	Coproporphyrinogen-III oxidase 1, chloroplastic OS=Arabidopsis thaliana GN=CPX1 PE=2 SV=1	11	---	----	-0,003	0,98010	2778,04	74,00%
P56791	50S ribosomal protein L2, chloroplastic OS=Arabidopsis thaliana GN=rpl2-A PE=3 SV=1	4	---	----	-0,004	0,97661	2768,15	74,00%
Q9SUA1	DEK domain-containing chromatin associated protein OS=Arabidopsis thaliana GN=At4g26630 PE=1 SV=1	5	---	----	-0,004	0,97810	2772,38	74,00%
F4KH14	Phosphoglucosamine mutase family protein OS=Arabidopsis thaliana GN=At5g17530 PE=4 SV=1	5	---	----	-0,005	0,97810	2772,38	74,00%
P56754	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic OS=Arabidopsis thaliana GN=ndhJ PE=3 SV=1	3	---	----	-0,006	0,97610	2766,71	74,00%
P82873	Mitochondrial import receptor subunit TOM20-2 OS=Arabidopsis thaliana GN=TOM20-2 PE=1 SV=2	2	---	----	-0,006	0,97810	2772,38	74,00%
Q9LPL8	AT1G21350 protein OS=Arabidopsis thaliana GN=F24J8.1 PE=2 SV=1	2	---	----	-0,007	0,97341	2759,08	74,00%
O22711;Q9XEX2	Peroxiredoxin-2D OS=Arabidopsis thaliana GN=PRXIID PE=1 SV=2	1	---	----	-0,008	0,98010	2778,04	74,00%
Q06588;Q41931	1-aminocyclopropane-1-carboxylate oxidase 4 OS=Arabidopsis thaliana GN=ACO4 PE=1 SV=2	1	---	----	-0,009	0,97410	2761,04	74,00%
Q0WT48	DnaJ protein ERDJ2A OS=Arabidopsis thaliana GN=ERDJ2A PE=1 SV=1	1	---	----	-0,009	0,97901	2774,95	74,00%
Q39054	Molybdopterin biosynthesis protein CNX1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=2	2	---	----	-0,012	0,97210	2755,37	74,00%
Q9STH7	AT4g12340/T4C9_180 OS=Arabidopsis thaliana GN=T4C9.180 PE=2 SV=1	1	---	----	-0,012	0,97410	2761,04	74,00%

Q9SJ62	At2g35880/F11F19.21 OS=Arabidopsis thaliana GN=At2g35880 PE=2 SV=2	2	---	----	-0,012	0,97410	2761,04	74,00%
F4JNE1	Uncharacterized protein OS=Arabidopsis thaliana GN=At4g17100 PE=4 SV=1	2	---	----	-0,013	0,96810	2744,03	74,00%
F4JA39	Uncharacterized protein OS=Arabidopsis thaliana GN=At3g25680 PE=4 SV=1	1	---	----	-0,013	0,97610	2766,71	74,00%
Q9MBA3	Cell cycle checkpoint protein RAD17 OS=Arabidopsis thaliana GN=RAD17 PE=2 SV=1	1	---	----	-0,014	0,97410	2761,04	74,00%
O04420	Uricase OS=Arabidopsis thaliana GN=At2g26230 PE=1 SV=2	1	---	----	-0,016	0,97210	2755,37	74,00%
Q9LQF2	Alkaline/neutral invertase CINV1 OS=Arabidopsis thaliana GN=CINV1 PE=1 SV=1	1	SVLDTPLSSAR	Phospho S1	-0,019	0,97410	2761,04	74,00%
rev_P29976	reversed Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=	1	---	----	-0,031	0,97210	2755,37	74,00%
Q9ZUL3	Protein indeterminate-domain 5, chloroplastic OS=Arabidopsis thaliana GN=IDD5 PE=1 SV=1	1	TPNSDAEVIALSPK	Phospho S12	-0,039	0,97010	2749,70	74,00%
Q9M1X3	AT3g63160/F16M2_10 OS=Arabidopsis thaliana GN=F16M2_10 PE=1 SV=1	1	KSDSDDATVPPPSG	Phospho S3	0,036	0,97810	2772,38	74,10%
Q8RXZ8	At3g09980 OS=Arabidopsis thaliana GN=At3g09980 PE=1 SV=1	1	---	----	0,016	0,97810	2772,38	74,10%
F4JXP5	ACT domain-containing protein OS=Arabidopsis thaliana GN=At5g04740 PE=4 SV=1	1	---	----	0,011	0,97610	2766,71	74,10%
Q8W455	Expressed protein OS=Arabidopsis thaliana GN=At2g36835 PE=2 SV=1	1	---	----	-0,003	0,97810	2772,38	74,10%
Q8RU07	Putative malonyl-CoA OS=Arabidopsis thaliana GN=At2g30200 PE=2 SV=1	9	---	----	-0,003	0,98010	2778,04	74,10%
Q9C639	At1g45474/F2G19.4 OS=Arabidopsis thaliana GN=F2G19.4 PE=2 SV=1	2	---	----	-0,004	0,98010	2778,04	74,10%
F4JKW0	Thioredoxin family protein OS=Arabidopsis thaliana GN=At4g10000 PE=4 SV=1	2	---	----	-0,006	0,98210	2783,71	74,10%
Q9FR53	Serine/threonine-protein kinase TOR OS=Arabidopsis thaliana GN=TOR PE=1 SV=1	1	---	----	-0,007	0,98221	2784,02	74,10%
F4K6Z5	L-ascorbate oxidase OS=Arabidopsis thaliana GN=At5g21105 PE=4 SV=1	2	---	----	-0,009	0,97210	2755,37	74,10%
Q9SZ51	Early nodulin-like protein 15 OS=Arabidopsis thaliana GN=ENODL15 PE=2 SV=1	1	---	----	-0,009	0,97610	2766,71	74,10%
O22727	Probable disease resistance protein At1g61190 OS=Arabidopsis thaliana GN=At1g61190 PE=3 SV=1	1	---	----	-0,01	0,97410	2761,04	74,10%
Q9LZW6	AT5g01800/T20L15_70 OS=Arabidopsis thaliana GN=T20L15_70 PE=2 SV=1	1	---	----	0,009	0,98410	2789,38	74,20%
O23404	Pyruvate, phosphate dikinase 1, chloroplastic OS=Arabidopsis thaliana GN=PPDK PE=1 SV=2	1	GGMTSHAAVVAR	none	0,008	0,98410	2789,38	74,20%
Q38896	Cold shock domain-containing protein 4 OS=Arabidopsis thaliana GN=CSP4 PE=1 SV=1	1	---	----	0,007	0,98610	2795,05	74,20%
Q9ASV5	AT4g39690/T19P19_80 OS=Arabidopsis thaliana GN=At4g39690 PE=2 SV=1	2	---	----	0,005	0,98410	2789,38	74,20%
Q9LPT6	F11F12.1 protein OS=Arabidopsis thaliana GN=F11F12.1 PE=2 SV=1	4	---	----	-0,003	0,98410	2789,38	74,20%
Q9FIG9	Protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6, chloroplastic OS=Arabidopsis thaliana GN=ARC6 PE=	2	---	----	-0,003	0,98610	2795,05	74,20%
Q94F49	Probable histone H2A.5 OS=Arabidopsis thaliana GN=At5g27670 PE=1 SV=1	2	---	----	-0,005	0,98610	2795,05	74,20%
O48721	Uroporphyrinogen-III synthase, chloroplastic OS=Arabidopsis thaliana GN=UROS PE=2 SV=2	1	---	----	-0,006	0,98610	2795,05	74,20%
Q9SS61	At3g03590 OS=Arabidopsis thaliana GN=T12J13.13 PE=2 SV=1	1	---	----	-0,011	0,98610	2795,05	74,20%
Q9FGJ3	Nuclear transcription factor Y subunit B-2 OS=Arabidopsis thaliana GN=NFYB2 PE=2 SV=1	1	---	----	0,007	0,98610	2795,05	74,30%
Q8L7Z3	Anamorsin homolog OS=Arabidopsis thaliana GN=At5g18400 PE=1 SV=1	1	---	----	0,004	0,99010	2806,39	74,30%
Q9C505	Eukaryotic translation initiation factor 5A-3 OS=Arabidopsis thaliana GN=ELF5A-3 PE=2 SV=1	1	---	----	0,003	0,98610	2795,05	74,30%
Q9SAD7	Eukaryotic initiation factor 4B2 OS=Arabidopsis thaliana GN=F3F19.4 PE=1 SV=1	4	---	----	0,003	0,98610	2795,05	74,30%
Q9LP45	26S proteasome non-ATPase regulatory subunit 11 homolog OS=Arabidopsis thaliana GN=RPN6 PE=1 SV=1	5	---	----	-0,001	0,98610	2795,05	74,30%
Q38871	Calcium-dependent protein kinase 5 OS=Arabidopsis thaliana GN=CPK5 PE=2 SV=1	1	---	----	-0,005	0,98810	2800,72	74,30%
Q39025	Mitogen-activated protein kinase 5 OS=Arabidopsis thaliana GN=MPK5 PE=2 SV=2	1	---	----	-0,006	0,98810	2800,72	74,30%
Q9SYG5	At1g54090 OS=Arabidopsis thaliana GN=F15I1.17 PE=2 SV=1	1	---	----	0,012	0,99410	2817,72	74,40%
Q9M817	Protein NRT1/ PTR FAMILY 1.2 OS=Arabidopsis thaliana GN=NPF1.2 PE=1 SV=1	1	---	----	0,009	0,99061	2807,83	74,40%
Q9SGW5	F1N19.7 OS=Arabidopsis thaliana GN=At1g64500 PE=1 SV=1	1	---	----	0,006	0,99210	2812,05	74,40%
Q8L9X2	Chaperonin-like RbcX protein OS=Arabidopsis thaliana GN=At5g19855 PE=1 SV=1	2	---	----	0,002	0,99010	2806,39	74,40%
Q9M2T9	Methionyl-tRNA synthetase OS=Arabidopsis thaliana GN=T22E16.60 PE=3 SV=1	5	---	----	0,002	0,99010	2806,39	74,40%
O23629;Q9FFC0;Q9SI96	Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	1	---	----	0,002	0,99181	2811,23	74,40%
O48528	Outer envelope pore protein 16-3, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OEP163 PE=1 SV=1	4	---	----	0,002	0,99210	2812,05	74,40%
Q9FUS9	Glutathione S-transferase U18 OS=Arabidopsis thaliana GN=GSTU18 PE=2 SV=1	3	---	----	0,002	0,99210	2812,05	74,40%
Q9FM19	Hypersensitive-induced response protein 1 OS=Arabidopsis thaliana GN=HIR1 PE=1 SV=1	2	---	----	-0,001	0,99810	2829,06	74,40%
Q8VZ49	Alcohol dehydrogenase-like 4 OS=Arabidopsis thaliana GN=At1g64710 PE=2 SV=1	3	---	----	-0,002	0,99210	2812,05	74,40%
Q8LFQ6	Glutaredoxin-C4 OS=Arabidopsis thaliana GN=GRXC4 PE=2 SV=2	1	---	----	-0,003	0,99610	2823,39	74,40%
A2RVM0	Short-chain dehydrogenase TIC 32, chloroplastic OS=Arabidopsis thaliana GN=TIC32 PE=2 SV=1	2	---	----	-0,005	0,99010	2806,39	74,40%
P04778;P0CJ48;Q39142;C	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1	1	---	----	0,006	0,99610	2823,39	74,50%
P58049	Cytochrome P450 71B11 OS=Arabidopsis thaliana GN=CYP71B11 PE=2 SV=1	1	---	----	0,005	0,99410	2817,72	74,50%
Q9C5N2	Transmembrane 9 superfamily member 9 OS=Arabidopsis thaliana GN=TMN9 PE=2 SV=1	2	---	----	0,002	0,99810	2829,06	74,50%
Q9C9I5	AT1G71480 protein OS=Arabidopsis thaliana GN=F26A9.14 PE=2 SV=1	2	---	----	0,001	0,99410	2817,72	74,50%
B3LFA4	At5g38830 OS=Arabidopsis thaliana GN=At5g38830 PE=2 SV=1	1	---	----	0,001	1,00010	2834,73	74,50%
Q9LY66	50S ribosomal protein L1, chloroplastic OS=Arabidopsis thaliana GN=RPL1 PE=1 SV=1	11	---	----	0	0,99410	2817,72	74,50%
P0DKI3	Tropinone reductase homolog At1g07440 OS=Arabidopsis thaliana GN=At1g07440 PE=1 SV=1	4	---	----	0	0,99610	2823,39	74,50%
Q38820	Mitochondrial import inner membrane translocase subunit TIM23-2 OS=Arabidopsis thaliana GN=TIM23-2 PE=1 SV=1	1	---	----	0	0,99810	2829,06	74,50%

Q9M329	At3g53980 OS=Arabidopsis thaliana GN=F5K20_280 PE=2 SV=1	1	---	----	0	0,99901	2831,64	74,50%
Q944G9;Q9SJU4;Q9ZU52	Probable fructose-bisphosphate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=FBA2 PE=1 SV=2	2	---	----	-0,001	0,99610	2823,39	74,50%
Q9LR91	Acyl-CoA N-acyltransferases-like protein OS=Arabidopsis thaliana GN=At1g24040 PE=2 SV=1	1	---	----	-0,001	0,99610	2823,39	74,50%
F4JU03	Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=At4g19880 PE=1 SV=1	1	---	----	-0,001	0,99810	2829,06	74,50%
Q9LSW8	Electron transfer flavoprotein subunit beta, mitochondrial OS=Arabidopsis thaliana GN=ETFB PE=1 SV=1	1	---	----	-0,001	0,99810	2829,06	74,50%
O22912	Probable cytochrome c oxidase subunit 5C-1 OS=Arabidopsis thaliana GN=At2g47380 PE=3 SV=1	1	---	----	-0,001	0,99810	2829,06	74,50%
P49599	Protein phosphatase 2C 57 OS=Arabidopsis thaliana GN=PPH1 PE=2 SV=2	1	---	----	-0,001	1,00010	2834,73	74,50%
P92966	Serine/arginine-rich splicing factor RS41 OS=Arabidopsis thaliana GN=RS41 PE=1 SV=2	1	ERTSPDYGR	Phospho S4	-0,002	1,00010	2834,73	74,50%
Q38950;Q38951	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Arabidopsis thaliana GN=PP2A	2	---	----	-0,003	0,99610	2823,39	74,50%
Q93Z30	AT4g18950/F13C5_120 OS=Arabidopsis thaliana GN=At4g18950 PE=2 SV=1	1	---	----	0,001	1,00010	2834,73	74,60%
Q940V1;Q9SJZ7	AT4g39960/T5J17_130 OS=Arabidopsis thaliana GN=At4g39960 PE=2 SV=1	2	---	----	-0,001	0,99610	2823,39	74,60%
Q9LDY9	Protein Iojap, chloroplastic OS=Arabidopsis thaliana GN=IJ PE=2 SV=1	1	---	----	-0,001	0,99801	2828,80	74,60%
P93032	Isocitrate dehydrogenase [NAD] regulatory subunit 2, mitochondrial OS=Arabidopsis thaliana GN=IDH2 PE=2 SV=2	1	---	----	-0,002	0,99610	2823,39	74,60%

Supplemental Table S3: Subcellular localizations and functions of the proteins differentially regulated by *A. alternata* VOCs

ID	Biological Process	Cellular Component	Molecular Function	INTERPRO
A8MS32		GO:0005886~plasma membrane,		IPR012482:Lg106-like,
GT7;B9DHQ0;P11139;P2	GO:0000226~microtubule cytoskeleton organizati	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0	GO:0000166~nucleotide binding,GO:0003924~GTPase activity,GO:0005198~structural molecule ac	IPR000217:Tubulin,IPR002452:Alpha tubulin,IPR003008:Tubulin/FtsZ, GTPase domain,IPR017975:Tub
F4INE2;O03042;P93292	GO:0009853~photorespiration,GO:0015977~carb	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000287~magnesium ion binding,GO:0016831~carboxy-lyase activity,GO:0016984~ribulose-bis	IPR000685:Ribulose bisphosphate carboxylase, large subunit, C-terminal,IPR017443:Ribulose bisphos
O04130	GO:0006563~L-serine metabolic process,GO:0006	GO:0005829~cytosol,GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0004617~phosphoglycerate dehydrogenase activity,GO:0016	IPR002912:Amino acid-binding ACT,IPR006139:D-isomer specific 2-hydroxyacid dehydrogenase, catal
O04151	GO:0006457~protein folding,GO:0006970~respon	GO:0005739~mitochondrion,GO:0005783~endoplasmic reticulum,GO:0005788~endoplasmic re	GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008270~zinc ion binding,GO:00	IPR000886:Endoplasmic reticulum, targeting sequence,IPR001580:Calreticulin/calnexin,IPR009033:C
O04499	GO:0005996~monosaccharide metabolic process,	GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005829~cytosol,GO:00	GO:0004619~phosphoglycerate mutase activity,GO:0016866~intramolecular transferase activity,G	IPR005995:Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent,IPR006124:Metalloenzy
O04846	GO:0006163~purine nucleotide metabolic process	GO:0005783~endoplasmic reticulum,GO:0005886~plasma membrane,GO:0009507~chloroplast	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR000695:ATPase, P-type, H+ transporting proton pump,IPR001148:Carbonic anhydrase, alpha-class
O04905	GO:0006220~pyrimidine nucleotide metabolic pro		GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000850:Adenylate kinase,IPR006266:UMP-CMP kinase,
O04922	GO:0006979~response to oxidative stress,GO:005	GO:0005829~cytosol,	GO:0004601~peroxidase activity,GO:0004602~glutathione peroxidase activity,GO:0016209~antiox	IPR000889:Glutathione peroxidase,IPR012335:Thioredoxin fold,
O22788	GO:0006631~fatty acid metabolic process,GO:000	GO:0000267~cell fraction,GO:0005624~membrane fraction,GO:0005626~insoluble fraction,GO	GO:0005509~calcium ion binding,GO:0016165~lipoxygenase activity,GO:0016701~oxidoreductase	IPR007736:Caleosin related,
O22832	GO:0002252~immune effector process,GO:00066	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor	GO:0004768~stearoyl-CoA 9-desaturase activity,GO:0016717~oxidoreductase activity, acting on pa	IPR005067:Fatty acid desaturase, type 2,IPR005803:Stearoyl-ACP desaturase, conserved site,IPR0123
O23255	GO:0003006~reproductive developmental proces	GO:0005773~vacuole,GO:0005886~plasma membrane,	GO:0004013~adenosylhomocysteinase activity,GO:0005507~copper ion binding,GO:0016801~hydr	IPR000043:S-adenosyl-L-homocysteine hydrolase,IPR015878:S-adenosyl-L-homocysteine hydrolase,
O23324	GO:0000103~sulfate assimilation,GO:0006790~su	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0004779~sulfate adenylyltransferase activity,GO:0004781~sulfate adenylyltransferase (ATP) ac	IPR002650:ATP-sulfurylase,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,
O23515	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma membrane,GO:0015934~lar	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000439:Ribosomal protein L15e,
629;Q9FFC0;Q9SI96;Q9Z	GO:0006323~DNA packaging,GO:0006325~chrom	GO:0000785~chromatin,GO:0000786~nucleosome,GO:0005694~chromosome,GO:0005730~nu	GO:0003677~DNA binding,	IPR000558:Histone H2B,IPR007125:Histone core,IPR009072:Histone-fold,
O23684		GO:0005618~cell wall,GO:0009505~plant-type cell wall,GO:0009507~chloroplast,GO:0009536~		
O24457	GO:0005996~monosaccharide metabolic process,	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009536~plastid,GO:0009941~chl	GO:0004738~pyruvate dehydrogenase activity,GO:0004739~pyruvate dehydrogenase (acetyl-trans	IPR001017:Dehydrogenase, E1 component,IPR017597:Pyruvate dehydrogenase (acetyl-transferring)
O24521	GO:0009719~response to endogenous stimulus,G		GO:0005344~oxygen transporter activity,GO:0005506~iron ion binding,GO:0019825~oxygen bindin	IPR000971:Globin, subset,IPR001032:Leghaemoglobin,IPR012292:Globin,IPR019824:Leghaemoglobin
O48549	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma men	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001377:Ribosomal protein S6e,IPR014401:Ribosomal protein S6, eukaryotic,IPR018282:Ribosoma
O48741	GO:0006778~porphyrin metabolic process,GO:000	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009534~chloroplast thylakoid,GO	GO:0003959~NADPH dehydrogenase activity,GO:0016628~oxidoreductase activity, acting on the C	IPR002198:Short-chain dehydrogenase/reductase SDR,IPR002347:Glucose/ribitol dehydrogenase,IPR
O48917	GO:0006643~membrane lipid metabolic process,	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0008146~sulfotransferase activity,GO:0016782~transferase activity, transferring sulfur-contain	IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
O49304	GO:0006952~defense response,			IPR000916:Bet v I allergen,
O49499	GO:0006575~cellular amino acid derivative metab	GO:0005829~cytosol,	GO:0008171~O-methyltransferase activity,GO:0042409~caffeoyl-CoA O-methyltransferase activity,	IPR002935:O-methyltransferase, family 3,
O49562		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR005177:Protein of unknown function DUF299,IPR017409:Pyruvate Pi dikinase regulator,
O49629		GO:0009507~chloroplast,GO:0009534~chloroplast thylakoid,GO:0009535~chloroplast thylakoi	GO:0005198~structural molecule activity,	IPR006843:PAP fibrillin,
O49675	GO:0055114~oxidation reduction,	GO:0009507~chloroplast,GO:0009536~plastid,GO:0010287~plastoglobule,GO:0044434~chloro	GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxyg	IPR004294:Carotenoid oxygenase,
O64688	GO:0003006~reproductive developmental proces	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009536~plastid,GO:0009941~chl	GO:0004738~pyruvate dehydrogenase activity,GO:0004739~pyruvate dehydrogenase (acetyl-trans	IPR005475:Transketolase, central region,IPR005476:Transketolase, C-terminal,IPR015941:Transketol
O80517	GO:0006091~generation of precursor metabolites	GO:0005886~plasma membrane,GO:0031224~intrinsic to membrane,GO:0031225~anchored t	GO:0005507~copper ion binding,GO:0009055~electron carrier activity,GO:0043167~ion binding,G	IPR000923:Blue (type 1) copper domain,IPR003245:Plastocyanin-like,IPR008972:Cupredoxin,
O80533	GO:0006575~cellular amino acid derivative metab	GO:0012505~endomembrane system,	GO:0004022~alcohol dehydrogenase (NAD) activity,GO:0045551~cinnamyl-alcohol dehydrogenase	IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
O80585	GO:0000096~sulfur amino acid metabolic process		GO:0004489~methylenetetrahydrofolate reductase (NADPH) activity,GO:0016645~oxidoreductase	IPR003171:Methylenetetrahydrofolate reductase,IPR004621:Eukaryotic-type methylenetetrahydrof
O80626	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:002262	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001854:Ribosomal protein L29,IPR018254:Ribosomal protein L29, conserved site,
O80845	GO:0007031~peroxisome organization,GO:00165	GO:0005739~mitochondrion,GO:0005777~peroxisome,GO:0005778~peroxisomal membrane,G		IPR008733:Peroxisomal biogenesis factor 11,
O80852	GO:0006952~defense response,GO:0009404~toxi	GO:0005576~extracellular region,GO:0005773~vacuole,GO:0005886~plasma membrane,GO:00	GO:0004364~glutathione transferase activity,GO:0004601~peroxidase activity,GO:0004602~glutat	IPR004045:Glutathione S-transferase, N-terminal,IPR004046:Glutathione S-transferase, C-terminal,IP
O81439	GO:0009266~response to temperature stimulus,G	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009532~plastid stroma,GO:00095	GO:0005198~structural molecule activity,	IPR006843:PAP fibrillin,
O81852	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001048:Aspartate/glutamate/uridylate kinase,IPR001341:Aspartate kinase region,IPR001342:Hom
O82089	GO:0000041~transition metal ion transport,GO:00	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0005507~copper ion binding,GO:0016530~metallochaperone activity,GO:0016531~copper cha	IPR006121:Heavy metal transport/detoxification protein,
O82392	GO:0006766~vitamin metabolic process,GO:0006	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor	GO:0019144~ADP-sugar diphosphatase activity,GO:0051536~iron-sulfur cluster binding,GO:00515	IPR002817:Thiamine biosynthesis protein ThiC,
O82514, Q9SF85	GO:0006166~purine ribonucleoside salvage,GO:00	GO:0005576~extracellular region,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0005	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR000719:Protein kinase, core,IPR000850:Adenylate kinase,IPR001805:Adenosine kinase,IPR002173
P16127	GO:0006778~porphyrin metabolic process,GO:000	GO:0005618~cell wall,GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plast	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000523:Magnesium chelatase, ChlI subunit,IPR003593:ATPase, AAA+ type, core,IPR011775:Magn
P16181	GO:0003006~reproductive developmental proces	GO:0005618~cell wall,GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small ribosom	GO:0003723~RNA binding,GO:0003735~structural constituent of ribosome,GO:0005198~structura	IPR000266:Ribosomal protein S17,IPR012340:Nucleic acid-binding, OB-fold,IPR019979:Ribosomal pr
P17094	GO:0003006~reproductive developmental proces	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000597:Ribosomal protein L3,IPR019926:Ribosomal protein L3, conserved site,
P17562	GO:0000096~sulfur amino acid metabolic process	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0030312~external encapsulating structure,G	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR002133:S-adenosylmethionine synthetase,
P17597	GO:0008652~cellular amino acid biosynthetic pro	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR000399:TPP-binding enzymes, conserved site,IPR011766:Thiamine pyrophosphate enzyme, C-term
P19456	GO:0006163~purine nucleotide metabolic process	GO:0005886~plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR000695:ATPase, P-type, H+ transporting proton pump,IPR001757:ATPase, P-type, K/Mg/Cd/Cu/Zn
P21218	GO:0006778~porphyrin metabolic process,GO:000	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009527~plastid outer membrane,	GO:0016628~oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as accep	IPR002198:Short-chain dehydrogenase/reductase SDR,IPR002347:Glucose/ribitol dehydrogenase,IPR
P22953	GO:0006457~protein folding,GO:0009266~respon	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005829~c	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001023:Heat shock protein Hsp70,IPR013126:Heat shock protein 70,IPR018181:Heat shock protei
P23586	GO:0008643~carbohydrate transport,GO:005508	GO:0005773~vacuole,GO:0005886~plasma membrane,GO:0016021~integral to membrane,GO:	GO:0005351~sugar:hydrogen symporter activity,GO:0005402~cation:sugar symporter activity,GO:	IPR003663:Sugar/inositol transporter,IPR005828:General substrate transporter,IPR005829:Sugar tra
P23686	GO:0000096~sulfur amino acid metabolic process	GO:0005618~cell wall,GO:0005886~plasma membrane,GO:0030312~external encapsulating str	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR002133:S-adenosylmethionine synthetase,
P24806	GO:0005976~polysaccharide metabolic process,G	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0005886~plasma membrane,GO:00	GO:0016762~xyloglucan:xyloglucosyl transferase activity,	IPR000757:Glycoside hydrolase, family 16,IPR008263:Glycoside hydrolase, family 16, active site,IPR0
P25702	GO:0006631~fatty acid metabolic process,GO:000	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000036~acyl carrier activity,GO:0016597~amino acid binding,GO:0019842~vitamin binding,G	IPR003231:Acyl carrier protein (ACP),IPR006162:Phosphopantetheine attachment site,IPR006163:Ph
P25819	GO:0000302~response to reactive oxygen species	GO:0000325~plant-type vacuole,GO:0005739~mitochondrion,GO:0005773~vacuole,GO:00057	GO:0004096~catalase activity,GO:0004601~peroxidase activity,GO:0005275~amine transmembran	IPR002226:Catalase,IPR002293:Amino acid/polyamine transporter I,IPR004841:Amino acid permease
P25853	GO:0000272~polysaccharide catabolic process,G	GO:0012505~endomembrane system,	GO:0016160~amylase activity,GO:0016161~beta-amylase activity,GO:0043167~ion binding,GO:004	IPR001371:Glycoside hydrolase, family 14B, plant,IPR001554:Glycoside hydrolase, family 14,IPR0137
P25855;Q9LQL0	GO:0006544~glycine metabolic process,GO:00065	GO:0005739~mitochondrion,GO:0005960~glycine cleavage complex,GO:0009507~chloroplast,	GO:0004375~glycine dehydrogenase (decarboxylating) activity,GO:0016638~oxidoreductase activit	IPR002930:Glycine cleavage H-protein,IPR003016:2-oxo acid dehydrogenase, lipoyl-binding site,IPR0
P25858	GO:0000302~response to reactive oxygen species	GO:0005576~extracellular region,GO:0005739~mitochondrion,GO:0005740~mitochondrial env	GO:0000166~nucleotide binding,GO:0004365~glyceraldehyde-3-phosphate dehydrogenase (phosp	IPR000173:Glyceraldehyde 3-phosphate dehydrogenase,IPR006424:Glyceraldehyde-3-phosphate de
P28185	GO:0007242~intracellular signaling cascade,GO:00	GO:0005886~plasma membrane,GO:0009898~internal side of plasma membrane,GO:0044459	GO:0000166~nucleotide binding,GO:0005525~GTP binding,GO:0017076~purine nucleotide binding	IPR001806:Ras GTPase,IPR003579:Ras small GTPase, Rab type,IPR005225:Small GTP-binding protein,
P29402	GO:0006457~protein folding,	GO:0000267~cell fraction,GO:0005618~cell wall,GO:0005624~membrane fraction,GO:0005626	GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0030246~carbohydrate binding,G	IPR001580:Calreticulin/calnexin,IPR009033:Calreticulin/calnexin, P,IPR013320:Concanavalin A-like le
P29514	GO:0006461~protein complex assembly,GO:0006	GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0005886~plasma membrane,GO:001	GO:0000166~nucleotide binding,GO:0003924~GTPase activity,GO:0005198~structural molecule ac	IPR000217:Tubulin,IPR002453:Beta tubulin,IPR003008:Tubulin/FtsZ, GTPase domain,IPR013838:Beta
P29515	GO:0006461~protein complex assembly,GO:0006	GO:0005618~cell wall,GO:0005773~vacuole,GO:0005856~cytoskeleton,GO:0005874~microtub	GO:0000166~nucleotide binding,GO:0003924~GTPase activity,GO:0005198~structural molecule ac	IPR000217:Tubulin,IPR002453:Beta tubulin,IPR003008:Tubulin/FtsZ, GTPase domain,IPR013838:Beta
P29976	GO:0008652~cellular amino acid biosynthetic pro	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0003849~3-deoxy-7-phosphoheptulonate synthase activity,GO:0016765~transferase activity, t	IPR002480:DAHP synthetase, class II,
P32961	GO:0009683~indoleacetic acid metabolic process,	GO:0005576~extracellular region,GO:0005886~plasma membrane,GO:0009507~chloroplast,G	GO:0000257~nitrilase activity,GO:0016815~hydrolase activity, acting on carbon-nitrogen (but not	IPR000132:Nitrilase/cyanide hydratase, conserved site,IPR003010:Nitrilase/cyanide hydratase and ap
P32962	GO:0009617~response to bacterium,GO:0009683	GO:0005886~plasma membrane,GO:0009898~internal side of plasma membrane,GO:0044459	GO:0000257~nitrilase activity,GO:0016815~hydrolase activity, acting on carbon-nitrogen (but not	IPR000132:Nitrilase/cyanide hydratase, conserved site,IPR003010:Nitrilase/cyanide hydratase and ap
P38418	GO:0006631~fatty acid metabolic process,GO:000	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009532~plastid stroma,GO:00095	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0016165~lipoxygenase acti	IPR000907:Lipoxygenase,IPR001024:Lipoxygenase, LH2,IPR001246:Lipoxygenase, plant,IPR013819:Li
P41127	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001380:Ribosomal protein L13e,IPR018256:Ribosomal protein L13e, conserved site,
P42733	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small ribosomal subunit,GO:002262	GO:0003723~RNA binding,GO:0003735~structural constituent of ribosome,GO:0005198~structura	IPR000266:Ribosomal protein S17,IPR012340:Nucleic acid-binding, OB-fold,IPR019979:Ribosomal pr
P42761	GO:0009404~toxin metabolic process,GO:000940	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0005773~vacuole,GO:0005886~pla	GO:0004364~glutathione transferase activity,GO:0005507~copper ion binding,GO:0016765~transf	IPR004045:Glutathione S-transferase, N-terminal,IPR004046:Glutathione S-transferase, C-terminal,IP
P42762		GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009532~plastid stroma,GO:00095	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001270:Chaperonin clpA/B,IPR003593:ATPase, AAA+ type, core,IPR003959:ATPase, AAA-type, cor
P42801	GO:0006020~inositol metabolic process,GO:0006		GO:0004512~inositol-3-phosphate synthase activity,GO:0016872~intramolecular lyase activity,	IPR002587:Myo-inositol-1-phosphate synthase,IPR013021:Myo-inositol-1-phosphate synthase, GAPD
P46286	GO:0003006~reproductive developmental proces	GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO:	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR002171:Ribosomal protein L2,IPR012340:Nucleic acid-binding, OB-fold,IPR014726:Ribosomal prot
P46312	GO:0006631~fatty acid metabolic process,GO:000	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009528~plastid inner membrane,	GO:0045485~omega-6 fatty acid desaturase activity,	IPR005804:Fatty acid desaturase, type 1,
P46644	GO:0007568~aging,GO:0010149~senescence,GO:	GO:0005777~peroxisome,GO:0009507~chloroplast,GO:0009536~plastid,GO:0042579~microbo	GO:0004069~L-aspartate:2-oxoglutarate aminotransferase activity,GO:0008483~transaminase acti	IPR000796:Aspartate/other aminotransferase,IPR004838:Aminotransferases, class-I, pyridoxal-phosp

P48006	GO:0006412~translation,GO:0006414~translation	GO:0005853~eukaryotic translation elongation factor 1 complex,GO:0005886~plasma membra	GO:0003746~translation elongation factor activity,GO:0008135~translation factor activity, nucleic	IPR001326:Translation elongation factor EF1B, beta/delta chains, conserved site,IPR014038:Translati
P48421	GO:0006790~sulfur metabolic process,GO:00093	GO:0005783~endoplasmic reticulum,GO:0016021~integral to membrane,GO:0031224~intrinsi	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0019825~oxygen binding,G	IPR001128:Cytochrome P450,IPR002401:Cytochrome P450, E-class, group I,IPR017972:Cytochrome P
P49078	GO:0006528~asparagine metabolic process,GO:0		GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000583:Glutamine amidotransferase, class-II,IPR001962:Asparagine synthase,IPR006426:Asparagi
P49201	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small ribosomal subunit,GO:002262	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR005680:Ribosomal protein S23, eukaryotic/archaeal,IPR006032:Ribosomal protein S12/S23,IPR01
P49637	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:00226	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001196:Ribosomal protein L15,
P49688;Q8L8Y0	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small riboso	GO:0003723~RNA binding,GO:0003735~structural constituent of ribosome,GO:0005198~structura	IPR000851:Ribosomal protein S5,IPR005324:Ribosomal protein S5, C-terminal,IPR005711:Ribosomal
P49692	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma mem	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001921:Ribosomal protein L7A,IPR004037:Ribosomal protein L7Ae conserved site,IPR004038:Ribo
P51413	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001063:Ribosomal protein L22/L17,IPR005721:Ribosomal protein L22/L17, eukaryotic/archaeal,IP
P51418	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma membrane,GO:0015934~la	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR002670:Ribosomal protein L18ae,
P51420	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005618~cell wall,GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosom	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000054:Ribosomal protein L31e,
P51430	GO:0003006~reproductive developmental proces	GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma membrane,GO:0015935~sm	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001377:Ribosomal protein S6e,IPR014401:Ribosomal protein S6, eukaryotic,IPR018282:Ribosoma
P52032	GO:0006979~response to oxidative stress,GO:005	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009532~plastid stroma,GO:00095	GO:0004601~peroxidase activity,GO:0004602~glutathione peroxidase activity,GO:0016209~antiox	IPR000889:Glutathione peroxidase,IPR012335:Thioredoxin fold,
P53780	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0004121~cystathionine beta-lyase activity,GO:0016846~carbon-sulfur lyase activity,GO:001984	IPR000277:Cys/Met metabolism, pyridoxal phosphate-dependent enzyme,IPR006238:Cystathionine
P55217	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0003962~cystathionine gamma-synthase activity,GO:0016765~transferase activity, transferring	IPR000277:Cys/Met metabolism, pyridoxal phosphate-dependent enzyme,IPR015421:Pyridoxal phos
P56755	GO:0006091~generation of precursor metabolites	GO:0009507~chloroplast,GO:0009536~plastid,GO:0009579~thylakoid,GO:0019898~extrinsic to	GO:0003954~NADH dehydrogenase activity,GO:0005506~iron ion binding,GO:0008137~NADH deh	IPR001450:4Fe-4S ferredoxin, iron-sulphur binding, subgroup,IPR004497:NADH-plastoquinone oxido
P56780	GO:0010608~posttranscriptional regulation of ge	GO:0009507~chloroplast,GO:0009521~photosystem,GO:0009523~photosystem II,GO:000953	GO:0042301~phosphate binding,GO:0043167~ion binding,GO:0043168~anion binding,	IPR001056:Photosystem II phosphoprotein PsbH,
P57106	GO:0005996~monosaccharide metabolic process,	GO:0005886~plasma membrane,	GO:0016615~malate dehydrogenase activity,GO:0030060~L-malate dehydrogenase activity,	IPR001236:Lactate/malate dehydrogenase,IPR001252:Malate dehydrogenase, active site,IPR001557:
P59223;P59224	GO:0006412~translation,	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000589:Ribosomal protein S15,IPR012606:Ribosomal protein S13/S15, N-terminal,
P59230	GO:0003002~regionalization,GO:0006396~RNA p	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:00226	GO:0003723~RNA binding,GO:0003735~structural constituent of ribosome,GO:0005198~structura	IPR002143:Ribosomal protein L1,IPR016094:Ribosomal protein L1, 2-layer alpha/beta-sandwich,
P59232	GO:0006412~translation,GO:0006508~proteolysis	GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,GO:000	IPR000626:Ubiquitin,IPR001975:Ribosomal protein L40e,IPR002906:Ribosomal protein S27a,IPR0199
P60039	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,GO:003	IPR000517:Ribosomal protein L30p/L7e, N-terminal,IPR005998:Ribosomal protein L7, eukaryotic,IPR
P68209	GO:0006084~acetyl-CoA metabolic process,GO:0	GO:0005618~cell wall,GO:0005739~mitochondrion,GO:0030312~external encapsulating struct	GO:0000166~nucleotide binding,GO:0003878~ATP citrate synthase activity,GO:0004774~succinate	IPR003781:CoA-binding,IPR005810:Succinyl-CoA ligase, alpha subunit,IPR005811:ATP-citrate lyase/s
P81760		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009534~chloroplast thylakoid,GO:0		IPR001646:Pentapeptide repeat,
P82658		GO:0009507~chloroplast,GO:0009534~chloroplast thylakoid,GO:0009536~plastid,GO:0009543		IPR016123:Mog1/PsbP, alpha/beta/alpha sandwich,
P92980	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0009973~adenylyl-sulfate reductase activity,GO:0016667~oxidoreductase activity, acting on su	IPR002500:Phosphoadenosine phosphosulphate reductase,IPR004508:Thioredoxin-independent 5'-a
P92981	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009534~chloroplast thylakoid,GO:0	GO:0004604~phosphoadenylyl-sulfate reductase (thioredoxin) activity,GO:0009973~adenylyl-sulfa	IPR002500:Phosphoadenosine phosphosulphate reductase,IPR004508:Thioredoxin-independent 5'-a
P93836	GO:0006558~L-phenylalanine metabolic process,	GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0009507~chloroplast,GO:0009536~plast	GO:0003868~4-hydroxyphenylpyruvate dioxygenase activity,GO:0005506~iron ion binding,GO:001	IPR004360:Glyoxalase/bleomycin resistance protein/dioxygenase,IPR005956:4-hydroxyphenylpyruva
Q03250	GO:0003006~reproductive developmental proces	GO:0005777~peroxisome,GO:0009507~chloroplast,GO:0009536~plastid,GO:0012505~endome	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000504:RNA recognition motif, RNP-1,IPR000719:Protein kinase, core,IPR001245:Tyrosine protei
Q05431	GO:0000302~response to reactive oxygen species	GO:0005618~cell wall,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0009507~chlo	GO:0004601~peroxidase activity,GO:0005506~iron ion binding,GO:0005509~calcium ion binding,G	IPR002016:Haem peroxidase, plant/fungal/bacterial,IPR002207:Plant ascorbate peroxidase,IPR0197
Q07473	GO:0006091~generation of precursor metabolites	GO:0009507~chloroplast,GO:0009521~photosystem,GO:0009522~photosystem I,GO:0009523	GO:0000287~magnesium ion binding,GO:0016168~chlorophyll binding,GO:0043167~ion binding,G	IPR001344:Chlorophyll A-B binding protein,
Q1H537	GO:0006778~porphyrin metabolic process,GO:00	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009536~plastid,GO:0009941~chl	GO:0016564~transcription repressor activity,GO:0030528~transcription regulator activity,GO:0051	IPR008030:NmrA-like,IPR016040:NAD(P)-binding domain,
Q37165	GO:0055114~oxidation reduction,	GO:0009507~chloroplast,GO:0009536~plastid,GO:0009579~thylakoid,GO:0016021~integral to	GO:0048037~cofactor binding,GO:0048038~quinone binding,	IPR001694:NADH:ubiquinone oxidoreductase, subunit 1,IPR018086:NADH:ubiquinone oxidoreducta
Q38814	GO:0006766~vitamin metabolic process,GO:0006	GO:0005739~mitochondrion,GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009	GO:0042802~identical protein binding,GO:0042803~protein homodimerization activity,GO:004698	IPR002922:Thiamine biosynthesis Thi4 protein,
Q38853	GO:0006979~response to oxidative stress,GO:000	GO:0009507~chloroplast,GO:0009536~plastid,		IPR001763:Rhodanese-like,
Q38924	GO:0009267~cellular response to starvation,GO:0	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0009505~plant-type cell wall,GO:0	GO:0003993~acid phosphatase activity,GO:0004721~phosphoprotein phosphatase activity,GO:000	IPR004843:Metallophosphoesterase,IPR015914:Purple acid phosphatase, N-terminal,
Q38946	GO:0006970~response to osmotic stress,GO:0009	GO:0005739~mitochondrion,GO:0005886~plasma membrane,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR006095:Glutamate/phenylalanine/leucine/valine dehydrogenase,IPR006096:Glutamate/phenylal
Q39043	GO:0006457~protein folding,GO:0009266~respon	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005783~endoplasmic	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000886:Endoplasmic reticulum, targeting sequence,IPR001023:Heat shock protein Hsp70,IPR0131
Q39101	GO:0000041~transition metal ion transport,GO:0	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009534~chloroplast thylakoid,GO:0	GO:0004322~ferroxidase activity,GO:0005506~iron ion binding,GO:0008199~ferric iron binding,GO	IPR001519:Ferritin, N-terminal,IPR008331:Ferritin and Dps,IPR009040:Ferritin-like,IPR012347:Ferriti
Q39108	GO:0006720~isoprenoid metabolic process,GO:0	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0004311~farnesyltranstransferase activity,GO:0004659~prenyltransferase activity,GO:0016765	IPR000092:Polyprenyl synthetase,IPR008949:Terpenoid synthase,IPR017446:Polyprenyl synthetase-
Q39195	GO:0015979~photosynthesis,	GO:0009507~chloroplast,GO:0009521~photosystem,GO:0009523~photosystem II,GO:0009534		
Q39249	GO:0006631~fatty acid metabolic process,GO:000	GO:0009507~chloroplast,GO:0009521~photosystem,GO:0009523~photosystem II,GO:0009534	GO:0046422~violaxanthin de-epoxidase activity,	IPR002345:Lipocalin,IPR010788:Violaxanthin de-epoxidase,IPR012674:Calycin,
Q42112	GO:0006412~translation,GO:0006414~translation	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma mem	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001790:Ribosomal protein L10,IPR001813:Ribosomal protein 60S,
Q42340	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0009507~chloroplast,GO:0009536~plastid,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000754:Ribosomal protein S9,IPR014721:Ribosomal protein S5 domain 2-type fold,
Q42472	GO:0006536~glutamate metabolic process,GO:00		GO:0004351~glutamate decarboxylase activity,GO:0005516~calmodulin binding,GO:0016831~carb	IPR002129:Pyridoxal phosphate-dependent decarboxylase,IPR010107:Glutamate decarboxylase,IPR0
Q42523	GO:0006551~leucine metabolic process,GO:0006	GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005840~ribosome,GO:00	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000089:Biotin/lipoyl attachment,IPR001882:Biotin-binding site,IPR005479:Carbamoyl phosphate
Q42547	GO:0000302~response to reactive oxygen species	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0005739~mitochondrion,GO:0005	GO:0004096~catalase activity,GO:0004601~peroxidase activity,GO:0005275~amine transmembran	IPR002226:Catalase,IPR002293:Amino acid/polyamine transporter I,IPR004841:Amino acid permease
Q43295	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR002891:Adenylylsulphate kinase, C-terminal,
Q43349	GO:0006396~RNA processing,GO:0006397~mRNA	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor	GO:0000166~nucleotide binding,GO:0003723~RNA binding,GO:0003727~single-stranded RNA bind	IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait,
Q56WH4	GO:0003002~regionalization,GO:0006325~chrom	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005886~plasma mem	GO:0004407~histone deacetylase activity,GO:0016811~hydrolase activity, acting on carbon-nitrog	
Q56WK6	GO:0007049~cell cycle,GO:0051301~cell division,	GO:0005576~extracellular region,GO:0005773~vacuole,GO:0005886~plasma membrane,GO:0	GO:0008289~lipid binding,	IPR001251:Cellular retinaldehyde-binding/triple function, C-terminal,IPR008273:Cellular retinaldehy
Q56Y11	GO:0006720~isoprenoid metabolic process,GO:0	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0004659~prenyltransferase activity,GO:0016765~transferase activity, transferring alkyl or aryl	IPR001441:Di-trans-poly-cis-decaprenylcistransferase-like,IPR018520:Di-trans-poly-cis-decaprenylcis
Q56YU0	GO:0006575~cellular amino acid derivative meta	GO:0005829~cytosol,	GO:0004028~3-chloroallyl aldehyde dehydrogenase activity,GO:0004029~aldehyde dehydrogenas	IPR015590:Aldehyde dehydrogenase,IPR016160:Aldehyde dehydrogenase, conserved site,IPR016162
Q56Z59	GO:0007049~cell cycle,GO:0051301~cell division,	GO:0005886~plasma membrane,GO:0019898~extrinsic to membrane,	GO:0008289~lipid binding,	IPR001251:Cellular retinaldehyde-binding/triple function, C-terminal,IPR008273:Cellular retinaldehy
Q6NKS4	GO:0006091~generation of precursor metabolites	GO:0009507~chloroplast,GO:0009534~chloroplast thylakoid,GO:0009535~chloroplast thylakoi		
Q6STH5		GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000808:Mrp, conserved site,IPR002744:Protein of unknown function DUF59,IPR019591:ATPase-li
Q6ZY51	GO:0000272~polysaccharide catabolic process,G	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bi	IPR000121:PEP-utilizing enzyme,IPR002044:Glycoside hydrolase, carbohydrate-binding,IPR002192:P
Q7XA63		GO:0005773~vacuole,		IPR007493:Protein of unknown function DUF538,
Q84WM9	GO:0006412~translation,GO:0006414~translation	GO:0005853~eukaryotic translation elongation factor 1 complex,GO:0005886~plasma membra	GO:0003746~translation elongation factor activity,GO:0008135~translation factor activity, nucleic	IPR001326:Translation elongation factor EF1B, beta/delta chains, conserved site,IPR004046:Glutathi
Q8GW48				IPR009643:Heat shock factor binding 1,
Q8L7C9	GO:0009404~toxin metabolic process,GO:000940	GO:0005576~extracellular region,GO:0009507~chloroplast,GO:0009536~plastid,GO:0048046~	GO:0004364~glutathione transferase activity,GO:0016765~transferase activity, transferring alkyl o	IPR004045:Glutathione S-transferase, N-terminal,IPR004046:Glutathione S-transferase, C-terminal,IP
Q8L9E3				IPR008011:Complex 1 LYR protein,
Q8LCT3	GO:0006091~generation of precursor metabolites	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0016667~oxidoreductase activity, acting on sulfur group of donors,GO:0016671~oxidoreducta	IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain,IPR015467:Thioredoxin, core,IPR017936
Q8LDP4	GO:0006457~protein folding,	GO:0000267~cell fraction,GO:0005624~membrane fraction,GO:0005626~insoluble fraction,GO	GO:0003755~peptidyl-prolyl cis-trans isomerase activity,GO:0016859~cis-trans isomerase activity,	IPR002130:Peptidyl-prolyl cis-trans isomerase, cyclophilin-type,
Q8LDQ8		GO:0009507~chloroplast,GO:0009536~plastid,		
Q8LGG0	GO:0006457~protein folding,	GO:0009507~chloroplast,GO:0009534~chloroplast thylakoid,GO:0009536~plastid,GO:0009543	GO:0003755~peptidyl-prolyl cis-trans isomerase activity,GO:0005527~macrolide binding,GO:0005	IPR001179:Peptidyl-prolyl cis-trans isomerase, FKBP-type,
Q8RX87	GO:0009266~response to temperature stimulus,	GO:0009507~chloroplast,GO:0009536~plastid,		
Q8RXD5	GO:0006970~response to osmotic stress,GO:0009	GO:0005739~mitochondrion,	GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0030414	IPR002160:Proteinase inhibitor I3, Kunitz legume,
Q8RXD9	GO:0000023~maltose metabolic process,GO:0000	GO:0005829~cytosol,	GO:0001871~pattern binding,GO:0004133~glycogen debranching enzyme activity,GO:0004134~4-	IPR002044:Glycoside hydrolase, carbohydrate-binding,IPR003385:Glycoside hydrolase, family 77,IPR
Q8S4F6	GO:0006643~membrane lipid metabolic process,	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009536~plastid,GO:0009941~chl	GO:0046510~UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity,	IPR001296:Glycosyl transferase, group 1,
Q8VY70		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor		
Q8VY86	GO:0000302~response to reactive oxygen species	GO:0005829~cytosol,	GO:0008113~peptide-methionine-(S)-S-oxide reductase activity,GO:0016667~oxidoreductase activ	IPR002579:Methionine sulphoxide reductase B,
Q8VY88		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor		IPR002110:Ankyrin,
Q8VZ19	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:00226	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000231:Ribosomal protein L30e,IPR004038:Ribosomal protein L7Ae/L30e/S12e/Gadd45,

Q8W108	GO:0000096~sulfur amino acid metabolic process		GO:0005506~iron ion binding,GO:0010309~acireductone dioxygenase [iron(II)-requiring] activity,G	IPR004313:Acireductone dioxygenase, ARD,IPR014710:RmlC-like jelly roll fold,
Q8W4M5	GO:0005996~monosaccharide metabolic process,	GO:0005618~cell wall,GO:0005829~cytosol,GO:0005945~6-phosphofructokinase complex,GO:0	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000023:Phosphofructokinase,IPR011183:Pyrophosphate-dependent phosphofructokinase PfpB,
Q8W585	GO:0006508~proteolysis,GO:0009057~macromole	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009534~chloroplast thylakoid,GO	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000642:Peptidase M41,IPR003593:ATPase, AAA+ type, core,IPR003959:ATPase, AAA-type, core,IP
Q93V62		GO:0005829~cytosol,GO:0005886~plasma membrane,		
Q93VI3	GO:0006412~translation,	GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma memb	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001063:Ribosomal protein L22/L17,IPR005721:Ribosomal protein L22/L17, eukaryotic/archaeal,IP
Q93VK5	GO:0006720~isoprenoid metabolic process,GO:00	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0010291~carotene beta-rin	IPR001128:Cytochrome P450,IPR002401:Cytochrome P450, E-class, group I,IPR017972:Cytochrome P
Q93VP3	GO:0006412~translation,GO:0006413~translation		GO:0003723~RNA binding,GO:0003743~translation initiation factor activity,GO:0003746~translatio	IPR001884:Eukaryotic initiation factor 5A hypusine (eIF-5A),IPR001884:Translation elongation factor,
Q93VT9	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO:	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001197:Ribosomal protein L10e,IPR016180:Ribosomal protein L10e/L16,IPR018255:Ribosomal pro
Q93W28				
Q93W34			GO:0000166~nucleotide binding,GO:0003723~RNA binding,	IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait,
Q93XW5	GO:0006790~sulfur metabolic process,GO:001605			IPR006652:Kelch repeat type 1,IPR015915:Kelch-type beta propeller,
Q940B0	GO:0006412~translation,	GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosom	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000039:Ribosomal protein L18e,
Q941D3		GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009536~plastid,GO:0009941~chlo	GO:0005198~structural molecule activity,	IPR006843:PAP fibrillin,
Q944H0	GO:0006644~phospholipid metabolic process,GO:		GO:0000234~phosphoethanolamine N-methyltransferase activity,GO:0008170~N-methyltransfera	IPR013216:Methyltransferase type 11,
Q949U1	GO:0006790~sulfur metabolic process,GO:001605	GO:0005783~endoplasmic reticulum,GO:0016021~integral to membrane,GO:0031224~intrinsic	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0020037~heme binding,GO	IPR001128:Cytochrome P450,IPR002401:Cytochrome P450, E-class, group I,IPR017972:Cytochrome P
Q94A41	GO:0000272~polysaccharide catabolic process,GO	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0004556~alpha-amylase activity,GO:0005509~calcium ion binding,GO:0016160~amylase activit	IPR006047:Glycosyl hydrolase, family 13, catalytic region,IPR012850:Alpha-amylase, C-terminal beta-
Q94AQ3	GO:0006869~lipid transport,GO:0010876~lipid loc	GO:0012505~endomembrane system,	GO:0008289~lipid binding,	IPR003612:Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor,IPR013770:Plant
Q94AR8	GO:0006551~leucine metabolic process,GO:00086	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0003861~3-isopropylmalate dehydratase activity,GO:0005506~iron ion binding,GO:0016836~h	IPR001030:Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha,IPR006251:Hor
Q94K48		GO:0005730~nucleolus,GO:0005739~mitochondrion,GO:0009507~chloroplast,GO:0009536~pla	GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,	IPR004155:PBS lyase HEAT-like repeat,IPR011989:Armadillo-like helical,
Q96262	GO:0006952~defense response,GO:0009266~resp	GO:0005773~vacuole,GO:0005886~plasma membrane,GO:0009507~chloroplast,GO:0009536~	GO:0005507~copper ion binding,GO:0005509~calcium ion binding,GO:0005516~calmodulin bindin	IPR008469:DREPP plasma membrane polypeptide,
Q9ASR1	GO:0009266~response to temperature stimulus,G	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0009507~chl	GO:0000166~nucleotide binding,GO:0003746~translation elongation factor activity,GO:0003924~G	IPR000640:Translation elongation factor EFG/EF2, C-terminal,IPR000795:Protein synthesis factor, GT
Q9C4Z6	GO:0022621~shoot system development,GO:0022	GO:0005840~ribosome,GO:0022626~cytosolic ribosome,GO:0030529~ribonucleoprotein comp	GO:0000166~nucleotide binding,	IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like,IPR017986:WD40 repeat, region,IPR019
Q9C5C8		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0008113~peptide-methionine-(S)-S-oxide reductase activity,GO:0016667~oxidoreductase activ	IPR002579:Methionine sulphoxide reductase B,
Q9C6B9	GO:0006644~phospholipid metabolic process,GO:		GO:0000234~phosphoethanolamine N-methyltransferase activity,GO:0008170~N-methyltransfera	IPR013216:Methyltransferase type 11,
Q9C8L4	GO:0006081~cellular aldehyde metabolic process	GO:0005739~mitochondrion,	GO:0004416~hydroxyacylglutathione hydrolase activity,GO:0005506~iron ion binding,GO:0008270	IPR001279:Beta-lactamase-like,
Q9C9C9	GO:0006790~sulfur metabolic process,GO:001605		GO:0008146~sulfotransferase activity,GO:0016782~transferase activity, transferring sulfur-contain	IPR000863:Sulfotransferase,
Q9CAR7		GO:0005773~vacuole,GO:0005886~plasma membrane,GO:0009507~chloroplast,GO:0009536~		IPR001107:Band 7 protein,
Q9CAX6	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small riboso	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001971:Ribosomal protein S11,IPR018102:Ribosomal S11, conserved site,
Q9FE06		GO:0005618~cell wall,GO:0009505~plant-type cell wall,GO:0030312~external encapsulating str		IPR006766:Phosphate-induced protein 1 conserved region,
Q9FE58	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma men	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR002671:Ribosomal protein L22e,
Q9FE65	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma membrane,GO:0015934~lar	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR008195:Ribosomal protein L34e,IPR018065:Ribosomal protein L34e, conserved site,
Q9FEB5	GO:0005976~polysaccharide metabolic process,G	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0001871~pattern binding,GO:0004721~phosphoprotein phosphatase activity,GO:0008138~pro	IPR000340:Dual specificity phosphatase, catalytic domain,IPR000340:Protein-tyrosine phosphatase,
Q9FF55	GO:0006979~response to oxidative stress,GO:001	GO:0005739~mitochondrion,GO:0005783~endoplasmic reticulum,GO:0005886~plasma membr	GO:0003756~protein disulfide isomerase activity,GO:0016860~intramolecular oxidoreductase activ	IPR005788:Disulphide isomerase,IPR005792:Protein disulphide isomerase,IPR006662:Thioredoxin-lik
Q9FF90	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:002262	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR001380:Ribosomal protein L13e,IPR018256:Ribosomal protein L13e, conserved site,
Q9FG67	GO:0006790~sulfur metabolic process,GO:001605	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0003852~2-isopropylmalate synthase activity,GO:0010177~methylthioalkylmalate synthase act	IPR000891:Pyruvate carboxyltransferase,IPR002034:Alpha-isopropylmalate/homocitrate synthase, c
Q9FGY1	GO:0003006~reproductive developmental proces	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0009505~plant-type cell wall,GO:0	GO:0046556~alpha-N-arabinofuranosidase activity,	IPR001764:Glycoside hydrolase, family 3, N-terminal,IPR002772:Glycoside hydrolase, family 3, C-term
Q9FJ95	GO:0055114~oxidation reduction,		GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~	IPR002085:Alcohol dehydrogenase superfamily, zinc-containing,IPR002328:Alcohol dehydrogenase,
Q9FKC0	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:002262	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR005755:Ribosomal protein L13, eukaryotic/archaeal,IPR005822:Ribosomal protein L13,
Q9FKK7	GO:0005996~monosaccharide metabolic process,	GO:0005773~vacuole,GO:0005783~endoplasmic reticulum,GO:0005886~plasma membrane,	GO:0000287~magnesium ion binding,GO:0009045~xylose isomerase activity,GO:0016860~intramo	IPR001998:Xylose isomerase,IPR012307:Xylose isomerase-type TIM barrel,IPR013022:Xylose isomera
Q9FLF0	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small ribosomal subunit,GO:002262	GO:0003723~RNA binding,GO:0003735~structural constituent of ribosome,GO:0005198~structura	IPR001912:Ribosomal protein S4,IPR002942:RNA-binding S4,IPR005710:Ribosomal protein S4/S9, eu
Q9FLG1	GO:0000272~polysaccharide catabolic process,GO	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0030312~external encapsulating st	GO:0009044~xylan 1,4-beta-xylosidase activity,	
Q9FMT1	GO:0006551~leucine metabolic process,GO:00069	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0003862~3-isopropylma	IPR001804:Isocitrate/isopropylmalate dehydrogenase,IPR004429:Isopropylmalate dehydrogenase,IP
Q9FNB0	GO:0006778~porphyrin metabolic process,GO:00	GO:0005739~mitochondrion,GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:00095	GO:0016851~magnesium chelatase activity,GO:0051002~ligase activity, forming nitrogen-metal bo	IPR003672:CobN/magnesium chelatase,IPR011771:Magnesium-chelatase, subunit H,
Q9FVQ1	GO:0000469~cleavages during rRNA processing,G	GO:0005730~nucleolus,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,	GO:0000166~nucleotide binding,	IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait,
Q9FZ76	GO:0006412~translation,	GO:0005783~endoplasmic reticulum,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000915:Ribosomal protein L6E,IPR005568:Ribosomal protein L6, N-terminal,
Q9FZ80	GO:0006790~sulfur metabolic process,GO:001605		GO:0008146~sulfotransferase activity,GO:0016782~transferase activity, transferring sulfur-contain	IPR000863:Sulfotransferase,
Q9LDD8	GO:0006551~leucine metabolic process,GO:00065	GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0031974~membrane-enclo	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000022:Carboxyl transferase,IPR011762:Acetyl-coenzyme A carboxyltransferase, N-terminal,IPR0
Q9LE06	GO:0006790~sulfur metabolic process,GO:000908	GO:0005829~cytosol,	GO:0004084~branched-chain-amino-acid transaminase activity,GO:0008483~transaminase activity	IPR001544:Aminotransferase, class IV,IPR005786:Branched-chain amino acid aminotransferase II,IPR
Q9LF33		GO:0005618~cell wall,GO:0005829~cytosol,GO:0030312~external encapsulating structure,	GO:0000166~nucleotide binding,GO:0003979~UDP-glucose 6-dehydrogenase activity,GO:004803	IPR001732:UDP-glucose/GDP-mannose dehydrogenase, N-terminal,IPR013328:Dehydrogenase, mult
Q9LFW1	GO:0000271~polysaccharide biosynthetic process	GO:0005618~cell wall,GO:0005794~Golgi apparatus,GO:0005840~ribosome,GO:0005886~plasm		IPR004901:Alpha-1,4-glucan-protein synthase, UDP-forming,
Q9LIA8	GO:0055114~oxidation reduction,	GO:0005829~cytosol,	GO:0000166~nucleotide binding,GO:0003979~UDP-glucose 6-dehydrogenase activity,GO:004803	IPR001732:UDP-glucose/GDP-mannose dehydrogenase, N-terminal,IPR014026:UDP-glucose/GDP-ma
Q9LIB2	GO:0009266~response to temperature stimulus,G	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0004645~phosphorylase activity,GO:0019842~vitamin binding,GO:0030170~pyridoxal phospha	IPR000811:Glycosyl transferase, family 35,IPR011833:Glycogen/starch/alpha-glucan phosphorylase,
Q9LIK9	GO:0000103~sulfate assimilation,GO:0006790~su	GO:0005886~plasma membrane,GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:000	GO:0004779~sulfate adenylyltransferase activity,GO:0004781~sulfate adenylyltransferase (ATP) ac	IPR002650:ATP-sulfurylase,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,
Q9LK36	GO:0006730~one-carbon metabolic process,	GO:0005773~vacuole,GO:0005886~plasma membrane,	GO:0004013~adenosylhomocysteinase activity,GO:0016801~hydrolase activity, acting on ether bo	IPR000043:S-adenosyl-L-homocysteine hydrolase,IPR015878:S-adenosyl-L-homocysteine hydrolase, N
Q9LLR6	GO:0006869~lipid transport,GO:0009414~respons	GO:0012505~endomembrane system,	GO:0008289~lipid binding,	IPR000528:Plant lipid transfer protein/Par allergen,IPR003612:Plant lipid transfer protein/seed storag
Q9LMJ7		GO:0009507~chloroplast,GO:0009536~plastid,		
Q9LPG6	GO:0003006~reproductive developmental proces	GO:0000267~cell fraction,GO:0005625~soluble fraction,	GO:0010280~UDP-L-rhamnose synthase activity,GO:0010489~UDP-4-keto-6-deoxy-glucose-3,5-epi	IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
Q9LPL5			GO:0003863~3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity,G	IPR001017:Dehydrogenase, E1 component,
Q9LQ04	GO:0005996~monosaccharide metabolic process,	GO:0000267~cell fraction,GO:0005625~soluble fraction,GO:0005886~plasma membrane,	GO:0008830~dTDP-4-dehydrorhamnose 3,5-epimerase activity,GO:0008831~dTDP-4-dehydrorham	IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
Q9LQQ3			GO:0045735~nutrient reservoir activity,	IPR006044:11-S plant seed storage protein,IPR006045:Cupin 1,IPR014710:RmlC-like jelly roll fold,
Q9LU85		GO:0009507~chloroplast,GO:0009534~chloroplast thylakoid,GO:0009535~chloroplast thylakoi	GO:0005198~structural molecule activity,	IPR006843:PAP fibrillin,
Q9LUD4	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005829~cytosol,GO:0005840~ribosome,GO:0015934~large ribosomal subunit,GO:002262	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR002670:Ribosomal protein L18ae,
Q9LUT2	GO:0000096~sulfur amino acid metabolic process	GO:0005618~cell wall,GO:0005730~nucleolus,GO:0005886~plasma membrane,GO:0030312~ex	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR002133:S-adenosylmethionine synthetase,
Q9LV28	GO:0022621~shoot system development,GO:0022	GO:0005730~nucleolus,GO:0005834~heterotrimeric G-protein complex,GO:0005886~plasma m	GO:0000166~nucleotide binding,	IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like,IPR017986:WD40 repeat, region,IPR019
Q9LVQ8		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chloro	GO:0000287~magnesium ion binding,GO:0004721~phosphoprotein phosphatase activity,GO:0016	IPR000222:Protein phosphatase 2C, manganese/magnesium aspartate binding site,IPR001932:Prote
Q9LVT8		GO:0005886~plasma membrane,	GO:0003723~RNA binding,	IPR006861:Hyaluronan/mRNA binding protein,
Q9LX13	GO:0006631~fatty acid metabolic process,GO:000	GO:0005618~cell wall,GO:0009507~chloroplast,GO:0009536~plastid,GO:0030312~external enc	GO:0016836~hydro-lyase activity,GO:0019171~3-hydroxyacyl-[acyl-carrier-protein] dehydratase ac	IPR010084:Beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ,IPR013114:Beta-hydroxyacyl-(a
Q9LX31	GO:0006778~porphyrin metabolic process,GO:00	GO:0009507~chloroplast,GO:0009536~plastid,GO:0019898~extrinsic to membrane,	GO:0019899~enzyme binding,GO:0046906~tetrapyrrole binding,	IPR008629:GUN4-like,
Q9LY15	GO:0006979~response to oxidative stress,GO:005	GO:0005829~cytosol,	GO:0008113~peptide-methionine-(S)-S-oxide reductase activity,GO:0016667~oxidoreductase activ	IPR002569:Methionine sulphoxide reductase A,
Q9LYN2	GO:0000041~transition metal ion transport,GO:00	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009536~plastid,GO:0009941~chlo	GO:0004322~ferroxidase activity,GO:0005506~iron ion binding,GO:0008199~ferric iron binding,GO	IPR001519:Ferritin, N-terminal,IPR008331:Ferritin and Dps,IPR009040:Ferritin-like,IPR012347:Ferritin
Q9LYT7	GO:0006551~leucine metabolic process,GO:00086	GO:0005829~cytosol,GO:0009316~3-isopropylmalate dehydratase complex,GO:0009536~plasti	GO:0003861~3-isopropylmalate dehydratase activity,GO:0016836~hydro-lyase activity,	IPR000573:Aconitase A/isopropylmalate dehydratase small subunit, swivel,IPR012305:3-isopropylma
Q9LYU8	GO:0006566~threonine metabolic process,GO:00	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001048:Aspartate/glutamate/uridylate kinase,IPR001341:Aspartate kinase region,IPR002912:Ami
Q9LZ23		GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009534~chloroplast thylakoid,GO:0	GO:0016597~amino acid binding,GO:0031406~carboxylic acid binding,GO:0043176~amine binding	IPR002912:Amino acid-binding ACT,

Q9LZ57	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma membrane,GO:0015934~lar	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000509:Ribosomal protein L36e,
Q9LZ66	GO:0006790~sulfur metabolic process,GO:000697	GO:0005576~extracellular region,GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0016002~sulfite reductase	IPR005117:Nitrite/sulphite reductase, hemoprotein beta-component, ferrodoxin-like,IPR006066:Nitr
Q9LZG0	GO:0006166~purine ribonucleoside salvage,GO:0	GO:0005886~plasma membrane,	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bin	IPR001805:Adenosine kinase,IPR002173:Carbohydrate/puine kinase, PfkB, conserved site,IPR011611
Q9M0A5	GO:0000096~sulfur amino acid metabolic process	GO:0012505~endomembrane system,		IPR000991:Glutamine amidotransferase class-I, C-terminal,IPR017926:Glutamine amidotransferase t
Q9M0A7		GO:0012505~endomembrane system,		IPR000991:Glutamine amidotransferase class-I, C-terminal,IPR017926:Glutamine amidotransferase t
Q9M0S5	GO:0000272~polysaccharide catabolic process,G	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009569~chlor	GO:0004133~glycogen debranching enzyme activity,GO:0004556~alpha-amylase activity,GO:00161	
Q9M1G8		GO:0012505~endomembrane system,		IPR002818:ThiJ/PfpI,
Q9M2D8		GO:0005773~vacuole,GO:0005886~plasma membrane,		IPR005516:Remorin, C-terminal region,IPR005518:Remorin, N-terminal,IPR005518:Remorin, N-termi
Q9M2F1	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005618~cell wall,GO:0005829~cytosol,GO:0005840~ribosome,GO:0015935~small ribosom	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,GO:000	IPR000592:Ribosomal protein S27e,
Q9M2Z4		GO:0005886~plasma membrane,GO:0009507~chloroplast,GO:0009534~chloroplast thylakoid,	GO:0005496~steroid binding,GO:0005506~iron ion binding,GO:0008289~lipid binding,GO:002003	IPR001199:Cytochrome b5,IPR018506:Cytochrome b5, heme-binding site,
Q9M352	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma membrane,GO:0015934~lar	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000509:Ribosomal protein L36e,
Q9M356	GO:0006508~proteolysis,	GO:0005618~cell wall,GO:0009505~plant-type cell wall,GO:0030312~external encapsulating st	GO:0004175~endopeptidase activity,GO:0004190~aspartic-type endopeptidase activity,GO:00082	IPR001461:Peptidase A1,IPR001969:Peptidase aspartic, active site,IPR009007:Peptidase aspartic, cat
Q9M401	GO:0008652~cellular amino acid biosynthetic pro	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0004084~branched-chain-amino-acid transaminase activity,GO:0008483~transaminase activity	IPR001544:Aminotransferase, class IV,IPR005786:Branched-chain amino acid aminotransferase II,IPR
Q9M591	GO:0006778~porphyrin metabolic process,GO:000	GO:0009507~chloroplast,GO:0009526~plastid envelope,GO:0009528~plastid inner membrane,	GO:0003677~DNA binding,GO:0005506~iron ion binding,GO:0043167~ion binding,GO:0043169~ca	IPR003251:Rubrerythrin,IPR008434:Magnesium-protoporphyrin IX monomethyl ester aerobic oxidati
Q9M885	GO:0006412~translation,	GO:0005829~cytosol,GO:0005840~ribosome,GO:0009507~chloroplast,GO:0009536~plastid,GO	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR000554:Ribosomal protein S7e,
Q9M9P3	GO:0005984~disaccharide metabolic process,GO:	GO:0005886~plasma membrane,	GO:0003983~UTP:glucose-1-phosphate uridylyltransferase activity,GO:0016779~nucleotidyltransf	IPR002618:UTP--glucose-1-phosphate uridylyltransferase,IPR016267:UTP--glucose-1-phosphate urid
Q9MAQ0	GO:0000271~polysaccharide biosynthetic process	GO:0009501~amyloplast,GO:0009507~chloroplast,GO:0009536~plastid,	GO:0009011~starch synthase activity,GO:0033840~NDP-glucose-starch glucosyltransferase activity	IPR001296:Glycosyl transferase, group 1,IPR011835:Glycogen/starch synthases, ADP-glucose type,IP
Q9S762	GO:0000105~histidine biosynthetic process,GO:0	GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000287~magnesium ion binding,GO:0003879~ATP phosphoribosyltransferase activity,GO:001	IPR001348:Histidine biosynthesis HisG: ATP phosphoribosyltransferase,IPR013115:Histidine biosynth
Q9S7C0	GO:0006457~protein folding,GO:0009266~respon	GO:0005886~plasma membrane,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001023:Heat shock protein Hsp70,IPR013126:Heat shock protein 70,
Q9SA18	GO:0000096~sulfur amino acid metabolic process	GO:0009507~chloroplast,GO:0009532~plastid stroma,GO:0009536~plastid,GO:0009570~chlor	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001048:Aspartate/glutamate/uridylate kinase,IPR001341:Aspartate kinase region,IPR001342:Hom
Q9SCV8		GO:0005576~extracellular region,GO:0009341~beta-galactosidase complex,GO:0012505~endo	GO:0004565~beta-galactosidase activity,GO:0015925~galactosidase activity,GO:0043167~ion bind	IPR001944:Glycoside hydrolase, family 35,IPR013781:Glycoside hydrolase, subgroup, catalytic core,I
Q9SCW1	GO:0006979~response to oxidative stress,	GO:0005576~extracellular region,GO:0005618~cell wall,GO:0009505~plant-type cell wall,GO:0	GO:0004565~beta-galactosidase activity,GO:0004601~peroxidase activity,GO:0005506~iron ion bi	IPR000922:D-galactoside/L-rhamnose binding SUEL lectin,IPR001944:Glycoside hydrolase, family 35,I
Q9SCX3	GO:0006412~translation,GO:0006414~translation	GO:0005576~extracellular region,GO:0005853~eukaryotic translation elongation factor 1 comp	GO:0003746~translation elongation factor activity,GO:0008135~translation factor activity, nucleic	IPR001326:Translation elongation factor EF1B, beta/delta chains, conserved site,IPR004046:Glutathi
Q9SE50	GO:0006952~defense response,GO:0009620~resp	GO:0005773~vacuole,GO:0005777~peroxisome,GO:0005783~endoplasmic reticulum,GO:0009	GO:0043167~ion binding,GO:0043169~cation binding,	IPR000886:Endoplasmic reticulum, targeting sequence,IPR001360:Glycoside hydrolase, family 1,IPR0
Q9SFB1		GO:0005618~cell wall,GO:0030312~external encapsulating structure,		IPR006946:Protein of unknown function DUF642,
Q9SFU1	GO:0006412~translation,	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0005840~ribosome,GO:0009507~chloroplast,	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR005755:Ribosomal protein L13, eukaryotic/archaeal,IPR005822:Ribosomal protein L13,
Q9SGE0	GO:0009225~nucleotide-sugar metabolic process,	GO:0005576~extracellular region,GO:0048046~apoplast,	GO:0016831~carboxy-lyase activity,GO:0048037~cofactor binding,GO:0048040~UDP-glucuronate	IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
Q9SIP7	GO:0006412~translation,GO:0006970~response t	GO:0005773~vacuole,GO:0005829~cytosol,GO:0005840~ribosome,GO:0005886~plasma memb	GO:0003723~RNA binding,GO:0003735~structural constituent of ribosome,GO:0005198~structura	IPR001351:Ribosomal protein S3, C-terminal,IPR004044:K Homology, type 2,IPR004087:K Homology,
Q9SIV0	GO:0001558~regulation of cell growth,GO:00015		GO:0008483~transaminase activity,GO:0016769~transferase activity, transferring nitrogenous grou	IPR001176:1-aminocyclopropane-1-carboxylate synthase,IPR004839:Aminotransferase, class I and II,
Q9SJL8	GO:0000096~sulfur amino acid metabolic process	GO:0005886~plasma membrane,	GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0001882~nucleoside bi	IPR002133:S-adenosylmethionine synthetase,
Q9SJW3	GO:0000902~cell morphogenesis,GO:0008361~re	GO:0005819~spindle,GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0005876~spind		
Q9SK84	GO:0008652~cellular amino acid biosynthetic pro		GO:0003849~3-deoxy-7-phosphoheptulonate synthase activity,GO:0016765~transferase activity, t	IPR002480:DAHP synthetase, class II,
Q9SKC1				IPR002213:UDP-glucuronosyl/UDP-glucosyltransferase,
Q9SRG3	GO:0006970~response to osmotic stress,GO:0009	GO:0005783~endoplasmic reticulum,GO:0005788~endoplasmic reticulum lumen,GO:0005886~	GO:0003756~protein disulfide isomerase activity,GO:0016860~intramolecular oxidoreductase acti	IPR000886:Endoplasmic reticulum, targeting sequence,IPR005788:Disulphide isomerase,IPR005792:
Q9SRV5	GO:0000096~sulfur amino acid metabolic process	GO:0005576~extracellular region,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:00	GO:0003871~5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,G	IPR002629:Methionine synthase, vitamin-B12 independent,IPR006276:5-methyltetrahydropteroyltri
Q9SSK7	GO:0006952~defense response,			IPR000916:Bet v I allergen,
Q9STX5	GO:0006457~protein folding,GO:0006970~respon	GO:0005739~mitochondrion,GO:0005773~vacuole,GO:0005783~endoplasmic reticulum,GO:00	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000886:Endoplasmic reticulum, targeting sequence,IPR001404:Heat shock protein Hsp90,IPR003
Q9SUQ9	GO:0006952~defense response,			IPR000916:Bet v I allergen,
Q9SUR0	GO:0006952~defense response,GO:0006970~resp	GO:0005773~vacuole,	GO:0005507~copper ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:00468	IPR000916:Bet v I allergen,
Q9SUR6	GO:0006970~response to osmotic stress,GO:000	GO:0005576~extracellular region,GO:0005773~vacuole,GO:0048046~apoplast,	GO:0004121~cystathionine beta-lyase activity,GO:0004838~L-tyrosine:2-oxoglutarate aminotransf	IPR001176:1-aminocyclopropane-1-carboxylate synthase,IPR004839:Aminotransferase, class I and II,
Q9SWG0	GO:0055114~oxidation reduction,	GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0031974~membrane-encl	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR006089:Acyl-CoA dehydrogenase, conserved site,IPR006090:Acyl-CoA oxidase/dehydrogenase, ty
Q9SXE1	GO:0006790~sulfur metabolic process,GO:00160	GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR000960:Flavin-containing monooxygenase FMO,
Q9SYG7	GO:0006081~cellular aldehyde metabolic process,		GO:0004028~3-chloroallyl aldehyde dehydrogenase activity,GO:0004029~aldehyde dehydrogenase	IPR015590:Aldehyde dehydrogenase,IPR016160:Aldehyde dehydrogenase, conserved site,IPR01616
Q9SYI5				IPR011042:Six-bladed beta-propeller, TolB-like,IPR011659:WD40-like Beta Propeller,
Q9SYM5	GO:0005996~monosaccharide metabolic process,	GO:0000267~cell fraction,GO:0005625~soluble fraction,	GO:0010280~UDP-L-rhamnose synthase activity,GO:0016836~hydro-lyase activity,GO:0048037~co	IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
Q9SZI2	GO:0006259~DNA metabolic process,GO:000628	GO:0005886~plasma membrane,	GO:0003677~DNA binding,	IPR002164:Nucleosome assembly protein (NAP),
Q9T043	GO:0006412~translation,GO:0022613~ribonucleo	GO:0005730~nucleolus,GO:0005773~vacuole,GO:0005783~endoplasmic reticulum,GO:000582	GO:0003735~structural constituent of ribosome,GO:0005198~structural molecule activity,	IPR002784:Ribosomal protein L14,
Q9T074	GO:0005996~monosaccharide metabolic process,	GO:0005730~nucleolus,GO:0005829~cytosol,GO:0031974~membrane-enclosed lumen,GO:003	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside	IPR001272:Phosphoenolpyruvate carboxykinase, ATP-utilising,IPR008210:Phosphoenolpyruvate carb
Q9XI42		GO:0005886~plasma membrane,		IPR015157:Translation machinery associated TMA7,
Q9ZPZ4		GO:0005576~extracellular region,GO:0048046~apoplast,		IPR007493:Protein of unknown function DUF538,
Q9ZUJ3		GO:0009507~chloroplast,GO:0009536~plastid,	GO:0000166~nucleotide binding,GO:0003723~RNA binding,	IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait,
Q9ZUP3	GO:0006259~DNA metabolic process,GO:000628	GO:0005886~plasma membrane,	GO:0003677~DNA binding,	IPR002164:Nucleosome assembly protein (NAP),
Q9ZVS4;Q9ZVS5	GO:0006508~proteolysis,GO:0006970~response t	GO:0005618~cell wall,GO:0005886~plasma membrane,GO:0009505~plant-type cell wall,GO:00	GO:0004175~endopeptidase activity,GO:0004190~aspartic-type endopeptidase activity,GO:00082	IPR001461:Peptidase A1,IPR009007:Peptidase aspartic, catalytic,
Q9ZW13	GO:0055114~oxidation reduction,			IPR002198:Short-chain dehydrogenase/reductase SDR,IPR002347:Glucose/ribitol dehydrogenase,IPR
Q9ZW84	GO:0006551~leucine metabolic process,GO:0008	GO:0005829~cytosol,GO:0009316~3-isopropylmalate dehydratase complex,GO:0009536~plast	GO:0003861~3-isopropylmalate dehydratase activity,GO:0016836~hydro-lyase activity,	IPR000573:Aconitase A/isopropylmalate dehydratase small subunit, swivel,IPR012305:3-isopropylma
Q9ZWC4		GO:0005618~cell wall,GO:0005773~vacuole,GO:0005886~plasma membrane,GO:0009505~pla	GO:0003993~acid phosphatase activity,GO:0016791~phosphatase activity,	IPR005519:Acid phosphatase (Class B),IPR010028:Acid phosphatase, plant,IPR014403:Vegetative sto
Q9ZWT2	GO:0006952~defense response,GO:0009617~resp	GO:0005783~endoplasmic reticulum,GO:0005789~endoplasmic reticulum membrane,GO:0012	GO:0005506~iron ion binding,GO:0020037~heme binding,GO:0043167~ion binding,GO:0043169~	IPR001199:Cytochrome b5,IPR018506:Cytochrome b5, heme-binding site,

ulin, conserved site,IPR018316:Tubulin/FtsZ, 2-layer sandwich domain,
phate carboxylase, large subunit, ferrodoxin-like N-terminal,IPR017444:Ribulose bisphosphate carboxylase, large subunit, N-terminal,
ytic region,IPR006140:D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding,IPR006236:D-3-phosphoglycerate dehydrogenase,IPR015508:D-3-phosphogylcerate Dehydrogenase,IPR016040:NAD(P)-binding domain,
lreticulin/calnexin, P,IPR009169:Calreticulin,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,IPR018124:Calreticulin/calnexin, conserved site,
me,IPR011258:BPG-independent PGAM, N-terminal,IPR017849:Alkaline phosphatase-like, alpha/beta/alpha,
, catalytic domain,IPR001757:ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter,IPR004014:ATPase, P-type cation-transporter, N-terminal,IPR005834:Haloacid dehalogenase-like hydrolase,IPR006068:ATPase, P-type cation-transporter, C-terminal,IPR006069:ATPase, P-type cation exchange, alpha subunit,IPR006408:ATPase, P-type, calcium-transporting, PMCA-type,IP

48:Ribonucleotide reductase-related,
AD binding,IPR016040:NAD(P)-binding domain,

E1 component, alpha subunit, subgroup y,
, iron-binding site,
protein S6e, conserved site,
005979:Light-dependent protochlorophyllide reductase,IPR016040:NAD(P)-binding domain,

ase C-terminal-like,

late reductase,

R010987:Glutathione S-transferase, C-terminal-like,IPR012335:Thioredoxin fold,IPR017933:Glutathione S-transferase/chloride channel, C-terminal,

oserine dehydrogenase, catalytic,IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site,IPR002912:Amino acid-binding ACT,IPR005106:Aspartate/homoserine dehydrogenase, NAD-binding,IPR011147:Bifunctional aspartokinase/homoserine dehydrogenase I,IPR016040:NAD(P)-binding domain,IPR018042:Aspartate kinase, conserved site,IPR019811:Homoserine dehy

:Carbohydrate/puine kinase, PfkB, conserved site,IPR006259:Adenylate kinase, subfamily,IPR007862:Adenylate kinase, zinc-finger lid region,IPR008271:Serine/threonine protein kinase, active site,IPR011611:Carbohydrate/purine kinase,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein kinase-related,
esium chelatase, ATPase subunit I,
tein S17, conserved site,

inal TPP-binding,IPR012000:Thiamine pyrophosphate enzyme, central region,IPR012001:Thiamine pyrophosphate enzyme, N-terminal TPP binding region,IPR012846:Acetolactate synthase, large subunit, biosynthetic,
/Na/Ca/Na/H-transporter,IPR004014:ATPase, P-type cation-transporter, N-terminal,IPR005834:Haloacid dehalogenase-like hydrolase,IPR006534:ATPase, P-type, plasma-membrane proton-efflux,IPR008250:ATPase, P-type, ATPase-associated region,IPR018303:ATPase, P-type phosphorylation site,
005979:Light-dependent protochlorophyllide reductase,IPR016040:NAD(P)-binding domain,
n 70, conserved site,
sporter, conserved site,

10713:Xyloglucan endo-transglycosylase, C-terminal,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,IPR016455:Xyloglucan endotransglucosylase/hydrolase,
sphopantetheine-binding,IPR009081:Acyl carrier protein-like,
-associated region,IPR010582:Catalase-related immune responsive,IPR011614:Catalase, N-terminal,IPR015606:Cationic amino acid transporter,IPR018028:Catalase related subgroup,IPR018130:Ribosomal protein S2, conserved site,
81:Glycoside hydrolase, subgroup, catalytic core,IPR018238:Glycoside hydrolase, family 14, conserved site,
17453:Glycine cleavage H-protein, subgroup,
ydrogenase, type I,
IPR013753:Ras,IPR015595:Rab11-related,
ctin/glucanase, subgroup,IPR018124:Calreticulin/calnexin, conserved site,
tubulin, autoregulation binding site,IPR017975:Tubulin, conserved site,IPR018316:Tubulin/FtsZ, 2-layer sandwich domain,
tubulin, autoregulation binding site,IPR017975:Tubulin, conserved site,IPR018316:Tubulin/FtsZ, 2-layer sandwich domain,

olipoprotein N-acyltransferase,
olipoprotein N-acyltransferase,
poxygenase, C-terminal,

tein S17, conserved site,
R010987:Glutathione S-transferase, C-terminal-like,IPR012335:Thioredoxin fold,IPR017933:Glutathione S-transferase/chloride channel, C-terminal,
e,IPR004176:Clp, N-terminal,IPR013093:ATPase associated with various cellular activities, AAA-2,IPR018368:Chaperonin ClpA/B, conserved site,IPR019489:Clp ATPase, C-terminal,
H-like,IPR016040:NAD(P)-binding domain,
ein L2, domain 3,

hate-binding site,IPR004839:Aminotransferase, class I and II,IPR015421:Pyridoxal phosphate-dependent transferase, major region, subdomain 1,

on elongation factor EF1B, beta and delta chains, guanine nucleotide exchange,IPR014717:Translation elongation factor EF1B/ribosomal protein S6,
P450, conserved site,IPR017973:Cytochrome P450, C-terminal region,
ine synthase, glutamine-hydrolyzing,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,IPR017932:Glutamine amidotransferase, type II,
2340:Nucleic acid-binding, OB-fold,

protein S5, eukaryotic/archaeal,IPR013810:Ribosomal protein S5, N-terminal,IPR014720:Double-stranded RNA-binding-like,IPR014721:Ribosomal protein S5 domain 2-type fold,IPR018192:Ribosomal protein S5, N-terminal, conserved site,
osomal protein L7Ae/L30e/S12e/Gadd45,IPR018492:Ribosomal protein L7A/RS6 family,
R018260:Ribosomal protein L22/L17, conserved site,

l protein S6e, conserved site,

eta-lyase, eukaryotic,IPR015421:Pyridoxal phosphate-dependent transferase, major region, subdomain 1,IPR015422:Pyridoxal phosphate-dependent transferase, major region, subdomain 2,
phate-dependent transferase, major region, subdomain 1,IPR015422:Pyridoxal phosphate-dependent transferase, major region, subdomain 2,
reductase, subunit I,IPR010226:NADH-quinone oxidoreductase, chain I,IPR017896:4Fe-4S ferredoxin, iron-sulpur binding domain,IPR017900:4Fe-4S ferredoxin, iron-sulphur binding, conserved site,

L-lactate/malate dehydrogenase,IPR010945:Malate dehydrogenase, NAD or NADP,IPR011274:Malate dehydrogenase, NAD-dependent, cytosolic,IPR015955:Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal,IPR016040:NAD(P)-binding domain,

54:Ubiquitin conserved site,IPR019955:Ubiquitin supergroup,IPR019956:Ubiquitin subgroup,
012988:Ribosomal protein L30, N-terminal,IPR018038:Ribosomal protein L30,
ccinyl-CoA ligase,IPR016040:NAD(P)-binding domain,IPR016102:Succinyl-CoA synthetase-like,IPR017440:ATP-citrate lyase/succinyl-CoA ligase, active site,

denylylsulphate reductase,IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,IPR017936:Thioredoxin-like,
denylylsulphate reductase,IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,IPR017936:Thioredoxin-like,
te dioxygenase,
kinase,IPR001368:TNFR/CD27/30/40/95 cysteine-rich region,IPR001509:NAD-dependent epimerase/dehydratase,IPR008271:Serine/threonine protein kinase, active site,IPR009091:Regulator of chromosome condensation/beta-lactamase-inhibitor protein II,IPR012677:Nucleotide-binding, alpha-beta plait,IPR015465:RNA recognition motif, glycine rich protein,IPR016040:NA
03:Peroxidases heam-ligand binding site,IPR019794:Peroxidase, active site,

e, subunit 1, conserved site,

anine/leucine/valine dehydrogenase, C-terminal,IPR006097:Glutamate/phenylalanine/leucine/valine dehydrogenase, dimerisation region,IPR014362:Glutamate dehydrogenase,IPR016040:NAD(P)-binding domain,
26:Heat shock protein 70,IPR018181:Heat shock protein 70, conserved site,
-related,IPR014034:Ferritin, conserved site,
elated,

15421:Pyridoxal phosphate-dependent transferase, major region, subdomain 1,
synthetase, large subunit, ATP-binding,IPR005481:Carbamoyl phosphate synthase, large subunit, N-terminal,IPR005482:Biotin carboxylase, C-terminal,IPR011761:ATP-grasp fold,IPR011764:Biotin carboxylation region,IPR013816:ATP-grasp fold, subdomain 2,IPR013817:Pre-ATP-grasp fold,
-associated region,IPR010582:Catalase-related immune responsive,IPR011614:Catalase, N-terminal,IPR013838:Beta tubulin, autoregulation binding site,IPR015606:Cationic amino acid transporter,IPR018028:Catalase related subgroup,

de-binding/triple function, N-terminal,IPR009038:GOLD,
ransferase-like, conserved site,
:Aldehyde dehydrogenase, N-terminal,
de-binding/triple function, N-terminal,IPR009038:GOLD,

ke, ParA/MinD,
ruvate phosphate dikinase, PEP/pyruvate-binding,IPR013783:Immunoglobulin-like fold,IPR013815:ATP-grasp fold, subdomain 1,IPR018274:PEP-utilising enzyme, mobile region, conserved site,

one S-transferase, C-terminal,IPR014038:Translation elongation factor EF1B, beta and delta chains, guanine nucleotide exchange,IPR014717:Translation elongation factor EF1B/ribosomal protein S6,

R010987:Glutathione S-transferase, C-terminal-like,IPR012335:Thioredoxin fold,IPR017933:Glutathione S-transferase/chloride channel, C-terminal,

:Thioredoxin-like,IPR017937:Thioredoxin, conserved site,

010916:TonB box, conserved site,IPR013781:Glycoside hydrolase, subgroup, catalytic core,IPR013783:Immunoglobulin-like fold, PR003960:ATPase, AAA-type, conserved site,IPR005936:Peptidase M41, FtsH,IPR006025:Peptidase M, neutral zinc metallopeptidases, zinc-binding site,IPR011546:Peptidase M41, FtsH extracellular,

PR018260:Ribosomal protein L22/L17, conserved site,
P450, conserved site,IPR017973:Cytochrome P450, C-terminal region,
IF5A,IPR012340:Nucleic acid-binding, OB-fold,IPR014722:Translation protein SH3-like, subgroup,IPR019769:Eukaryotic initiation factor 5A, hypusine site,IPR019769:Translation elongation factor, IF5A, hypusine site,
otein L10e, conserved site,

P450, conserved site,
-sheet,IPR013781:Glycoside hydrolase, subgroup, catalytic core,
lipid transfer protein and hydrophobic protein, helical,
moaconitase/3-isopropylmalate dehydratase, large subunit, subgroup,IPR015931:Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 1/3,IPR015932:Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 2,IPR015936:Homoaconitase/3-isopropylmalate dehydratase, small/large subunit,IPR015937:Aconitase-

P-binding,IPR004161:Translation elongation factor EFTu/EF1A, domain 2,IPR005517:Translation elongation factor EFG/EF2, domain IV,IPR014721:Ribosomal protein S5 domain 2-type fold,
9775:WD40 repeat, conserved site,IPR019781:WD40 repeat, subgroup,IPR019782:WD40 repeat 2,

dual specificity,IPR000387:Dual-specific/protein-tyrosine phosphatase, conserved region,IPR000387:Protein-tyrosine phosphatase,
e subdomain,IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain,IPR017936:Thioredoxin-like,IPR017937:Thioredoxin, conserved site,

onserved site,IPR013785:Aldolase-type TIM barrel,
inal,
zinc-containing, conserved site,IPR013149:Alcohol dehydrogenase, zinc-binding,IPR013154:Alcohol dehydrogenase GroES-like,

ase-like, TIM barrel,IPR013452:Xylose isomerase, bacterial type,IPR018115:Xylose isomerase, active site,
karyotic/archaeal,IPR018079:Ribosomal protein S4, conserved site,

R019818:Isocitrate/isopropylmalate dehydrogenase, conserved site,

11763:Acetyl-coenzyme A carboxyltransferase, C-terminal,
018300:Aminotransferase, class IV, conserved site,
ihelical,IPR014026:UDP-glucose/GDP-mannose dehydrogenase, dimerisation,IPR014027:UDP-glucose/GDP-mannose dehydrogenase, C-terminal,IPR014028:UDP-glucose/GDP-mannose dehydrogenase, dimerisation and substrate-binding,IPR016040:NAD(P)-binding domain,IPR017476:Nucleotide sugar dehydrogenase,

nnose dehydrogenase, dimerisation,IPR014027:UDP-glucose/GDP-mannose dehydrogenase, C-terminal,IPR014028:UDP-glucose/GDP-mannose dehydrogenase, dimerisation and substrate-binding,IPR016040:NAD(P)-binding domain,IPR017476:Nucleotide sugar dehydrogenase,

NAD binding,
ge/trypsin-alpha amylase inhibitor,IPR013770:Plant lipid transfer protein and hydrophobic protein, helical,

9775:WD40 repeat, conserved site,IPR019781:WD40 repeat, subgroup,IPR019782:WD40 repeat 2,
in phosphatase 2C-related,

cyl-carrier-protein) dehydratase, FabA/FabZ,

n-related,IPR014034:Ferritin, conserved site,
late dehydratase, small subunit,IPR015928:Aconitase/3-isopropylmalate dehydratase, swivel,IPR015937:Aconitase-like core,
no acid-binding ACT,IPR018042:Aspartate kinase, conserved site,

ite and sulphite reductase iron-sulphur/siroheme-binding site,IPR006067:Nitrite and sulphite reductase 4Fe-4S region,IPR011787:Sulphite reductase, ferredoxin dependent,
:Carbohydrate/purine kinase,
ype 1,
ype 1,

nal region,

alytic,
018300:Aminotransferase, class IV, conserved site,
ive cyclase,

ylyltransferase, subgroup,
R013534:Starch synthase catalytic region,
esis HisG, C-terminal,IPR013820:ATP phosphoribosyltransferase, catalytic region,IPR018198:ATP phosphoribosyltransferase, conserved site,

noserine dehydrogenase, catalytic,IPR002912:Amino acid-binding ACT,IPR005106:Aspartate/homoserine dehydrogenase, NAD-binding,IPR011147:Bifunctional aspartokinase/homoserine dehydrogenase I,IPR016040:NAD(P)-binding domain,IPR018042:Aspartate kinase, conserved site,IPR019811:Homoserine dehydrogenase, conserved site,
PR019801:Glycoside hydrolase, family 35, conserved site,
IPR013781:Glycoside hydrolase, subgroup, catalytic core,IPR019793:Peroxidases heam-ligand binding site,IPR019801:Glycoside hydrolase, family 35, conserved site,
one S-transferase, C-terminal,IPR014038:Translation elongation factor EF1B, beta and delta chains, guanine nucleotide exchange,IPR014717:Translation elongation factor EF1B/ribosomal protein S6,
13781:Glycoside hydrolase, subgroup, catalytic core,IPR018120:Glycoside hydrolase, family 1, active site,

IPR005703:Ribosomal protein S3, eukaryotic/archaeal,IPR018280:Ribosomal protein S3, conserved site,
IPR005958:Tyrosine/nicotianamine aminotransferase,IPR015421:Pyridoxal phosphate-dependent transferase, major region, subdomain 1,

rotein disulphide isomerase,IPR006662:Thioredoxin-like subdomain,IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain,IPR017936:Thioredoxin-like,IPR017937:Thioredoxin, conserved site,
glutamate--homocysteine S-methyltransferase,IPR013215:Cobalamin (vitamin B12)-independent methionine synthase MetE, N-terminal,

94:ATP-binding region, ATPase-like,IPR015566:Molecular chaperone, heat shock protein, endoplasmin,IPR019805:Heat shock protein Hsp90, conserved site,

IPR005958:Tyrosine/nicotianamine aminotransferase,IPR015421:Pyridoxal phosphate-dependent transferase, major region, subdomain 1,
pe 1,IPR006091:Acyl-CoA oxidase/dehydrogenase, central region,IPR006092:Acyl-CoA dehydrogenase, N-terminal,IPR013764:Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal,IPR013786:Acyl-CoA dehydrogenase/oxidase, N-terminal,

:Aldehyde dehydrogenase, N-terminal,

oxykinase, N-terminal,IPR013035:Phosphoenolpyruvate carboxykinase, C-terminal,IPR015994:Phosphoenolpyruvate carboxykinase (ATP), conserved site,

005829:Sugar transporter, conserved site,IPR016040:NAD(P)-binding domain,
late dehydratase, small subunit,IPR015928:Aconitase/3-isopropylmalate dehydratase, swivel,IPR015937:Aconitase-like core,
rage protein/acid phosphatase,

R008250:ATPase, P-type, ATPase-associated region,IPR018303:ATPase, P-type phosphorylation site,IPR018338:Carbonic anhydrase, alpha-class, conserved site,IPR018340:Carbonic anhydrase, CAH1-like,

drogenase, conserved site,

D(P)-binding domain,IPR017441:Protein kinase, ATP binding site,

-like core