Title: Volatiles from the fungal phytopathogen *Penicillium aurantiogriseum* modulate root metabolism and architecture through proteome resetting

Running title: Response of roots to fungal volatiles

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ABSTRACT

Volatile compounds (VCs) emitted by the fungal phytopathogen *Penicillium aurantiogriseum* promote root growth and developmental changes in Arabidopsis. Here we characterized the metabolic and molecular responses of roots to fungal volatiles. Proteomic analyses revealed that these compounds reduce the levels of aquaporins, the iron carrier IRT1 and apoplastic peroxidases. Fungal VCs also increased the levels of enzymes involved in the production of mevalonate (MVA)-derived isoprenoids, nitrogen assimilation and conversion of methionine to ethylene and cyanide. Consistently, fungal VC-treated roots accumulated high levels of hydrogen peroxide (H₂O₂), MVA-derived cytokinins, ethylene, cyanide and long-distance nitrogen transport amino acids. qRT-PCR analyses showed that many proteins differentially expressed by fungal VCs are encoded by VC non-responsive genes. Expression patterns of hormone reporters and developmental characterization of mutants provided evidence for the involvement of cyanide scavenging and enhanced auxin, ethylene, cytokinin and H₂O₂ signaling in the root architecture changes promoted by fungal VCs. Our findings show that VCs from *P. aurantiogriseum* modify root metabolism and architecture, and improve nutrient and water use efficiencies through transcriptionally and non-transcriptionally regulated proteome resetting mechanisms. Some of these mechanisms are subject to long-distance regulation by photosynthesis and differ from those triggered by VCs emitted by beneficial microorganisms.

Key-words: biostimulant, cyanide scavenging, growth promotion, hormone signaling, microbial volatile compounds, photosynthesis, plant-microbe interaction, proteomics

INTRODUCTION

The root system represents an important interface through which plants interact with the environment. It provides anchorage, facilitates the acquisition of water and mineral nutrients from the soil and allows the establishment of biotic relationships with the rhizosphere (van Dam & Bouwmeester, 2016). Physiological and genetic studies have provided strong evidence that auxin is a master regulator of root system architecture (RSA) (Saini, Sharma, Kaur, & Pati, 2013). Other phytohormones such as ethylene and cytokinins (CK), and reactive oxygen species (ROS) such as superoxide anion (O_2^-) and hydrogen peroxide (H_2O_2) interact with auxin to trigger cascades of events leading to root morphogenesis (Foreman et al., 2003; Liu, Moore, Chen, & Lindsey, 2017; Ma et al., 2014; Mangano et al., 2017; Stepanova, Hoyt, Hamilton, & Alonso, 2005). In response to environmental changes, roots reorganize their metabolism and architecture in order to maximize fitness and cope with and survive these changes (López-Bucio, Cruz-Ramírez, & Herrera-Estrella, 2003; Malamy, 2005). These adjustments involve long-distance communication with the aerial part of the plant (Gansel, Muños, Tillard, & Gojon, 2001; Kiba, Takebayashi, Kojima, & Sakakibara, 2019; Vert, Briat, & Curie, 2003), and are regulated at the transcriptional, post-transcriptional and post-translational levels through mechanisms involving shifts in phytohormone and ROS signaling (Bouguyon et al., 2016; Guerra et al., 2015; Lan, Li, & Schmidt, 2012; Mangano et al., 2017; Tsukagoshi, Busch, & Benfey, 2010; Žd'árská et al., 2013).

In soil, microorganisms communicate with plants by exchanging chemical signals throughout the rhizosphere. Such interactions are important for plant productivity (De-la-Peña & Loyola-Vargas, 2014). In the precolonization phase, before direct contact with plants occurs, beneficial bacteria and fungi emit diffusible substances (e.g. carbohydrates, proteins, fatty acids, flavonols, organic acids, amino acids and hormones) that cause massive lateral root (LR) formation and enhanced root hair (RH) growth, thus improving the root's capacity to explore for water and minerals and predisposing plants to microbial colonization and infection (Contreras-Cornejo, Macías-Rodríguez, Cortés-Penagos, & López-Bucio, 2009; López-Bucio et al., 2007).

85 These microorganisms also emit a large number of volatile compounds (VCs) with molecular
86 masses of less than 300 Da that promote growth and photosynthesis, induce systemic drought
87 tolerance, improve nutrient acquisition, and modulate RSA in both host and non-host plants
88 (Cho et al., 2008; Cordovez et al., 2018; Ditengou et al., 2015; Gutiérrez-Luna et al., 2010; Ryu
89 et al., 2003; Zhang et al., 2010, 2009). Recent studies have shown that this capacity is not
90 restricted to beneficial microbes; it also extends to phytopathogens and microbes that do not
91 normally interact mutualistically with plants (Cordovez et al., 2017; García-Gómez et al., 2019;
92 Li et al., 2018; Moisan et al., 2019; Sánchez-López, Baslam, et al., 2016).

93 RSA modulation by microbial VCs has frequently been associated with lipophilic
94 carbon-based compounds, which are known as volatile organic compounds (VOCs) (Bitas et al.,
95 2015; Cordovez et al., 2018; Ditengou et al., 2015; Garnica-Vergara et al., 2016; Gutiérrez-
96 Luna et al., 2010; Splivallo, Fischer, Göbel, Feussner, & Karlovsky, 2009; Zhang et al., 2007,
97 2008). In addition to VOCs, microorganisms also release a limited number of volatile inorganic
98 compounds (VICs) with molecular masses of less than 45 Da such as hydrogen sulfide (H₂S),
99 molecular hydrogen, nitric oxide (NO), nitrogen dioxide, nitrous oxide and carbon monoxide
100 (CO) (García-Gómez et al., 2019; Nandi & Sengupta, 1998; Shatalin, Shatalina, Mironov, &
101 Nudler, 2011). These compounds can act as signaling molecules that promote growth and
102 modulate RSA when applied individually and at low concentrations (Cao et al., 2007; Correa-
103 Aragunde, Graziano, & Lamattina, 2004; Dooley, Nair, & Ward, 2013; Guo, Kong, & Yang,
104 2009; Lin et al., 2014; Takahashi et al., 2014; Zhu et al., 2016). There is evidence that VIC
105 emissions from growth-promoting rhizobacteria promote changes in the RSA of their host
106 plants (Creus et al., 2005; Molina-Favero, Creus, Simontacchi, Puntarulo, & Lamattina, 2008).

107 Using a “box-in-box” co-cultivation system in which plants are grown in the vicinity of
108 microbial cultures covered with charcoal filters, we have recently provided evidence that VCs
109 with molecular masses of less than 45 Da are major determinants of plant responses to microbial
110 volatile emissions (García-Gómez et al., 2019). VOC-depleted volatile emissions from
111 *Penicillium aurantiogriseum* (a fungal phytopathogen that can be found in the rhizosphere
112 [Bodini, Cicalini, & Santori, 2011; Gharaei-Fathabad, Tajick-Ghanbary, & Shahrokhi, 2014;

Kłapeć, Cholewa, Cholewa, Dutkiewicz, & Wójcik-Fatla, 2018]) inhibit primary root (PR) and LR growth, stimulate *de novo* LR formation, and promote extensive proliferation and elongation of RHs leading to the development of a “cotton-like” external root phenotype caused by the formation of peculiar “brush-like” structures at the root tip (García-Gómez et al., 2019). These changes in RSA resemble those occurring in plants treated with exogenous auxins (Casimiro et al., 2001), CO (Guo et al., 2009), NO (Correa-Aragunde et al., 2004) and diffusible substances emitted by beneficial microorganisms (Ditengou et al., 2015; Garnica-Vergara et al., 2016; López-Bucio et al., 2007; Splivallo et al., 2009).

To date, the majority of studies on the root response to complex mixtures of microbial VCs have been conducted using beneficial microorganisms and focused mainly on analyses of reporters for auxin-inducible gene expression, RSA adjustments in ethylene and auxin transport/signaling mutants, transcriptome changes in roots of VC-exposed plants and identification of bioactive microbial VOCs (Bailly et al., 2014; Camarena-Pozos, Flores-Núñez, López, López-Bucio, & Partida-Martínez, 2019; Cordovez et al., 2018; Ditengou et al., 2015; Garnica-Vergara et al., 2016; Splivallo et al., 2009; Zhang et al., 2007). These studies have shown that RSA modulation promoted by VCs emitted by beneficial microorganisms is associated with changes in the root transcriptome, and involves processes wherein auxin, ethylene and ROS play important roles. However, although it is well established that adjustments of roots to changing environmental conditions are largely regulated at post-transcriptional and post-translational levels, nothing is known about proteome reprogramming following exposure to microbial VCs. Moreover, the metabolic and molecular adjustments made by roots in response to compounds (particularly VCs) emitted by microbial phytopathogens remain unknown. To obtain insights into the mechanisms involved in the response of roots to VCs emitted by microbial phytopathogens, we performed comprehensive proteomic, transcript, metabolic and developmental analyses of *Arabidopsis* plants exposed to VOC-depleted volatile emissions from *P. aurantiogriseum* cultures. We also characterized the response to fungal VCs in mutants with altered hormone and ROS status. Results presented in this work provide a holistic view of the biochemical and molecular mechanisms operating in roots of plants exposed

to VCs emitted by *P. aurantiogriseum*. Our findings show that VCs emitted by this fungal phytopathogen modify root metabolism and architecture, and enhance nutrient and water use efficiency by means of transcriptionally and non-transcriptionally regulated proteome resetting mechanisms that involve cyanide (HCN) scavenging, hormones and ROS signaling. Some of these mechanisms are subject to long-distance regulation by photosynthesis and differ from those involved in the response to VCs emitted by beneficial microorganisms.

MATERIALS AND METHODS

Plant and microbial cultures, growth conditions and sampling

The experiments were carried out using *Arabidopsis thaliana* L. (Heynh) WT plants (ecotype Col-0), the *aux1-T* auxin influx carrier mutant (N657534) (Fischer et al., 2006), the *etr1-3* ethylene receptor mutant (N3070) (Hua & Meyerowitz, 1998), the *eir1* ethylene insensitive and auxin efflux carrier mutant (N8058) (Luschnig, Gaxiola, Grisafi, & Fink, 1998), the *ahk2/3*, *ahk2/4* and *ahk3/4* CK signaling mutants (Riefler, Novak, Strnad, & Schmu, 2006), the *rhd2* mutant which is impaired in a plasma membrane NADPH oxidase (Foreman et al., 2003), the *cas-c1* mutant which is impaired in the mitochondrial β -cyanoalanine synthase (N522479) (García et al., 2010), the CK-inducible *ARR5:GUS* reporter (D'Agostino, Deruère, & Kieber, 2000) and the auxin-responsive reporter *DR5:GUS* (Ulmasov, Murfett, Hagen, & Guilfoyle, 1997). Unless otherwise indicated the plants were cultured in Petri dishes (92 x 16 mm, Ref. 82.1472.001, Sarstedt) containing sucrose-free half-strength solid Murashige and Skoog (MS) (Phytotechlab M519) medium in growth chambers providing 'long day' 16 h light (90 $\mu\text{mol photons sec}^{-1} \text{ m}^{-2}$), 22 °C /8 h dark, 18 °C cycles. For water stress treatments, seedlings were transferred onto solid MS growth medium that had been equilibrated with a 5% (w/v) polyethylene glycol (PEG) 6000 MS solution according to van der Weele, Spollen, Sharp, & Baskin (2000). *P. aurantiogriseum* was cultured in small Petri dishes (35 x 10 mm, Sarstedt, Ref. 82.1135.500) containing solid MS medium supplemented with 90 mM sucrose. Effects of microbial VOC-depleted VCs on plants were investigated using the "box-in-box" co-cultivation system as described in García-Gómez et al. (2019). Briefly, plant cultures 14 days after sowing

and fungal cultures in unlidded Petri dishes with a top layer of charcoal filter that adsorbs VCs with molecular masses greater than 45 Da were placed in sterile plastic boxes (200 x 150 x 50 mm IT200N Instrument Trays; AW Gregory, UK) sealed with polyvinyl chloride plastic wrap. As negative controls, Petri dishes containing plants were cultured in sealed boxes together with Petri dishes each containing sterile microbial culture media and a charcoal filter. After the incubation time indicated for each experiment, roots were harvested, 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

Gas exchange rates were determined as described by Sánchez-López et al. (2016) using a LI-COR 6400 gas exchange portable photosynthesis system (LI-COR, Lincoln, NE, USA). Net rates of CO₂ assimilation (A_n) and stomatal conductance (g_s) were calculated as described by von Caemmerer & Farquhar (1981). Intrinsic water use efficiency (WUE_i) was calculated as the ratio of A_n to g_s as described by Flexas et al. (2016).

Root morphological analysis

Ten days after sowing plants cultured on vertical square Petri dishes (10 x 10 x 2 cm, Sarstedt, Ref. 82.9923.422) were placed in vertical position in sealed plastic boxes containing fungal cultures placed in horizontal position covered with charcoal filters. After 6 days of co-cultivation, the numbers and lengths of the plants' roots and RHs were measured using an MVX10 stereomicroscope (Olympus, Japan). RHs lengths were measured on ca. 2 cm long LR. Photomicrographs were captured with a DP72 video camera (Olympus, Japan) and the Cell D package (Olympus, Japan). RHs were measured in a region of 5 mm from the LR tips.

O₂⁻ and H₂O₂ staining

O₂⁻ and H₂O₂ were semi-quantitatively detected in rosettes essentially as described by Nguyen et al. (2017). Briefly, O₂⁻ was detected by staining roots for 15 min with 0.05% nitro blue

tetrazolium (NBT) (w/v) in 50 mM potassium phosphate, pH 7.0, and H₂O₂ by staining for 5 h with 0.1% 3,3'-diaminobenzidine in 10 mM potassium phosphate, pH 7.0.

GUS expression analysis

Expression of the GUS reporter gene was monitored using the histochemical staining assay described by Jefferson, Kavanagh, & Bevan (1987).

Analytical procedures

The amino acids contents were determined from frozen powder samples (see above) as described by Loiret, Grimm, Hajirezaei, Kleiner, & Ortega (2009). To determine the levels of CKs, aliquots of the frozen powders were lyophilized and CKs were quantified according to the method described in Novák, Hauserová, Amakorová, Doležal, & Strnad (2008). HCN contents in roots and ethylene produced and released by roots were measured as described by García et al. (2010). Levels of UDP-glucose and TCA intermediates were measured as described by Ghaffari et al. (2016). Fe and Zn levels were measured as indicated in Eggert & Von Wirén, (2013).

Proteomic analysis

High-throughput, isobaric labeling-based differential proteomic analyses were conducted essentially as described in Sánchez-López, Bahaji, et al. (2016) for Arabidopsis leaves but with the following modifications. For protein sample preparation, samples were prepared by grinding 200 mg of root material into a fine powder under liquid nitrogen using a pre-cooled mortar and pestle. The tryptic peptides were labeled using a iTRAQ-4 plex Isobaric Mass Tagging Kit (SCIEX, Foster City, CA, USA). Search engines were configured to match potential peptide candidates with a 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 (¹³C) of 1, and also allowing for fixed MMTS modification of cysteine and variable oxidation of methionine, pyroglutamic acid from glutamine or glutamic acid at the peptide N-terminus, acetylation of the

protein N-terminus and modification of lysine and peptide N-terminus with iTRAQ 4-plex reagents. Statistical significance was measured using q-values (FDR). The cut-off for identifying differentially regulated proteins was established at a $FDR \leq 2.7\%$ and $\log_2$ ratios (+VC treatment vs. -VC treatment) of either > 0.4 (for proteins whose expression is up-regulated by fungal VCs) and < -0.4 (for proteins whose expression is down-regulated by VCs).

Real-time quantitative PCR

Total RNA was extracted from frozen Arabidopsis roots of *in vitro* cultured plants using the Trizol method according to the manufacturer's recommendations (Invitrogen), following treatment with RNAase-free DNAase (Takara). RNA (1.5 μg) was reverse-transcribed using polyT primers and an Expand Reverse Transcriptase kit (Roche) according to the manufacturer's instructions. RT-PCR amplification was performed as described by Sánchez-López, Baslam, et al. (2016) using primers listed in **Table S1**, and their specificity was checked by separating the obtained products on 1.8% agarose gels.

Statistical analysis

Unless otherwise indicated, data presented here are means ($\pm$ SE) obtained from 3-4 independent experiments, with 3-5 replicates for each experiment. The significance of differences between plants not exposed to VCs, and plants exposed to *P. aurantiogriseum* VCs, and between WT plants and mutants was statistically evaluated with Student's t-test using the SPSS package. Differences were considered significant if $P < 0.05$.

RESULTS

Fungal VCs promote changes in the root proteome and metabolome of exposed plants

We carried out high-throughput, isobaric labeling-based differential proteomic analysis of roots of Arabidopsis plants cultured in the absence, or presence for three days, of volatile emissions of adjacent cultures of *P. aurantiogriseum* covered with charcoal filters. As shown in **Table S2**, 178 out of the 2988 proteins identified in this study (**Table S3**) were proteins of known

functions that were differentially expressed in response to fungal VCs. Among them, 49 were up-regulated and 129 were down-regulated (**Table S2**). Using the broad categories outlined by the MapMan tool (<https://mapman.gabipd.org/>) (Thimm et al., 2004), the 178 differentially expressed proteins (DEPs) with known functions were assembled into 23 functional groups (**Figure 1**). The general trend indicates that RSA and root metabolic changes in plants treated with fungal VCs are associated with DEPs that fit into the following groups:

Transport

Fungal volatile emissions down-regulated the expression of plasma membrane and vacuolar aquaporins (e.g. PIP1-1, PIP1-2, PIP2-1, PIP2-2, PIP2-3, PIP2-7, TIP1-1, TIP1-2 and TIP2-2) involved in processes such as water transport (Péret et al., 2012; Reinhardt et al., 2016) and H₂O₂ transport and detoxification (Bienert et al., 2007; Rodrigues et al., 2017) (**Table S2** and **Figure 1**). Exposure to fungal VCs also reduced the expression of ACA8, a plasma membrane calcium pump that regulates cytosolic calcium concentration and signaling in response to environmental changes (Costa et al., 2017; Yang et al., 2017) and that of IRT1 (**Table S2** and **Figure 1**), a metal ion carrier protein that mediates the entry of Fe and Zn into roots and subsequent transport to leaves (Rogers, Eide, & Guerinot, 2000; Varotto et al., 2002). Consistent with this finding, leaves of VC-exposed plants had lower levels of Fe and Zn than controls (96.5 ± 4.0 and $166 \pm 9.4 \mu\text{g g}^{-1}$ dry weight (DW) of Fe in leaves of VC-treated and non-treated plants, respectively, and $86.3 \pm 2.3 \mu\text{g}$ and $129 \pm 18.2 \mu\text{g g}^{-1}$ DW of Zn in leaves of VC-treated and non-treated plants, respectively).

Major carbohydrate metabolism

Exposure to fungal VCs diminished the expression of the two vacuolar invertases involved in sucrose breakdown (**Table S2** and **Figure 1**), BFRUCT3 and BFRUCT4, the latter being an important determinant of root length in Arabidopsis (Sergeeva et al., 2006).

Redox metabolism

Exposure to charcoal-filtered fungal VCs down-regulated the expression of various extracellular peroxidases (e.g. PER3, PER32 and PER34) (**Table S2** and **Figure 1**). Some of them (e.g. PER34) are important determinants of root and RH growth (Passardi, Tognolli, De Meyer, Penel, & Dunand, 2006).

Cell wall metabolism

Fungal VCs down-regulated the expression of cell wall breakdown enzymes (e.g. BGLU20-23), and stimulated the expression of enzymes involved in the synthesis of precursors for cell wall biosynthesis (e.g. UGP2, UGD4 and UXS4) and cell wall loosening during cell growth (e.g. XTH14) (**Table S2** and **Figure 1**). In agreement with this observation, roots of fungal VC-exposed plants accumulated higher levels of cell wall precursor molecules than controls (81.1 ± 15.2 and 10.9 ± 3.2 nmol g⁻¹ DW of UDP-glucose in roots of VC-treated and non-treated plants, respectively, and 107 ± 8.8 and 46.6 ± 8.7 nmol g⁻¹ DW glucuronic acid in roots of VC-treated and non-treated plants, respectively).

Nitrogen assimilation

Fungal VCs increased the expression of enzymes involved in non-photorespiratory ammonium assimilation (e.g. GLUT1/NADH-GOGAT), the conversion of cytosolic citrate to Gln (e.g. ASP2 and GLN1-2) and the conversion of cytosolic Met and mitochondrial Cys to Asp and Asn (e.g. METK2, METK3, ACO2 and CAS-C1) (**Table S2** and **Figure 1**). Consistent with this observation, levels of Glu, Gln, Asp and Asn in roots of VC-treated plants were higher than those in controls (34.5 ± 1.0 and 23.4 ± 1.2 μmol g⁻¹ DW of Glu in roots of VC-treated and non-treated plants, respectively; 62.0 ± 1.4 and 38.9 ± 1.6 μmol g⁻¹ DW of Gln in roots of VC-treated and non-treated plants, respectively; 18.1 ± 0.7 and 14.5 ± 1.2 μmol g⁻¹ DW of Asp in roots of VC-treated and non-treated plants, respectively; 195.8 ± 2.9 and 164 ± 5.3 μmol g⁻¹ DW of Asn in roots of VC-treated and non-treated plants, respectively). Levels of citrate and other

TCA metabolic intermediates acting as amino acid precursors were higher in VC-exposed roots than in controls (**Table S4**).

Hormone metabolism

Fungal VCs increased the expression of ACLA-1, an enzyme that participates directly in the conversion of cytosolic citrate into the acetyl-CoA necessary for the synthesis of mevalonate (MVA)-derived isoprenoids (Fatland, Nikolau, & Wurtele, 2005). Fungal VCs also increased the expression of ethylene biosynthetic enzymes such as METK2, METK3 and ACO2 (**Table S2** and **Figure 1**); the latter catalyzes the rate-limiting step of ethylene biosynthesis in many processes in response to environmental changes and is an important determinant in plant-microbe interactions (Barry et al., 1996; Nascimento, Rossi, & Glick, 2018).

Changes in the root proteome promoted by fungal VCs are transcriptionally and non-transcriptionally regulated

To investigate the extent to which post-transcriptional and/or post-translational mechanisms are involved in proteome shifts promoted by fungal VCs, we analyzed by qRT-PCR the expression levels of genes encoding a selected group of fungal VC-responsive proteins. As shown in **Figure 2**, these analyses revealed that nearly 40% of these genes are not differentially expressed by fungal VCs and/or show expression patterns in response to fungal VCs that are different to those of the encoded proteins. This indicates that changes in the proteome of roots promoted by fungal VCs are subject to both transcriptional and non-transcriptional regulatory processes.

Down-regulation of water and iron transport systems in response to fungal VCs is associated with enhanced intrinsic photosynthetic water use efficiency and drought tolerance

Fe participates in electron transfer reactions starting from the photochemical water splitting occurring during photosynthesis. Down-regulation of the expression of aquaporins and IRT1 in roots and of Fe contents in leaves in response to fungal VCs suggested enhancement of

photosynthetic efficiency thus reducing the water and Fe demands of leaves. To test this hypothesis, we measured the WUE_i by analyzing A_n and g_s at varying intercellular CO_2 concentrations (C_i) in plants cultured in the absence or presence of adjacent cultures of *P. aurantiogriseum*. These analyses revealed that plants exposed to fungal VCs had higher A_n and similar g_s (and thus higher WUE_i) values than controls at all C_i levels (**Figure 3**). We also compared growth of plants cultured under water deficit conditions imposed by equilibrating the culture medium with PEG 6000 solutions. As expected, drought exerted a strong negative effect on plant growth in fungal VC untreated plants (**Figure 4**). Notably, treatment with fungal VCs highly stimulated growth under drought conditions (**Figure 4**).

Fungal VCs enhance auxin, ethylene and CK signaling

Fungal VC-promoted expression of enzymes involved in the synthesis of ethylene (e.g. METK2, METK3 and ACO2) and isoprenoids (e.g. ACLA1) suggested enhanced production and signaling of ethylene and isoprenoid hormones such as CKs. Because ethylene stimulates auxin production in roots (Růžicka et al., 2007; Swarup et al., 2007), fungal VC-promoted expression of ethylene biosynthetic enzymes also suggested enhanced auxin signaling. To test these hypotheses we analyzed GUS expression in roots of plants harboring the CK-inducible *ARR5:GUS* marker and the auxin-inducible *DR5:GUS* marker cultured in the absence or presence of adjacent cultures of *P. aurantiogriseum*. Furthermore, we measured ethylene emissions and CK contents in roots of VC-treated plants. As shown in **Figure 5**, *ARR5:GUS* and *DR5:GUS* plants grown with adjacent fungal cultures showed greater GUS expression in vascular tissues, root tips, LR primordia and RHs than controls. Furthermore, ethylene emissions by roots of plants treated with fungal VCs were substantially higher than in controls (**Figure 6**). CK content analyses revealed that treatment with fungal VCs causes a significant increase in the content of both MVA- and 2-C-methyl-D-erythritol 4-phosphate (MEP)-derived CKs (**Table 1**). The most strongly accumulated CK forms were the free bases of the biologically active cis-zeatin (cZ) and isopentenyladenine (iP), their ribosides (cZR and iPR

respectively), their precursors (*cZRMP* and *iPRMP*, respectively) and the precursor and transport forms of *tZ* (*tZR* and *tZRMP*, respectively) (**Table 1, Figure S1**).

Root developmental responses to fungal VCs in auxin, ethylene and CK signaling mutants

Whether enhanced ethylene, auxin and CK signaling plays an important role in the developmental responses of roots to fungal VCs was investigated by characterizing RSA in the *etr1-3* ethylene receptor mutant, the *aux1-T* auxin influx carrier mutant, the *eir1* ethylene insensitive and auxin efflux carrier mutant and the *ahk2/3*, *ahk2/4* and *ahk3/4* CK signaling mutants cultured in the absence or presence of adjacent cultures of *P. aurantiogriseum*. In keeping with García-Gómez et al. (2019), fungal VCs promoted root growth (on a fresh weight basis) and the development of a “cotton-like” external root phenotype caused by the formation of “brush-like” structures at the root tips, shortened the PR and LRs and increased the number of elongated LRs in WT plants (**Figure 7**). VCs promoted similar to WT enhancement of root growth and increased the number of elongated LRs in all mutants (**Figure 7, Figure S2**). Fungal volatile emissions did not shorten the PRs and LRs in *aux1-T*, *eir1* and *etr1-3* mutants and the LRs in CK mutants (**Figure 7 and Figure S2**).

Under non-induced conditions, roots of *aux1-T*, *eir1* and *etr1-3* mutants produced fewer and shorter RHs than WT plants (**Figure 7c**), which is consistent with Pitts, Cernac, & Estelle, (1998). As in WT plants, all mutants developed and elongated new RHs in response to fungal VCs, although the stimulatory effect in auxin and ethylene signaling mutants was weaker than in WT plants and CK signaling mutants (**Figure 7c and Figure S2c**). In the presence of fungal VCs, the auxin and ethylene mutants failed to form “brush-like” structures at the root tips (**Figure 7a**). It thus appears that the promotion of the “cotton-like” external root phenotype by fungal VCs caused by the strong proliferation and elongation of RHs at the root tips is auxin- and ethylene- dependent.

RSA changes promoted by fungal VCs are associated with enhanced O_2^- and H_2O_2 contents in roots and RHs

Fungal VCs promoted down-regulation of the expressions of calcium pumps, aquaporins and apoplastic peroxidases in roots (cf. **Table S2** and **Figure 1**) suggested enhanced O_2^- and H_2O_2 contents. This inference was corroborated by specific O_2^- and H_2O_2 staining analyses, which revealed higher levels of these compounds in roots and RHs of fungal VC-treated plants than in controls (**Figure 8**). Root and RH growth is associated with O_2^- and H_2O_2 accumulation (Foreman et al., 2003). To test the possible involvement of the accumulation of these compounds in the fungal VC-promoted RSA changes we characterized the root response of *rhd2* plants to fungal VCs. These plants lack an NADPH oxidase that contributes to O_2^- and H_2O_2 production in roots, and have shorter roots and RHs than WT plants (Foreman et al., 2003). As in WT plants, fungal VCs promoted root growth in *rhd2* plants (**Figure 9a,b**). As expected, in the absence of fungal VCs *rhd2* roots showed only a few short malformed RHs (**Figure 9a**) that accumulated low levels of O_2^- (**Figure S3**). Notably, unlike WT plants, this mutant was unresponsive in terms of O_2^- accumulation in RHs (**Figure S3**), RH growth stimulation (**Figure 9a,c**) and PR and LR shortening promoted by fungal VCs (**Figure 9c**). We also characterized the RH response of WT plants to nanomolar concentrations of the NADPH oxidase inhibitor diphenyleneiodonium (DPI) (Cross & Jones, 1986). As shown in **Figure S4**, enhancement of RH growth promoted by fungal VCs was weaker in DPI-treated plants than in controls.

RSA changes promoted by fungal VCs are associated with enhanced HCN content in roots

HCN is a toxic compound produced mainly by 1-aminocyclopropane-1-carboxylate oxidase (ACO) in the last step of the ethylene biosynthetic pathway. Mitochondrial β -cyanoalanine synthase (CAS-C1) is essential to maintain low HCN levels and allow for proper RH development (Arenas-Alfonseca, Gotor, Romero, & García, 2018; García et al., 2010). Fungal VC-promoted expression of ethylene biosynthetic enzymes (e.g. METK2, METK3 and ACO2) and CAS-C1 (cf. **Table S2** and **Figure 1**) suggested that up-regulation of CAS-C1 could play a role in the RH elongation process promoted by fungal VCs by removing excess HCN. To test this hypothesis, we measured HCN levels in roots of WT plants cultured in the absence or

presence of adjacent fungal cultures. We also characterized the RSA and O_2^- accumulation responses of *cas-cl* mutants to fungal VCs.

Fungal VCs caused a ca. 3-fold increase in HCN contents in roots (15.5 ± 5.9 and 42.3 ± 6.2 nmol g⁻¹ FW in non-treated and VC-treated plants, respectively). As in WT plants, fungal VCs promoted root growth in *cas-cl* plants (**Figure 10a,b**). In keeping with findings by García et al. (2010), *cas-cl* roots not treated with fungal VCs exhibited only a few short malformed RHs (**Figure 10a**) and accumulated low levels of O_2^- in the RHs (**Figure S3**). Notably, unlike WT plants, this mutant did not exhibit O_2^- accumulation in RHs (**Figure S3**), RH growth stimulation (**Figure 10a,c**) and LR shortening in response to exposure to fungal VCs (**Figure 10c**).

DISCUSSION

Results presented in this work provide a holistic view, schematically illustrated in **Figure 11**, of the biochemical and molecular mechanisms operating in roots of plants exposed to VCs from *P. aurantiogriseum*. Our findings strongly indicate that fungal VCs modify root metabolism and architecture, and improve nutrient and water use efficiency through transcriptionally and non-transcriptionally regulated proteome resetting mechanisms that involve long-distance photosynthetic signals, HCN scavenging and ROS and hormone signaling.

Fungal VCs promote changes in the root proteome that are associated with enhanced nutrient and photosynthetic water use efficiencies

The uptake of mineral nutrients relies on regulatory mechanisms controlling the abundance and activity of transporters on the root cells to adjust the uptake to the demands of the plant's aerial part. Evidence for the occurrence of shoot-borne photosynthetic signals (presumably sugars) regulating nutrient uptake in roots according to the shoot demand for nutrients has been provided by expression analyses of the Nrt2.1 and IRT1 NO_3^- and Fe transporters, respectively (Gansel et al., 2001; Vert et al., 2003).

We have previously shown that VCs emitted by microbial phytopathogens enhance photosynthesis through mechanisms involving redox activation of the Calvin-Benson enzymes and proteins involved in photochemical reactions (Ameztoy et al., 2019). Here we found that fungal VCs enhance WUE_i, and down-regulate the expression of IRT1 and aquaporins in roots. Fungal VCs did not alter the stomatal conductance, strongly indicating that the enhancement of photosynthetic activity promoted by fungal VCs is due to improved efficiency of the photosynthetic machinery, but not to an increased passage of CO₂ entering through the stomata. Therefore, one possible explanation for the fungal VC-promoted down-regulation of expression of IRT1 and aquaporins in roots is that fungal VCs greatly enhance the photosynthetic water and Fe use efficiencies and thus reduce the water and Fe demands. According to this view, production and release of signals (presumably sugars) of enhanced photosynthetic efficiency in leaves would activate pathways leading to repression of genes encoding water and Fe transporters in roots as illustrated in **Figure 11**. That plants exposed to fungal VCs were more tolerant to drought than controls further supports the idea that the enhanced photosynthetic water use efficiency promoted by fungal VCs reduces water demands. Because (i) CKs and auxin transcriptionally down-regulate the expression of *IRT1* and aquaporin genes, respectively (Nemhauser, Hong, & Chory, 2006; Péret et al., 2012; Séguéla, Briat, Vert, & Curie, 2008) and (ii) fungal VCs enhance CK and auxin signaling, it is likely that fungal VC-promoted reduction of IRT1 and aquaporin expression is primarily due to enhanced CK and auxin signaling.

As illustrated in **Figure 11**, fungal VCs promoted the expression of enzymes involved in non-photorespiratory ammonium assimilation (e.g. GLUT1/NADH-GOGAT) and the conversion of cytosolic citrate and Met to Asp and the long-distance nitrogen transport amino acids Asn, Glu and Gln (e.g. ASP2, GLN1-2, METK2, METK3, ACO2 and CAS-C1). Some of these enzymes (e.g. GLUT1, GLN1-2 and ASP2) are major determinants of nitrogen use efficiency (NUE) (Li, Hu, & Chu, 2017). Consistently, fungal VCs promoted the accumulation of high levels of Asp, Glu, Asn and Gln. Because (i) CKs post-transcriptionally and/or post-translationally up-regulate METK2, METK3 and ACO2 expression (Žd'árská et al., 2013), and (ii) fungal VCs enhance CK signaling, it is conceivable that fungal VC-promoted growth is

partly the consequence of enhanced NUE due to up-regulation of METK2, METK3 and ACO2 expression caused by the increase in CK levels and signaling.

Root shortening promoted by fungal VCs involves enhanced auxin, ethylene and CK production and signaling caused by proteome shifts

Results presented in this work showing enhanced CK, ethylene and auxin signaling promoted by fungal VCs, and weak root developmental responses of hormone signaling mutants strongly indicate that root shortening promoted by fungal VCs involve hormone actions. Fungal VCs enhanced the levels of ethylene biosynthetic enzymes (e.g. METK2, METK3 and ACO2) and ethylene production in roots. It is thus conceivable that the enhanced ethylene production and signaling promoted by fungal VCs is due, at least in part, to augmented METK2, METK3 and ACO2 expression as schematically illustrated in **Figure 11**. Fungal VCs also enhanced ACLA-1 expression and levels of MVA-derived CKs, which indicates that enhanced levels of MVA-derived CKs and signaling promoted by fungal VCs is due to up-regulation of ACLA-1 expression (**Figure 11**). Recent studies have shown that plants employ a long-distance signaling system to regulate growth in response to elevated photosynthesis in which photosynthetically generated sugars induce *de novo* CK biosynthesis in roots (Kiba et al., 2019). Because fungal VCs enhance photosynthesis and the production of sugars (Sánchez-López, Baslam, et al., 2016), we propose that enhanced CK levels in roots promoted by fungal VCs is due to long-distance signaling of enhanced photosynthesis.

Root shortening promoted by fungal VCs involves reduction of osmotic water uptake

Root elongation occurs as individual cells along the growing zone increase in volume. This increase is controlled by water uptake driven by the osmotic potential of the cells. Fungal VCs down-regulated the expression of BFRUCT4. This vacuolar invertase converts sucrose to fructose and glucose leading to osmotic water uptake and a subsequent increase in turgor as a driving force for root elongation (Sergeeva et al., 2006). In addition, fungal VCs down-regulated the expression of tonoplast and plasma membrane aquaporins that contribute to cell

elongation by allowing water influx to maintain adequate turgor pressure (Péret et al., 2012; Reinhardt et al., 2016). We therefore propose that root shortening in response to fungal VCs is due, at least to some extent, to reduced osmotic water uptake caused by down-regulation of the expressions of aquaporins and BFRUCT4. Because aquaporin genes are repressed by auxin it is conceivable that root shortening promoted by fungal VCs is due, at least in part, to down-regulation of the expression of aquaporins caused by enhanced auxin signaling.

RH proliferation and elongation promoted by fungal VCs involves hormone signaling independent mechanisms

VCS emitted by *P. aurantiogriseum* strongly promoted RH formation and elongation in auxin, ethylene and CK mutants, which suggests the operation of important hormone signaling independent mechanisms in the promotion of proliferation and elongation of RHs by fungal VCs.

RH proliferation and elongation promoted by fungal VCs is ROS-dependent

O_2^- and H_2O_2 accumulation in the apoplast, mediated through the activity of redox metabolism-related enzymes (e.g. NADPH oxidases and apoplastic peroxidases) and plasma membrane H_2O_2 transporting aquaporins (Bienert et al., 2007; Rodrigues et al., 2017) play important roles in root and RH growth and development (Foreman et al., 2003; Passardi et al., 2006). Here we found that fungal VCs enhanced O_2^- and H_2O_2 levels in roots and RHs. Fungal VCs also down-regulated the expression of plasma membrane aquaporins and apoplastic peroxidases, some of which (e.g. PER34) are directly involved in root growth and RH formation and development (Passardi et al., 2006). Furthermore, fungal VCs reduced the expression of ACA8, a calcium pump that determines the concentration of the cytosolic calcium that regulates NADPH oxidase activity through calcium-dependent protein kinases (Costa et al., 2017; Dubiella et al., 2013; Yang et al., 2017). We also found that the NADPH oxidase inhibitor DPI prevents the RH elongation promoted by *P. aurantiogriseum* VCs and that *rhb2* plants lacking a root-expressed NADPH oxidase do not show O_2^- accumulation in RHs, RH growth stimulation in response to

528 fungal VCs. Overall the data indicate that an apoplastic oxidative burst due to down-regulation
529 of plasma membrane aquaporins and apoplastic peroxidases, and activation of NADPH oxidases
530 by calcium-dependent protein kinases (**Figure 11**), are major determinants of the RH response
531 to fungal VCs.

532 H_2O_2 may function as a downstream component in auxin-mediated signal transduction
533 (Ma et al., 2014; Mangano et al., 2017). As auxin down-regulates plasma membrane H_2O_2
534 transporting aquaporin gene expression (Nemhauser et al., 2006; Péret et al., 2012) and fungal
535 VCs enhance auxin signaling, it is conceivable that the fungal VC-promoted root response
536 caused by an apoplastic oxidative burst is due, at least in part, to down-regulation of expression
537 of plasma membrane aquaporins caused by enhanced auxin signaling.

538
539 ***RH proliferation and elongation promoted by fungal VCs involve HCN scavenging***
540 ***mechanisms mediated by CAS-C1***

541 Synthesis of ethylene results in the production of HCN, which is a potent toxin. To prevent self-
542 poisoning, plants maintain an endogenous HCN detoxification pathway involving CAS-C1,
543 which catalyzes the addition of HCN to Cys to produce H_2S and β -cyanoalanine, the latter being
544 transported from mitochondria to the cytosol where it is converted to Asp or Asn by β -
545 cyanoalanine nitrilase (Piotrowski, Schönfelder, & Weiler, 2001) (**Figure 11**). CAS-C1 null
546 mutants accumulate 40-60% more HCN and produce fewer and shorter RHs than WT plants
547 (Arenas-Alfonseca et al., 2018; García et al., 2010). Thus, it has been suggested that CAS-C1 is
548 essential in maintaining HCN at low levels that allow proper RH development (García et al.,
549 2010).

550 Fungal VCs enhanced the expression of ethylene biosynthetic enzymes (e.g. METK2,
551 METK3 and ACO2) and CAS-C1. In addition, fungal VCs did not promote RH elongation in
552 *cas-c1* plants.. These findings suggest that enhanced CAS-C1 expression may play a role in the
553 fungal VC-promoted RH elongation by removing excess HCN generated by VC-promoted
554 ethylene synthesis. However, fungal VCs caused a ca. 3-fold increase in HCN contents in the
555 roots of WT plants, which strongly indicates that (a) roots of WT plants exposed to fungal VCs

are capable of accumulating high levels of HCN without inhibiting RH formation and elongation, and (b) CAS-C1 operates in the fungal VC-promoted RH formation and elongation through mechanisms other than maintaining low levels of HCN. HCN is recognized as a broad-spectrum antimicrobial biocontrol agent produced by some prokaryotes that has been implicated in the suppression of different root diseases caused by fungal phytopathogens (Flaishman, Eyal, Zilberstein, Voisard, & Haas, 1996; Voisard, Keel, Haas, & Dèfago, 1989). It is therefore conceivable that HCN over-accumulation in roots in response to fungal VC is a strategy to protect the plant against fungal attack. Clearly, further experiments are necessary to test this hypothesis.

In *Arabidopsis*, enhanced flux from HCN to Asn and Asp by the ectopic expression of β -cyanoalanine nitrilase promotes RH elongation (O’Leary, Preston, & Sweetlove, 2014). One possible explanation for the fungal VC-promoted RH formation and elongation could therefore involve the conversion of HCN produced by ACO2 to cytosolic Asp, Asn, Glu and Gln through the coupled reactions of CAS-C1, β -cyanoalanine nitrilase, ASP2 and GLN1-2 as schematically illustrated in **Figure 11**. Lack of CAS-C1 prevents not only the scavenging of HCN molecules produced in the last step of the ethylene biosynthetic pathway but also the formation of O_2^- by hitherto unknown mechanisms (Arenas-Alfonseca et al., 2018). Here we found that *cas-c1* plants are unresponsive in terms of O_2^- accumulation in RHs. Therefore, another possible explanation for the RH formation and elongation promoted by fungal VCs could involve the enhancement of O_2^- production and signaling by as yet to be identified CAS-C1 dependent mechanisms. At low concentrations H_2S can act as a signaling molecule that promotes growth and RSA changes (Chen et al., 2011; Mei, Chen, Shen, Shen, & Huang, 2017). Therefore, a third explanation for the fungal VC-promoted RH changes could involve the enhancement of CAS-C1-mediated H_2S production and signaling (**Figure 11**).

Metabolic and root developmental responses promoted by VCs from *P. aurantiogriseum* differ from those triggered by VCs emitted by beneficial microorganisms

Several factors indicate that the mechanisms involved in RSA and metabolic adjustments promoted by VCs emitted by beneficial microorganisms and by *P. aurantiogriseum* are different. First, whereas VCs emitted by growth promoting bacteria induce stomatal closure and up-regulate the expression of enzymes involved in the synthesis of osmoprotectants to avoid water loss and enhance drought tolerance (Cho et al., 2008; Zhang et al., 2010), no such changes are observed in plants exposed to *P. aurantiogriseum* VCs. Instead, it appears that enhanced drought tolerance induced by fungal VCs is due to reduced water demands (and thus reduced water uptake by roots) caused by enhanced WUE_i in leaves. Second, our findings contrast with those of reports showing that complex mixtures of VCs or discrete (individual) VOCs emitted by beneficial microorganisms exert a null or minor effect on LR formation and RH formation and elongation in auxin and ethylene signaling mutants (Contreras-Cornejo et al., 2015; Garnica-Vergara et al., 2016; Splivallo et al., 2009). Third, our results differ from those of studies showing that complex mixtures of VOCs emitted by the symbiotic fungus *Trichoderma atroviride* inhibit PR growth in ethylene signaling mutants (Contreras-Cornejo et al., 2015). Fourth, results presented in this work showing that *P. aurantiogriseum* inhibit IRT1 expression at both transcript and protein levels contrast with those of reports showing that VCs from beneficial rhizobacteria and rhizofungi enhance the levels of *IRT1* transcripts (Martínez-Medina, van Wees, & Pieterse, 2017; Zamioudis et al., 2015; Zhang et al., 2009). The discovery that VCs from pathogenic microorganisms can promote plant growth and root developmental changes through mechanisms different to those triggered by beneficial microorganisms raise questions regarding the evolution of the mechanisms involved in modulation of the response of plants to microbes and their ecological significance. At present we can just speculate that plant growth promotion by microbial VCs prepares the plant to host the microorganism, which in the case of phytopathogenic microorganisms ensures proper continuation into the pathogenic phase. Alternatively, it is possible that VCs emitted by microbial phytopathogens act as alert signals to plants.

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612

613 **AUTHORS' CONTRIBUTIONS:**

614 P G-G, A B and J P-R designed the experiments and analyzed the data; P G-G, A B, S G-A, FJ
615 M, ÁM S-L, G A, K A, E B-F, N DD, L U, L S, K D, M-R H, LC R and I G performed most of
616 the experiments; A B and J P-R supervised the experiments; P G-G and J P-R wrote the article
617 with contributions from all the authors; J P-R conceived the project and research plans.

618

619 **CONFLICT OF INTEREST STATEMENT**

620 The authors declare that the research was conducted in the absence of any commercial
621 or financial relationships that could be construed as a potential conflict of interest.

622

REFERENCES

- Ameztoy, K., Baslam, M., Sánchez-López, Á. M., Muñoz, F. J., Bahaji, A., Almagro, G., ... Pozueta-Romero, J. (2019). Plant responses to fungal volatiles involve global post-translational thiol redox proteome changes that affect photosynthesis. *Plant, Cell & Environment*, (4) doi: <https://doi.org/10.1111/pce.13601>.
- Arenas-Alfonseca, L., Gotor, C., Romero, L. C., & García, I. (2018). β -cyanoalanine synthase action in root hair elongation is exerted at early steps of the root hair elongation pathway and is independent of direct cyanide inactivation of NADPH oxidase. *Plant and Cell Physiology*, 59(5), 1072–1083.
- Bailly, A., Groenhagen, U., Schulz, S., Geisler, M., Eberl, L., & Weiskopf, L. (2014). The inter-kingdom volatile signal indole promotes root development by interfering with auxin signalling. *Plant Journal*, 80(5), 758–771.
- Barry, C. S., Blume, B., Bouzayen, M., Cooper, W., Hamilton, A. J., & Grierson, D. (1996). Differential expression of the 1-aminocyclopropane-1-carboxylate oxidase gene family of tomato. *Plant Journal*, 9(4), 525–535.
- Bienert, G. P., Møller, A. L. B., Kristiansen, K. A., Schulz, A., Møller, I. M., Schjoerring, J. K., & Jahn, T. P. (2007). Specific aquaporins facilitate the diffusion of hydrogen peroxide across membranes. *Journal of Biological Chemistry*, 282(2), 1183–1192.
- Bitas, V., McCartney, N., Li, N., Demers, J., Kim, J. E., Kim, H. S., ... Kang, S. (2015). *Fusarium oxysporum* volatiles enhance plant growth via affecting auxin transport and signaling. *Frontiers in Microbiology*, 10;6:1248.
- Bodini, S. F., Cicalini, A. R., & Santori, F. (2011). Rhizosphere dynamics during phytoremediation of olive mill wastewater. *Bioresource Technology*, 102(6), 4383–4389.
- Bouguyon, E., Perrine-Walker, F., Pervent, M., Rochette, J., Cuesta, C., Benkova, E., ... Nacry, P. (2016). Nitrate controls root development through post-transcriptional regulation of the NRT1.1/NPF6.3 transporter/sensor. *Plant Physiology*, 172(2), 1237–1248.
- Camarena-Pozos, D. A., Flores-Núñez, V. M., López, M. G., López-Bucio, J., & Partida-Martínez, L. P. (2019). Smells from the desert: microbial volatiles that affect plant growth

651 and development of native and non-native plant species. *Plant Cell and Environment*,
652 42(4), 1368–1380.

653 Cao, Z. Y., Xuan, W., Liu, Z. Y., Li, X. N., Zhao, N., Xu, P., ... Shen, W. B. (2007). Carbon
654 monoxide promotes lateral root formation in rapeseed. *Journal of Integrative Plant*
655 *Biology*, 49(7), 1070–1079.

656 Casimiro, I., Marchant, A., Bhalerao, R. P., Beeckman, T., Dhooge, S., Swarup, R., ... Bennett,
657 M. (2001). Auxin transport promotes Arabidopsis lateral root initiation. *The Plant Cell*,
658 13(4), 843–852.

659 Chen, J., Wu, F. H., Wang, W. H., Zheng, C. J., Lin, G. H., Dong, X. J., ... Zheng, H. L. (2011).
660 Hydrogen sulphide enhances photosynthesis through promoting chloroplast biogenesis,
661 photosynthetic enzyme expression, and thiol redox modification in *Spinacia oleracea*
662 seedlings. *Journal of Experimental Botany*, 62(13), 4481–4493.

663 Cho, S. M., Kang, B. R., Han, S. H., Anderson, A. J., Park, J. Y., Lee, Y. H., ... Kim, Y. C.
664 (2008). 2R,3R-butanediol, a bacterial volatile produced by *Pseudomonas chlororaphis* O6,
665 is involved in induction of systemic tolerance to drought in *Arabidopsis thaliana*.
666 *Molecular Plant-Microbe Interactions*, 21(8), 1067–1075.

667 Contreras-Cornejo, H. A., López-Bucio, J. S., Méndez-Bravo, A., Macías-Rodríguez, L.,
668 Ramos-Vega, M., Guevara-García, Á. A., & López-Bucio, J. (2015). Mitogen-activated
669 protein kinase 6 and ethylene and auxin signaling pathways are involved in Arabidopsis
670 root-system architecture alterations by *Trichoderma atroviride*. *Molecular Plant-Microbe*
671 *Interactions*, 28(6), 701–710.

672 Contreras-Cornejo, H. A., Macías-Rodríguez, L., Cortés-Penagos, C., & López-Bucio, J. (2009).
673 *Trichoderma virens*, a plant beneficial fungus, enhances biomass production and promotes
674 lateral root growth through an auxin-dependent mechanism in Arabidopsis. *Plant*
675 *Physiology*, 149(3), 1579–1592.

676 Cordovez, V., Mommer, L., Moisan, K., Lucas-Barbosa, D., Pierik, R., Mumm, R., ...
677 Raaijmakers, J. M. (2017). Plant phenotypic and transcriptional changes induced by
678 volatiles from the fungal root pathogen *Rhizoctonia solani*. *Frontiers in Plant Science*,

8(1262), doi: <https://doi.org/10.3389/fpls.2017.01262>

- Cordovez, V., Schop, S., Hordijk, K., de Boulois, H. D., Coppens, F., Hanssen, I., ... Carrióna, V. J. (2018). Priming of plant growth promotion by volatiles of root-associated *Microbacterium* spp. *Applied and Environmental Microbiology*, 84(22). doi: <https://doi.org/10.1128/AEM.01865-18>.
- Correa-Aragunde, N., Graziano, M., & Lamattina, L. (2004). Nitric oxide plays a central role in determining lateral root development in tomato. *Planta*, 218(6), 900–905.
- Costa, A., Luoni, L., Marrano, C. A., Hashimoto, K., Köster, P., Giacometti, S., ... Bonza, M. C. (2017). Ca^{2+} -dependent phosphoregulation of the plasma membrane Ca^{2+} -ATPase ACA8 modulates stimulus-induced calcium signatures. *Journal of Experimental Botany*, 68(12), 3215–3230.
- Creus, C. M., Graziano, M., Casanovas, E. M., Pereyra, M. A., Simontacchi, M., Puntarulo, S., ... Lamattina, L. (2005). Nitric oxide is involved in the *Azospirillum brasilense*-induced lateral root formation in tomato. *Planta*, 221(2), 297–303.
- Cross, A. R., & Jones, O. T. G. (1986). The effect of the inhibitor diphenylene iodonium on the superoxide-generating system of neutrophils. Specific labelling of a component polypeptide of the oxidase. *Biochemical Journal*, 237(1), 111–116.
- D'Agostino, I. B., Deruère, J., & Kieber, J. J. (2000). Characterization of the response of the Arabidopsis response regulator gene family to cytokinin. *Plant Physiology*, 124(4), 1706–1717.
- De-la-Peña, C., & Loyola-Vargas, V. M. (2014). Biotic interactions in the rhizosphere: a diverse cooperative enterprise for plant productivity. *Plant Physiology*, 166(2), 701–709.
- Ditengou, F. A., Müller, A., Rosenkranz, M., Felten, J., Lasok, H., Van Doorn, M. M., ... Polle, A. (2015). Volatile signalling by sesquiterpenes from ectomycorrhizal fungi reprogrammes root architecture. *Nature Communications*, 6(6279). doi:<https://doi.org/10.1038/ncomms7279>
- Dooley, F. D., Nair, S. P., & Ward, P. D. (2013). Increased growth and germination success in plants following hydrogen sulfide administration. *PLoS ONE*, 8, e62048. doi:

707 <https://doi.org/10.1371/journal.pone.0062048>

708 Dubiella, U., Seybold, H., Durian, G., Komander, E., Lassig, R., Witte, C.-P., ... Romeis, T.
709 (2013). Calcium-dependent protein kinase/NADPH oxidase activation circuit is required
710 for rapid defense signal propagation. *Proceedings of the National Academy of Sciences*,
711 *110*(21), 8744–8749.

712 Eggert, K., & Von Wirén, N. (2013). Dynamics and partitioning of the ionome in seeds and
713 germinating seedlings of winter oilseed rape. *Metallomics*, *5*(9), 1316–1325.

714 Fatland, B. L., Nikolau, B. J., & Wurtele, E. S. (2005). Reverse genetic characterization of
715 cytosolic acetyl-CoA generation by ATP-citrate lyase in Arabidopsis. *The Plant Cell*,
716 *17*(1), 182–203.

717 Fischer, U., Ikeda, Y., Ljung, K., Serralbo, O., Singh, M., Heidstra, R., ... Grebe, M. (2006).
718 Vectorial information for Arabidopsis planar polarity is mediated by combined *AUX1*,
719 *EIN2*, and *GNOM* activity. *Current Biology*, *16*(21), 2143–2149.

720 Flaishman, M. A., Eyal, Z., Zilberstein, A., Voisard, C., & Haas, D. (1996). Suppression of
721 septoria tritici blotch and leaf rust of wheat by recombinant cyanide-producing strains of
722 *Pseudomonas putida*. *Molecular Plant-Microbe Interactions*, *9*(7), 642–645.

723 Flexas, J., Díaz-Espejo, A., Conesa, M. A., Coopman, R. E., Douthe, C., Gago, J., ...
724 Niinemets, Ü. (2016). Mesophyll conductance to CO₂ and Rubisco as targets for
725 improving intrinsic water use efficiency in C₃ plants. *Plant Cell and Environment*. *39*(5),
726 965–982.

727 Foreman, J., Demidchik, V., Bothwell, J. H. F., Mylona, P., Miedema, H., Torres, M. A., ...
728 Dolan, L. (2003). Reactive oxygen species produced by NADPH oxidase regulate plant
729 cell growth. *Nature*, *422*(6930), 442–446.

730 Gansel, X., Muños, S., Tillard, P., & Gojon, A. (2001). Differential regulation of the NO₃⁻ and
731 NH₄⁺ transporter genes *AtNrt2.1* and *AtAmt1.1* in Arabidopsis: relation with long-distance
732 and local controls by N status of the plant. *Plant Journal*, *26*(2), 143–155.

733 García-Gómez, P., Almagro, G., Sánchez-López, Á. M., Bahaji, A., Amezttoy, K., Ricarte-
734 Bermejo, A., ... Pozueta-Romero, J. (2019). Volatile compounds other than CO₂ emitted

735 by different microorganisms promote distinct posttranscriptionally regulated responses in
 736 plants. *Plant Cell and Environment*, 42(5), 1729–1746.

737 García, I., Castellano, J. M., Vioque, B., Solano, R., Gotor, C., & Romero, L. C. (2010).
 738 Mitochondrial β -cyanoalanine synthase is essential for root hair formation in *Arabidopsis*
 739 *thaliana*. *The Plant Cell*, 22(10), 3268–3279.

740 Garnica-Vergara, A., Barrera-Ortiz, S., Muñoz-Parra, E., Raya-González, J., Méndez-Bravo, A.,
 741 Macías-Rodríguez, L., ... López-Bucio, J. (2016). The volatile 6-pentyl-2H-pyran-2-one
 742 from *Trichoderma atroviride* regulates *Arabidopsis thaliana* root morphogenesis via auxin
 743 signaling and *ETHYLENE INSENSITIVE 2* functioning. *New Phytologist*, 209(4), 1496–
 744 1512.

745 Ghaffari, M. R., Shahinnia, F., Usadel, B., Junker, B., Schreiber, F., Sreenivasulu, N., &
 746 Hajirezaei, M. R. (2016). The metabolic signature of biomass formation in barley. *Plant*
 747 *and Cell Physiology*, 57(9), 1943–1960.

748 Gharaei-Fathabad, E., Tajick-Ghanbary, M. A., & Shahrokhi, N. (2014). Antimicrobial
 749 properties of *Penicillium* species isolated from agricultural soils of northern Iran. *Research*
 750 *Journal of Toxins*, 6(1), 1–7.

751 Guerra, D., Crosatti, C., Khoshro, H. H., Mastrangelo, A. M., Mica, E., & Mazzucotelli, E.
 752 (2015). Post-transcriptional and post-translational regulations of drought and heat response
 753 in plants: A spider's web of mechanisms. *Frontiers in Plant Science*, 11(6), doi:
 754 <https://doi.org/10.3389/fpls.2015.00057>

755 Guo, K., Kong, W. W., & Yang, Z. M. (2009). Carbon monoxide promotes root hair
 756 development in tomato. *Plant, Cell and Environment*, 32(8), 1033–1045.

757 Gutiérrez-Luna, F. M., López-Bucio, J., Altamirano-Hernández, J., Valencia-Cantero, E., Reyes
 758 de La Cruz, H., & Macías-Rodríguez, L. (2010). Plant growth-promoting rhizobacteria
 759 modulate root-system architecture in *Arabidopsis thaliana* through volatile organic
 760 compound emission. *Symbiosis*, 51(1), 75–83.

761 Hua, J., & Meyerowitz, E. M. (1998). Ethylene responses are negatively regulated by a receptor
 762 gene family in *Arabidopsis thaliana*. *Cell*, 94(2), 261–271.

763 Jefferson, R. A., Kavanagh, T. A., & Bevan, M. W. (1987). GUS fusions: β -glucuronidase as a
 764 sensitive and versatile gene fusion marker in higher plants. *The EMBO Journal*, 6(13),
 765 3901–3907.

766 Kiba, T., Takebayashi, Y., Kojima, M., & Sakakibara, H. (2019). Sugar-induced de novo
 767 cytokinin biosynthesis contributes to Arabidopsis growth under elevated CO₂. *Scientific*
 768 *Reports*, 23;9(1):77, doi: <https://doi.org/10.1038/s41598-019-44185-4>

769 Kłapeć, T., Cholewa, G., Cholewa, A., Dutkiewicz, J., & Wójcik-Fatla, A. (2018). Fungal
 770 diversity of root vegetables and soil rhizosphere collected from organic and conventional
 771 farms in eastern Poland. *Annals of Agricultural and Environmental Medicine*, 25(2), 374–
 772 381.

773 Lan, P., Li, W., & Schmidt, W. (2012). Complementary proteome and transcriptome profiling in
 774 phosphate-deficient Arabidopsis roots reveals multiple levels of gene regulation.
 775 *Molecular & Cellular Proteomics*, 11(11), 1156–1166.

776 Li, H., Hu, B., & Chu, C. (2017). Nitrogen use efficiency in crops: Lessons from Arabidopsis
 777 and rice. *Journal of Experimental Botany*, 68(10), 2477–2488.

778 Li, N., Wang, W., Bitas, V., Subbarao, K., Liu, X. & Kang, S. (2018) Volatile compounds
 779 emitted by diverse *Verticillium* species enhance plant growth by manipulating auxin
 780 signaling. *Molecular Plant-Microbe Interactions*, 31(10), 1021–1031.

781 Lin, Y., Zhang, W., Qi, F., Cui, W., Xie, Y., & Shen, W. (2014). Hydrogen-rich water regulates
 782 cucumber adventitious root development in a heme oxygenase-1/carbon monoxide-
 783 dependent manner. *Journal of Plant Physiology*, 171(2), 1–8.

784 Liu, J., Moore, S., Chen, C., & Lindsey, K. (2017). Crosstalk complexities between auxin,
 785 cytokinin, and ethylene in Arabidopsis root development: from experiments to systems
 786 modeling, and back again. *Molecular Plant*, 10(12), 1480–1496.

787 Loiret, F. G., Grimm, B., Hajirezaei, M. R., Kleiner, D., & Ortega, E. (2009). Inoculation of
 788 sugarcane with *Pantoea* sp. increases amino acid contents in shoot tissues; serine, alanine,
 789 glutamine and asparagine permit concomitantly ammonium excretion and nitrogenase
 790 activity of the bacterium. *Journal of Plant Physiology*, 166(11), 1152–1161.

791 López-Bucio, J., Campos-Cuevas, J. C., Hernández-Calderón, E., Velásquez-Becerra, C.,
 792 Farías-Rodríguez, R., Macías-Rodríguez, L. I., & Valencia-Cantero, E. (2007). *Bacillus*
 793 *megaterium* rhizobacteria promote growth and alter root-system architecture through an
 794 auxin- and ethylene-independent signaling mechanism in *Arabidopsis thaliana*. *Molecular*
 795 *Plant-Microbe Interactions*, 20(2), 207–212.

796 López-Bucio, J., Cruz-Ramírez, A., & Herrera-Estrella, L. (2003). The role of nutrient
 797 availability in regulating root architecture. *Current Opinion in Plant Biology*, 6(3), 280–
 798 287.

799 Luschnig, C., Gaxiola, R. A., Grisafi, P., & Fink, G. R. (1998). EIR1, a root-specific protein
 800 involved in auxin transport, is required for gravitropism in *Arabidopsis thaliana*. *Genes*
 801 *and Development*, 12(14), 2175–2187.

802 Ma, F., Wang, L., Li, J., Samma, M. K., Xie, Y., Wang, R., ... Shen, W. (2014). Interaction
 803 between HY1 and H₂O₂ in auxin-induced lateral root formation in *Arabidopsis*. *Plant*
 804 *Molecular Biology*, 85((1-2)), 49–61.

805 Malamy, J. E. (2005) Intrinsic and environmental responses pathways that regulate root system
 806 architecture. *Plant, Cell and Environment*, 28, 66–77.

807 Mangano, S., Denita-Juarez, S. P., Choi, H.-S., Marzol, E., Hwang, Y., Ranocha, P., ... Estevez,
 808 J. M. (2017). Molecular link between auxin and ROS-mediated polar growth. *Proceedings*
 809 *of the National Academy of Sciences*, 114(20), 5289–5294.

810 Martínez-Medina, A., Van Wees, S. C. M., & Pieterse, C. M. J. (2017). Airborne signals from
 811 *Trichoderma fungi* stimulate iron uptake responses in roots resulting in priming of
 812 jasmonic aciddependent defences in shoots of *Arabidopsis thaliana* and *Solanum*
 813 *lycopersicum*. *Plant Cell and Environment*, 40(11), 2691–2705.

814 Mei, Y., Chen, H., Shen, W., Shen, W., & Huang, L. (2017). Hydrogen peroxide is involved in
 815 hydrogen sulfide-induced lateral root formation in tomato seedlings. *BMC Plant Biology*,
 816 17(1), 1–12.

817 Moisan, K., Cordovez, V., van de Zande, E. M., Raaijmakers, J. M., Dicke, M., & Lucas-
 818 Barbosa, D. (2019). Volatiles of pathogenic and non-pathogenic soil-borne fungi affect

819 plant development and resistance to insects. *Oecologia*, 190(3), 589–604.

820 Molina-Favero, C., Creus, C. M., Simontacchi, M., Puntarulo, S., & Lamattina, L. (2008).
821 Aerobic nitric oxide production by *Azospirillum brasilense* Sp245 and its influence on root
822 architecture in tomato. *Molecular Plant-Microbe Interactions*, 21(7), 1001–1009.

823 Nandi, R., & Sengupta, S. (1998). Microbial production of hydrogen: an overview. *Critical*
824 *Reviews in Microbiology*, 24(1), 61–84.

825 Nascimento, F. X., Rossi, M. J., & Glick, B. R. (2018). Ethylene and 1-aminocyclopropane-1-
826 carboxylate (ACC) in plant–bacterial interactions. *Frontiers in Plant Science*. doi:
827 <https://www.frontiersin.org/article/10.3389/fpls.2018.00114>.

828 Nemhauser, J. L., Hong, F., & Chory, J. (2006). Different plant hormones regulate similar
829 processes through largely nonoverlapping transcriptional responses. *Cell*. doi:
830 <https://www.frontiersin.org/article/10.3389/fpls.2018.00114>.

831 Nguyen, H. M., Sako, K., Matsui, A., Suzuki, Y., Mostofa, M. G., Ha, C. Van, ... Seki, M.
832 (2017). Ethanol enhances high-salinity stress tolerance by detoxifying reactive oxygen
833 species in *Arabidopsis thaliana* and rice. *Frontiers in Plant Science*. doi:
834 <https://www.frontiersin.org/article/10.3389/fpls.2017.01001>.

835 Novák, O., Hauserová, E., Amakorová, P., Doležal, K., & Strnad, M. (2008). Cytokinin
836 profiling in plant tissues using ultra-performance liquid chromatography-electrospray
837 tandem mass spectrometry. *Phytochemistry*, 69(11), 2214–2224.

838 O’Leary, B., Preston, G. M., & Sweetlove, L. J. (2014). Increased β -cyanoalanine nitrilase
839 activity improves cyanide tolerance and assimilation in *Arabidopsis*. *Molecular Plant*,
840 7(1), 231–243.

841 Passardi, F., Tognolli, M., De Meyer, M., Penel, C., & Dunand, C. (2006). Two cell wall
842 associated peroxidases from *Arabidopsis* influence root elongation. *Planta*, 223(5), 965–
843 974.

844 Péret, B., Li, G., Zhao, J., Band, L. R., Voß, U., Postaire, O., ... Bennett, M. J. (2012). Auxin
845 regulates aquaporin function to facilitate lateral root emergence. *Nature Cell Biology*,
846 14(10), 991–998.

847 Piotrowski, M., Schönfelder, S., & Weiler, E. W. (2001). The *Arabidopsis thaliana* isogene
848 *NIT4* and its orthologs in tobacco encode β -cyano-L-alanine hydratase/nitrilase. *Journal of*
849 *Biological Chemistry*, 276(4), 2616–2621.

850 Pitts, R. J., Cernac, A., & Estelle, M. (1998). Auxin and ethylene promote root hair elongation
851 in *Arabidopsis*. *The Plant Journal*, 16(5), 553–560.

852 Reinhardt, H., Hachez, C., Bienert, M. D., Beebo, A., Swarup, K., Voß, U., ... Chaumont, F.
853 (2016). Tonoplast aquaporins facilitate lateral root emergence. *Plant Physiology*, 170(3),
854 1640–1654.

855 Riefler, M., Novak, O., Strnad, M., & Schmu, T. (2006). *Arabidopsis* cytokinin receptor
856 mutants reveal functions in shoot growth, leaf senescence, seed size, germination, root
857 development, and cytokinin metabolism. *Plant Cell*, 18(1), 40–54.

858 Rodrigues, O., Reshetnyak, G., Grondin, A., Saijo, Y., Leonhardt, N., Maurel, C., & Verdoucq,
859 L. (2017). Aquaporins facilitate hydrogen peroxide entry into guard cells to mediate ABA-
860 and pathogen-triggered stomatal closure. *Proceedings of the National Academy of*
861 *Sciences*, 114(34), 9200–9205.

862 Rogers, E. E., Eide, D. J., & Guerinot, M. Lou. (2000). Altered selectivity in an *Arabidopsis*
863 metal transporter. *Proceedings of the National Academy of Sciences*, 97(22), 12356–
864 12360.

865 Růžička, K., Ljung, K., Vanneste, S., Podhorská, R., Beeckman, T., Friml, J., & Benková, E.
866 (2007). Ethylene regulates root growth through effects on auxin biosynthesis and
867 transport-dependent auxin distribution. *Plant Cell*, 19(7), 2197–2212.

868 Ryu, C.-M., Farag, M. A., Hu, C.-H., Reddy, M. S., Wei, H.-X., Pare, P. W., & Kloepper, J. W.
869 (2003). Bacterial volatiles promote growth in *Arabidopsis*. *Proceedings of the National*
870 *Academy of Sciences*, 100(8), 4927–4932.

871 Saini, S., Sharma, I., Kaur, N., & Pati, P. K. (2013). Auxin: a master regulator in plant root
872 development. *Plant Cell Reports*, 32(6), 741–757.

873 Sánchez-López, Á. M., Bahaji, A., De Diego, N., Baslam, M., Li, J., Muñoz, F. J., ... Pozueta-

874 Romero, J. (2016). *Arabidopsis* responds to *Alternaria alternata* volatiles by triggering
875 plastid phosphoglucose isomerase-independent mechanisms. *Plant Physiology*, 172(3),
876 1989–2001.

877 Sánchez-López, Á. M., Baslam, M., De Diego, N., Muñoz, F. J., Bahaji, A., Almagro, G., ...
878 Pozueta-Romero, J. (2016). Volatile compounds emitted by diverse phytopathogenic
879 microorganisms promote plant growth and flowering through cytokinin action. *Plant Cell*
880 *and Environment*, 39(12), 2592–2608.

881 Séguéla, M., Briat, J.-F., Vert, G., & Curie, C. (2008). Cytokinins negatively regulate the root
882 iron uptake machinery in *Arabidopsis* through a growth-dependent pathway. *The Plant*
883 *Journal*, 55(2), 289–300.

884 Sergeeva, L. I., Keurentjes, J. J. B., Bentsink, L., Vonk, J., van der Plas, L. H. W., Koornneef,
885 M., & Vreugdenhil, D. (2006). Vacuolar invertase regulates elongation of *Arabidopsis*
886 *thaliana* roots as revealed by QTL and mutant analysis. *Proceedings of the National*
887 *Academy of Sciences of the United States of America*, 103(8), 2994–2999.

888 Shatalin, K., Shatalina, E., Mironov, A., & Nudler, E. (2011). H₂S: a universal defense against
889 antibiotics in bacteria. *Science*, 334(6058), 986–990.

890 Splivallo, R., Fischer, U., Göbel, C., Feussner, I., & Karlovsky, P. (2009). Truffles regulate
891 plant root morphogenesis via the production of auxin and ethylene. *Plant Physiology*,
892 150(4), 2018–2029.

893 Stepanova, A. N., Hoyt, J. M., Hamilton, A. A., & Alonso, J. M. (2005). A link between
894 ethylene and auxin uncovered by the characterization of two root-specific ethylene-
895 insensitive mutants in *Arabidopsis*. *The Plant Cell*, 17(8), 2230–2242.

896 Swarup, R., Perry, P., Hagenbeek, D., Van Der Straeten, D., Beemster, G. T. S., Sandberg, G.,
897 ... Bennett, M. J. (2007) Ethylene upregulates auxin biosynthesis in *Arabidopsis* seedlings
898 to enhance inhibition of root cell elongation. *The Plant Cell*, 19(7), 2186–2196.

899 Takahashi, M., Furuhashi, T., Ishikawa, N., Horiguchi, G., Sakamoto, A., Tsukaya, H., &
900 Morikawa, H. (2014). Nitrogen dioxide regulates organ growth by controlling cell
901 proliferation and enlargement in *Arabidopsis*. *New Phytologist*, 201(4), 1304–1315.

902 Thimm, O., Bläsing, O., Gibon, Y., Nagel, A., Meyer, S., Krüger, P., ... Stitt, M. (2004).
 903 MAPMAN: A user-driven tool to display genomics data sets onto diagrams of metabolic
 904 pathways and other biological processes. *Plant Journal*, 37(6), 914–939.

905 Tsukagoshi, H., Busch, W., & Benfey, P. N. (2010). Transcriptional regulation of ROS controls
 906 transition from proliferation to differentiation in the root. *Cell*, 143(4), 606–616.

907 Ulmasov, T., Murfett, J., Hagen, G., & Guilfoyle, T. J. (1997). Aux/IAA proteins repress
 908 expression of reporter genes containing natural and highly active synthetic auxin response
 909 elements. *The Plant Cell*, 9(11), 1963–1971.

910 van Dam, N. M., & Bouwmeester, H. J. (2016). Metabolomics in the rhizosphere: tapping into
 911 belowground chemical communication. *Trends in Plant Science*, 21(3):256-265.

912 van der Weele, C. M., Spollen, W. G., Sharp, R. E., & Baskin, T. I. (2000). Growth of
 913 *Arabidopsis thaliana* seedlings under water deficit studied by control of water potential in
 914 nutrient-agar media. *Journal of Experimental Botany*, 51(350), 1555–1562.

915 Varotto, C., Maiwald, D., Pesaresi, P., Jahns, P., Salamini, F., & Leister, D. (2002). The metal
 916 ion transporter IRT1 is necessary for iron homeostasis and efficient photosynthesis in
 917 *Arabidopsis thaliana*. *The Plant Journal*, 31(5), 589–599.

918 Vert, G. A., Briat, J. F., & Curie, C. (2003). Dual regulation of the Arabidopsis high-affinity
 919 root iron uptake system by local and long-distance signals. *Plant Physiology*, 132(2), 796–
 920 804.

921 Voisard, C., Keel, C., Haas, D., & Dèfago, G. (1989). Cyanide production by *Pseudomonas*
 922 *fluorescens* helps suppress black root rot of tobacco under gnotobiotic conditions. *The*
 923 *EMBO Journal*, 8(2), 351–358.

924 von Caemmerer, S., & Farquhar, G. D. (1981). Some relationships between the biochemistry of
 925 photosynthesis and the gas exchange of leaves. *Planta*, 153(4), 376–387.

926 Yang, D.-L., Shi, Z., Bao, Y., Yan, J., Yang, Z., Yu, H., ... Hua, J. (2017). Calcium pumps and
 927 interacting BON1 protein modulate calcium signature, stomatal closure, and plant
 928 immunity. *Plant Physiology*, 175(1), 424–437.

929 Zamioudis, C., Korteland, J., Van Pelt, J. A., Van Hamersveld, M., Dombrowski, N., Bai, Y., ...

Pieterse, C. M. J. (2015). Rhizobacterial volatiles and photosynthesis-related signals coordinate MYB72 expression in Arabidopsis roots during onset of induced systemic resistance and iron-deficiency responses. *Plant Journal*, 84(2), 309–322.

Žd'árská, M., Zatloukalová, P., Benítez, M., Šedo, O., Potěšil, D., Novák, O., ... Hejátko, J. (2013). Proteome analysis in Arabidopsis reveals shoot- and root-specific targets of cytokinin action and differential regulation of hormonal homeostasis. *Plant Physiology*, 161(2), 918–930.

Zhang, H., Kim, M.-S., Krishnamachari, V., Payton, P., Sun, Y., Grimson, M., ... Paré, P. W. (2007). Rhizobacterial volatile emissions regulate auxin homeostasis and cell expansion in Arabidopsis. *Planta*, 226(4), 839–851.

Zhang, H., Murzello, C., Sun, Y., Kim, M. S., Xie, X., Jeter, R. M., ... Paré, P. W. (2010). Choline and osmotic-stress tolerance induced in Arabidopsis by the soil microbe *Bacillus subtilis* (GB03). *Molecular Plant-Microbe Interactions*, 23(8), 1097–1104.

Zhang, H., Sun, Y., Xie, X., Kim, M. S., Dowd, S. E., & Paré, P. W. (2009). A soil bacterium regulates plant acquisition of iron via deficiency-inducible mechanisms. *Plant Journal*, 58(4), 568–577.

Zhang, H., Xie, X., Kim, M. S., Kornyejev, D. A., Holaday, S., & Paré, P. W. (2008). Soil bacteria augment Arabidopsis photosynthesis by decreasing glucose sensing and abscisic acid levels in planta. *Plant Journal*, 56(2), 264–273.

Zhu, Y., Liao, W., Wang, M., Niu, L., Xu, Q., & Jin, X. (2016). Nitric oxide is required for hydrogen gas-induced adventitious root formation in cucumber. *Journal of Plant Physiology*, 195, 50–58.

FIGURE LEGENDS

Figure 1. Functional categorization of proteins differentially expressed by VCs emitted by *P. aurantiogriseum* in roots. Proteins that were significantly down- or up-regulated following VC exposure were sorted according to the putative functional categories assigned by MapMan software. The numbers of up- and down-regulated proteins in each categorical group are indicated by gray and black bars, respectively. Proteins discussed here are boxed. Plants were cultured in the absence or continuous presence of fungal VCs for 3 days.

Figure 2. Relative abundance of transcripts encoding proteins differentially expressed by fungal VCs in roots. Fold change values are differences in levels of transcripts (measured by quantitative RT-PCR) in roots of plants cultured in the presence of VCs relative to those of roots of plants cultured in the absence of VCs. Gray dashed lines indicate the threshold of $\log_2$ -fold change = 1 (2-fold change) to consider genes as significantly regulated by fungal VCs. Values are means $\pm$ SE for three biological replicates. White and black bars correspond to genes encoding proteins that are down- and up-regulated by fungal VCs, respectively. Plants were cultured in the absence or continuous presence of fungal VCs for 3 days.

Figure 3. *P. aurantiogriseum* VCs enhance photosynthetic water use efficiency. Curves of (a) A_n , (b) g_s and (c) WUE_i versus intercellular CO_2 concentration (C_i) in leaves of plants cultured in the absence or continuous presence of adjacent cultures of *P. aurantiogriseum* covered with charcoal filters for 3 days. Treatment with VCs began 28 days after seeds were sown. Values are means $\pm$ SE for four plants.

Figure 4. Fungal VCs enhance plant tolerance to drought. (a) External phenotypes and (b) rosette FW of plants cultured in MS with or without supplementation with PEG 6000 in the absence or continuous presence for one week of VCs emitted by adjacent *P. aurantiogriseum* cultures covered with charcoal filters. Values in panel (b) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Asterisks (*)

indicate significant differences, according to Student's t-test ($P < 0.05$), between VC-treated and non-treated plants.

Figure 5. Fungal VCs enhance CK and auxin/ethylene signaling in roots. GUS staining in roots of plants harboring (a) the CK-inducible *ARR5::GUS* reporter and (b) the auxin-inducible *DR5::GUS* reporter, cultured in the absence or presence of adjacent cultures of *P. aurantiogriseum* covered with charcoal filters for one week. The experiment was repeated three times (each a pool of 5 plants) with similar results. Scale bars: left panels: 5 mm. Right panels: 1 mm.

Figure 6. Fungal VCs enhance ethylene production in roots. The graph represents the time-course of ethylene accumulation in sealed vials containing roots of WT plants that had previously been cultured in the absence or presence for 3 days of adjacent cultures of *P. aurantiogriseum*. Values are means $\pm$ SE for three biological replicates obtained from three independent experiments.

Figure 7. Changes in RSA promoted by fungal VCs involve enhanced auxin and ethylene signaling. (a) External phenotypes, (b) root FW and (c) root architecture parameters of WT, *aux1-T*, *eir1* and *etr1-3* plants cultured in the absence or continuous presence for one week of VCs emitted by adjacent *P. aurantiogriseum* cultures. Values in panels (b) and (c) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters "a", "b" and "c" indicate significant differences, according to Student's t-test ($P < 0.05$), between: "a" WT plants and mutants cultured without fungal VC treatment, "b" VC-treated and non-treated plants, and "c" VC-treated WT and mutant plants. RH number and length data were obtained from a pool of 6 first order LR per plant. Scale bars in "A", 2 mm. Plants providing data shown in (a) and (b) were grown on horizontal plates whereas those providing data in (c) were grown on vertical plates.

Figure 8. Fungal VCs promote ROS accumulation in roots. (a) NBT staining of O_2^- and (b) 3,3'-diaminobenzidine staining of H_2O_2 in roots of WT plants cultured in the absence or presence for one week of adjacent cultures of *P. aurantiogriseum* with charcoal filters for one week. The experiment was repeated three times (each a pool of 5 plants) with similar results. Scale bars: left panels, 5 mm. Right panels, 1 mm.

Figure 9. RSA adjustment promoted by fungal VCs is a ROS dependent process. (a) External phenotypes, (b) root FW, (c) root architecture parameters of WT and *rhd2* plants cultured in the absence or continuous presence for one week of VCs emitted by adjacent *P. aurantiogriseum* cultures. Values in panels (b) and (c) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters “a”, “b” and “c” indicate significant differences, according to Student’s t-test ($P < 0.05$), between: “a” WT and *rhd2* plants cultured without fungal VC treatment, “b” VC-treated and non-treated plants, and “c” VC-treated WT and *rhd2* plants. RH number and length data were obtained from a pool of 6 first order LR per plant. Plants providing data shown in (a) and (b) were grown on horizontal plates, whereas those providing data in (c) were grown on vertical plates. Scale bars in (a), 500 μ m.

Figure 10. CAS-C1 is an important mediator of the root response to fungal VCs. (a) External phenotypes, (b) root FW, (c) root architecture parameters of WT and *cas-c1* plants cultured in the absence or continuous presence of VCs emitted by adjacent *P. aurantiogriseum* cultures for one week. Values in panels (b) and (c) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters “a”, “b” and “c” indicate significant differences, according to Student’s t-test ($P < 0.05$), between: “a” WT and *cas-c1* plants cultured without fungal VC treatment, “b” VC-treated and non-treated plants, and “c” VC-treated WT and *cas-c1* plants. RH number and length data were obtained from a pool of 6 first order LR per plant. Plants providing data shown in (a) and (b) were grown on horizontal plates, whereas those providing data in (c) were grown on vertical plates. Scale bars in (a), 500 μ m.

Figure 11. Suggested model for regulation of root proteomic and metabolic responses to fungal VCs. Mixtures of VOC-depleted fungal VCs (VICs and/or VOCs with molecular masses of less than 45 Da) and signals (presumably sugars) of enhanced photosynthesis promoted by fungal VCs from the aerial parts of the plant up-regulate the expression of ACLA-1, which regulates the metabolic flux from mitochondrially synthesized citrate to MVA-derived isoprenoids such as CKs. The resulting enhanced CK content down-regulates the expression of IRT1, thus restricting the uptake and subsequent transport of Fe to the aerial part of the plant. CKs up-regulate the expression of enzymes involved in the conversion of cytosolic Met to ethylene and HCN (METK2, METK and ACO2) the latter being converted to Asp, Glu and the long-distance nitrogen transport amino acids Asn and Gln by means of the ethylene-induced CAS-C1, ASP2 and GLN1-2. Fungal VCs down-regulate the expression of aquaporins through enhanced auxin signaling action, thus reducing H₂O and H₂O₂ uptake by root cells. Fungal VCs also down-regulate the expression of apoplastic peroxidases (e.g. PER3, PER32 and PER34) and the ACA8 calcium pump. Activation of plasma membrane NADPH oxidases by the resulting high cytoplasmic calcium concentrations, and down-regulation of aquaporins and apoplastic peroxidases leads to apoplastic oxidative burst due to the accumulation H₂O₂ and O₂⁻, which promotes root and RH growth and elongation. Fungal VCs down-regulate the expression of vacuolar invertases (e.g. BFRUCT 3 and 4), thus limiting glucose and fructose production from sucrose. This, and the reduction of water uptake due to down-regulation of aquaporin expression, leads to a reduction in turgor as a driving force for root elongation. Genes, metabolic pathways, enzymatic activities and metabolites that are up-regulated by fungal VCs are highlighted in red, whereas those that are down-regulated by VCs are highlighted in green. Multistep enzymatic reactions and signaling cascades are depicted with dashed arrows. DMAPP: dimethylallyl diphosphate.

SUPPORTING INFORMATION

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

Figure S1. VCs emitted by *P. aurantiogriseum* augment the levels of CKs in roots. Scheme representing pathways of CK biosynthesis through the plastidic MEP and cytosolic MVA pathways is shown. Metabolites whose levels are higher in roots exposed to fungal VCs than in controls are highlighted in red, and metabolites whose levels are lower in roots exposed to fungal VCs than in controls are highlighted in green. Data from Table 1. Multistep reactions are depicted with dashed arrows.

Figure S2. (a) external phenotypes, (b) root FW and (c) root architecture parameters of WT, *ahk2/3*, *ahk2/4* and *ahk3/4* plants cultured in the absence or continuous presence of VCs emitted by adjacent *P. aurantiogriseum* cultures for one week. Values in panels (b) and (c) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters “a”, “b” and “c” indicate significant differences, according to Student’s t-test ($P < 0.05$), between: “a” WT plants and mutants cultured without fungal VC treatment, “b” VC-treated and non-treated plants, and “c” VC-treated WT and mutant plants. RH number and length data were obtained from a pool of 6 first order LR per plant. Plants providing data shown in (a) and (b) were grown on horizontal plates, whereas those providing data in (c) were grown on vertical plates. Scale bars in (a), 2 mm.

Figure S3. Fungal VCs promote superoxide anion (O_2^-) accumulation in WT RHs but not in *rhd2* and *cas-cl* RHs. NBT staining of O_2^- in RHs of WT, *rhd2* and *cas-cl* plants cultured in the absence or presence for one week of adjacent cultures of *P. aurantiogriseum* with charcoal filters for one week. Red arrowheads indicate diformazan precipitates formed by NBT reduction by O_2^- . Scale bars 200 μ m.

Figure S4. DPI treatment inhibits the fungal VC-promoted elongation of RHs. (a) Photographs of roots and (b) RH lengths of WT plants cultured in the absence or continuous presence for one week of VCs emitted by adjacent *P. aurantiogriseum* cultures for one week, with or without

DPI supplementation. Values in panel (b) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letter “b” and “c” indicate significant differences, according to Student’s t-test ($P < 0.05$), between: “b” VC-treated and non-treated plants, and “c” VC-treated plants without DPI treatment and VC-treated plants with DPI treatment. RH length data were obtained from a pool of 6 first order LRs per plant. Plants were grown on vertical plates. Scale bars in (a), 500 μm .

1102 **Table 1.** CK content (pmol g⁻¹ DW) in roots of plants cultured in solid MS medium in the absence or presence of adjacent cultures of *P. aurantiogriseum*
1103 covered with charcoal filters for 3 days. Values represent the mean $\pm$ SE of determinations in 3 independent experiments. Asterisks indicate significant
1104 differences, according to Student's t-test (P<0.05), between VC-treated and non-treated plants. iPRMP, *N*⁶-isopentenyladenosine-5'-monophosphate; tZRMP,
1105 *tZ*-riboside-5'-monophosphate; iPR, *N*⁶-isopentenyladenosine; tZR, *tZ*-riboside; DHZR, dihydrozeatin-riboside; iP, isopentenyladenine; tZ, *trans*-zeatin; DZ,
1106 dihydrozeatin; iP7G, *N*⁶-isopentenyladenosine-7-glucoside; iP9G, *N*⁶-isopentenyladenosine-9-glucoside; tZROG, *trans*-zeatin-O-glucoside riboside; tZ7G,
1107 *trans*-zeatin-7-glucoside; DHZ7G, dihydrozeatin-7-glucoside; tZ9G, *trans*-zeatin-9-glucoside; DHZ9G, dihydrozeatin-9-glucoside

		MEP pathway (plastid) derived CKs			MVA pathway (cytosol) derived CKs	
		-VCs	+VCs		-VCs	+VCs
Precursors	iPRMP	41.5 $\pm$ 4.8	243 $\pm$ 34*			
	tZRMP	83.1 $\pm$ 8.3	252 $\pm$ 64*	cZRMP	88.7 $\pm$ 7.3	145.9 $\pm$ 8.5*
	DHZMP	0.49 $\pm$ 0.09	0.65 $\pm$ 0.17			
	Σ (%)	125	621		88.7	145.9
Transport forms	iPR	11.6 $\pm$ 0.4	51.3 $\pm$ 6.6*			
	tZR	31.7 $\pm$ 5.3	68.9 $\pm$ 15.2*	cZR	47.2 $\pm$ 1.3	57.3 $\pm$ 1.7*
	DHZR	3.55 $\pm$ 0.16	3.39 $\pm$ 0.19			
	Σ (%)	46.9	123.6		47.2	57.3
Active forms	iP	34.9 $\pm$ 1.9	76.9 $\pm$ 10.0*			
	tZ	69.5 $\pm$ 6.6	53.3 $\pm$ 9.1	cZ	26.0 $\pm$ 1.3	53.2 $\pm$ 1.5*
	DZ	0.76 $\pm$ 0.13	0.77 $\pm$ 0.16			
	Σ (%)	105	131		26.0	53.2
	iP7G	128 $\pm$ 5	138 $\pm$ 3			
	tZ7G	238 $\pm$ 15	88.9 $\pm$ 3.5*			
	DHZ7G	33.9 $\pm$ 1.9	11.7 $\pm$ 0.2*			

Glycosylated (inactive) forms	iP9G	31.4 ± 0.9	$46.5 \pm 1.2^*$	cZ9G	60.9 ± 2.6	52.8 ± 4.2
	tZ9G	373 ± 20	$172 \pm 13^*$			
	DHZ9G	24.8 ± 2.5	$10.9 \pm 1.0^*$			
	tZROG	6.89 ± 0.34	5.91 ± 0.27	cZROG	42.7 ± 2.6	$21.2 \pm 0.8^*$
	Σ (%)	837	473		103	74.1
TOTAL	Σ (%)	1,114	1,350		265	330

Figure 1

Figure 2

Figure 3

Figure 4

a

-VCs

+VCs

b

-VCs

+VCs

Figure 5

Figure 6

Figure 7

a

-VCs

+VCs

b

-VCs

+VCs

Figure 8

Figure 9

Figure 10

Figure S2: (a) external phenotypes, (b) root FW and (c) root architecture parameters of WT, *ahk2/3*, *ahk2/4* and *ahk3/4* plants cultured in the absence or continuous presence of VCs emitted by adjacent *P. aurantiogriseum* cultures for one week. Values in panels (b) and (c) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters “a”, “b” and “c” indicate significant differences, according to Student’s t-test ($P < 0.05$), between: “a” WT plants and mutants cultured without fungal VC treatment, “b” VC-treated and non-treated plants, and “c” VC-treated WT and mutant plants. RH number and length data were obtained from a pool of 6 first order LRs per plant. Plants providing data shown in (a) and (b) were grown on horizontal plates, whereas those providing data in (c) were grown on vertical plates. Scale bars in (a), 2 mm.

Figure S3: Fungal VCs promote superoxide anion (O_2^-) accumulation in WT RHs but not in *rhd2* and *cas-c1* RHs. NBT staining of O_2^- in RHs of WT, *rhd2* and *cas-c1* plants cultured in the absence or presence for one week of adjacent cultures of *P. aurantiogriseum* with charcoal filters for one week. Red arrowheads indicate diformazan precipitates formed by NBT reduction by O_2^- . Scale bars 200 μ m.

Figure S4: DPI treatment inhibits the fungal VC-promoted elongation of RHs. (a) Photographs of roots and (b) RH lengths of WT plants cultured in the absence or continuous presence for one week of VCs emitted by adjacent *P. aurantiogriseum* cultures for one week, with or without DPI supplementation. Values in panel (b) are means $\pm$ SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letter “b” and “c” indicate significant differences, according to Student’s t-test ($P < 0.05$), between: “b” VC-treated and non-treated plants, and “c” VC-treated plants without DPI treatment and VC-treated plants with DPI treatment. RH length data were obtained from a pool of 6 first order LR per plant. Plants were grown on vertical plates. Scale bars in (a), 500 μ m.

Supplemental Table S1. Primers used in qRT-PCR

Gene		Sequence
EF-1 alfa	Forward	TTCGTCTCCCACTTCAGGAT
At1g07940	Reverse	GGAGCAAAGGTCACAACCAT
ACO2	Forward	GAAGTCGAAGATGTCGATTGG
At1g62380	Reverse	ATGGCCGTCCTGTATTCATC
AHB1	Forward	GCAAGAAGCTTTGGTGAAGG
At2g16060	Reverse	CCTTTTGCTGCTGGTGCTAT
ASP2	Forward	TAAATGGGAACCGACAAAGG
At5g19550	Reverse	CACAGCTGCTTTAGGCAACA
BFRUCT4	Forward	TAAAGGTCTCCTCGCCGTCT
At1g12240	Reverse	TGTTTCATCGATCCCTTCGT
BGLU21	Forward	TGACAACAGCGGTTGATGAT
At1g66270	Reverse	ACCTGAAACGCAGCAGTAGC
CAS-C1	Forward	GGGAATCAGTTTGGCTTTCA
At3g61440	Reverse	GCACCAAAGGATCTCATCGT
GLN1-2	Forward	TGAGAAGCAAAGCCAGGACT
At1g66200	Reverse	TCTTGACCAGGAGCTTGACC
GPT2	Forward	TTAGACCAGATTTGCGCGTTA
At1g61800	Reverse	GTTGAATCGGGGTATGGAAA
IRT1	Forward	GAACCGGTTTTATGCACGTT
At4g19690	Reverse	TAGCGAGAAATCCGGAGAAA
METK2	Forward	TGCTGACAAATGCAAAGTCC
At4g01850	Reverse	GGTCACCAGCTCCAATGTCT
METK3	Forward	ATCCACTTGCAGGGAGATTG
At2g36880	Reverse	AATGTCAGGGCTCTGTTGCT
PER34	Forward	ATCTTTGTCCGCTGCTCAAC
At3g49120	Reverse	ACGAGGGTCCGACCTTAAC

PHT1-1	Forward	TGGAACCCTTTCTGGTCAAC
At5g43350	Reverse	CAGAAGCGACAGAGCACAAG
PIP1-2	Forward	GGAACTTCGGCTCAGAGTGA
At2g45960	Reverse	CAATCCCAGCTCTCCAGAAG
PIP2-3	Forward	GACCTGATGGATTTTCAGACGA
At2g37180	Reverse	CGGCGATGACTGCTCTGTAT
TIP2-2	Forward	CTCTTGCTTTTGCCAAGCTC
At4g17340	Reverse	TGGAAACACCAACGAAAAGG
UGP2	Forward	TCACAAATAACAATCCTCTCTTCG
At5g17310	Reverse	TTGAGGGAGATTCTCAGTGG
UXS4	Forward	CGATCCGTTACATGCTCAGA
At2g47650	Reverse	GGTGGTTGGATGATTTGGAG

Supplemental Table S2: list of proteins differentially expressed by VCs of *P. aurantiigriseum* in Arabidopsis roots. DEPs are classified according to their functions. DEPs that are discussed in the main text are highlighted in yellow.

Accession number	Protein ID	Fold change (log2)	qValue (FDR)	Subcellular location	Description
Amino acid metabolism					
AT3G04520	Q9FPH3	1,497	0,019	Cytosol	Q9FPH3 THA2_ARATH Probable low-specificity L-threonine aldolase 2 OS=Arabidopsis thaliana GN=THA2 PE=1 SV=1
AT1G66200	Q8LCE1	0,968	0,011	Cytosol	Q8LCE1 GLN1-2_ARATH Glutamine synthetase cytosolic isozyme 1-2 OS=Arabidopsis thaliana GN=GLN1-2 PE=1 SV=2
AT5G53460	Q9LV03	0,626	0,014	Plastid	Q9LV03 GLUT1_ARATH Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana GN=GLUT1 PE=1 SV=2
AT3G61440	Q9S757	0,52	0,025	Mitochondrion	Q9S757 CAS-C1_ARATH Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial OS=Arabidopsis thaliana GN=CAS-C1 PE=1 SV=1
AT5G19550	P46645	0,419	0,05	Cytosol	P46645 AAT2_ARATH Aspartate aminotransferase, cytoplasmic isozyme 1 OS=Arabidopsis thaliana GN=ASP2 PE=1 SV=2
AT2G43910	Q0WP12	-0,558	0,015	Cytosol	Q0WP12-2 HOL1_ARATH Isoform 2 of Thiocyanate methyltransferase 1 OS=Arabidopsis thaliana GN=HOL1
AT1G23310	Q9LR30	-0,873	0,013	Peroxisome	Q9LR30 GGT1_ARATH Glutamate--glyoxylate aminotransferase 1 OS=Arabidopsis thaliana GN=GGAT1 PE=1 SV=1
AT3G45300	Q9SWG0	-0,942	0,002	Mitochondrion	Q9SWG0 IVD_ARATH Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2
AT4G29840	Q9S7B5	-2,352	0,013	Plastid	Q9S7B5 THRC1_ARATH Threonine synthase 1, chloroplastic OS=Arabidopsis thaliana GN=TS1 PE=1 SV=1
Biodegradation of xenobiotics					
AT1G53580	Q9C8L4	-0,633	0,02	Mitochondrion	Q9C8L4 ETHE1_ARATH Persulfide dioxygenase ETHE1 homolog, mitochondrial OS=Arabidopsis thaliana GN=GLY3 PE=1 SV=3
Cell					
AT5G39510	Q9SEL6	1,218	0,048	ER, Golgi	Q9SEL6 VTI11_ARATH Vesicle transport v-SNARE 11 OS=Arabidopsis thaliana GN=VTI11 PE=1 SV=2
AT1G52360	Q9C827	0,843	0,024	Golgi	Q9C827 COB22_ARATH Coatomer subunit beta'-2 OS=Arabidopsis thaliana GN=At1g52360 PE=1 SV=1
AT4G34870	Q42406	0,609	0,005	Golgi	Q42406 CP18D_ARATH Peptidyl-prolyl cis-trans isomerase CYP18-4 OS=Arabidopsis thaliana GN=CYP18-4 PE=1 SV=1
AT1G35720	Q9SYT0	0,502	0,008	Apoplast	Q9SYT0 ANXD1_ARATH Annexin D1 OS=Arabidopsis thaliana GN=ANN1 PE=1 SV=1
Cell Wall					
AT4G25820	Q9ZSU4	1,857	0,044	Extracellular	Q9ZSU4 XTH14_ARATH Xyloglucan endotransglucosylase/hydrolase protein 14 OS=Arabidopsis thaliana GN=XTH14 PE=1 SV=1
AT5G44130	Q9FFH6	0,941	0,045	Plasma membrane	Q9FFH6 FLA13_ARATH Fasciclin-like arabinogalactan protein 13 OS=Arabidopsis thaliana GN=FLA13 PE=1 SV=1
AT2G47650	Q8S8T4	0,711	0,003	Golgi	Q8S8T4 UXS4_ARATH UDP-glucuronic acid decarboxylase 4 OS=Arabidopsis thaliana GN=UXS4 PE=2 SV=1
AT5G39320	Q9FM01	0,705	0,004	Cytosol	Q9FM01 UGDH4_ARATH UDP-glucose 6-dehydrogenase 4 OS=Arabidopsis thaliana GN=UGD4 PE=1 SV=1
AT3G03250	Q9M9P3	0,414	0,05	Cytosol	Q9M9P3 UGPA2_ARATH UTP--glucose-1-phosphate uridylyltransferase 2 OS=Arabidopsis thaliana GN=UGP2 PE=1 SV=1
AT3G10740	Q9SG80	-0,621	0,022	Apoplast	Q9SG80 ASD1_ARATH Alpha-L-arabinofuranosidase 1 OS=Arabidopsis thaliana GN=ASD1 PE=1 SV=1
AT1G66280	Q9C8Y9	-0,674	0,014	ER	Q9C8Y9 BGL22_ARATH Beta-glucosidase 22 OS=Arabidopsis thaliana GN=BGLU22 PE=1 SV=1
AT5G06860	Q9M5J9	-0,744	0,005	Golgi, cell wall	Q9M5J9 PGIP1_ARATH Polygalacturonase inhibitor 1 OS=Arabidopsis thaliana GN=PGIP1 PE=1 SV=1
AT3G09260	Q9SR37	-0,857	0,006	ER	Q9SR37 BGL23_ARATH Beta-glucosidase 23 OS=Arabidopsis thaliana GN=BGLU23 PE=1 SV=1
AT5G58090	Q93Z08	-0,934	0,034	Plasma membrane	Q93Z08 E136_ARATH Glucan endo-1,3-beta-glucosidase 6 OS=Arabidopsis thaliana GN=At5g58090 PE=1 SV=2
AT1G66270	Q9C525	-1,312	0,013	ER	Q9C525 BGL21_ARATH Beta-glucosidase 21 OS=Arabidopsis thaliana GN=BGLU21 PE=1 SV=1
AT5G04970	Q9FF77	-1,689	0,005	Cell wall	Q9FF77 PME47_ARATH Probable pectinesterase/pectinesterase inhibitor 47 OS=Arabidopsis thaliana GN=PME47 PE=2 SV=1
AT1G75940	Q84WV2	-1,834	0,005	ER	Q84WV2 BGL20_ARATH Beta-glucosidase 20 OS=Arabidopsis thaliana GN=BGLU20 PE=2 SV=1
Co-factor and vitamine metabolism					
AT3G14990	Q9FPF0	-1,147	0,001	Golgi	Q9FPF0 DJ1A_ARATH Protein DJ-1 homolog A OS=Arabidopsis thaliana GN=DJ1A PE=1 SV=1
AT5G50960	Q8H1Q2	-1,605	0,008	Cytosol	Q8H1Q2 NBP35_ARATH Cytosolic Fe-S cluster assembly factor NBP35 OS=Arabidopsis thaliana GN=NBP35 PE=1 SV=1
Development					
AT3G03340	A0A1I9LRM4	1,555	0,013	Nucleus	A0A1I9LRM4 A0A1I9LRM4_ARATH LUC7 related protein OS=Arabidopsis thaliana GN=UNE6 PE=4 SV=1
AT2G23810	Q8S8Q6	-0,97	0,016	Plasma membrane	Q8S8Q6 TET8_ARATH Tetraspanin-8 OS=Arabidopsis thaliana GN=TET8 PE=2 SV=1
AT4G37070	O23179	-1,076	0,001	Plasma membrane	O23179 PLP1_ARATH Patatin-like protein 1 OS=Arabidopsis thaliana GN=PLP1 PE=1 SV=2
DNA					
AT3G54560	O23628	-0,68	0,014	Nucleus	O23628 H2AV1_ARATH Histone H2A variant 1 OS=Arabidopsis thaliana GN=H2AV PE=1 SV=1
AT3G15950	Q9LSB4	-0,691	0,001	ER	Q9LSB4 NAI2_ARATH TSA1-like protein OS=Arabidopsis thaliana GN=NAI2 PE=1 SV=1
At1g07660	P59259	-0,845	0,001	Nucleus	P59259 H4_ARATH Histone H4 OS=Arabidopsis thaliana GN=At1g07660 PE=1 SV=2
AT1G08880	O04848	-1,149	0,017	Nucleus	O04848 H2AXA_ARATH Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1
AT5G28740	Q9LKU3	-1,356	0,031	Nucleus	Q9LKU3 Q9LKU3_ARATH Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=T32B20.g PE=4 SV=1
Fermentation					
AT1G77120	P06525	1,312	0,001	Cytosol	P06525 ADH1_ARATH Alcohol dehydrogenase class-P OS=Arabidopsis thaliana GN=ADH1 PE=1 SV=2
Glycolysis					
AT2G29560	Q9ZW34	2,122	0,027	Cytosol	Q9ZW34 ENO3_ARATH Cytosolic enolase 3 OS=Arabidopsis thaliana GN=ENO3 PE=1 SV=1
Hormone metabolism					

AT1G62380	Q41931	1,025	0,002	Golgi	Q41931 ACCO2_ARATH 1-aminocyclopropane-1-carboxylate oxidase 2 OS=Arabidopsis thaliana GN=ACO2 PE=1 SV=2
AT4G01850	P17562	0,896	0,014	Cytosol	P17562 METK2_ARATH S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1
AT1G10670	Q9SGY2	0,598	0,05	Cytosol	Q9SGY2 ACLA1_ARATH ATP-citrate synthase alpha chain protein 1 OS=Arabidopsis thaliana GN=ACLA-1 PE=1 SV=1
AT2G36880	Q9SJL8	0,435	0,049	Cytosol	Q9SJL8 METK3_ARATH S-adenosylmethionine synthase 3 OS=Arabidopsis thaliana GN=METK3 PE=1 SV=1
AT3G44320	P46010	-0,776	0,027	Cytosol	P46010 NRL3_ARATH Nitrilase 3 OS=Arabidopsis thaliana GN=NIT3 PE=1 SV=1
AT3G44310	P32961	-1,114	0,003	Cytosol	P32961 NRL1_ARATH Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2
Lipid metabolism					
AT1G65290	O80800	1,298	0,021	Mitochondrion	O80800 ACPM2_ARATH Acyl carrier protein 2, mitochondrial OS=Arabidopsis thaliana GN=MTACP2 PE=1 SV=1
AT2G33150	Q56WD9	-0,539	0,024	Peroxisome	Q56WD9 THIK2_ARATH 3-ketoacyl-CoA thiolase 2, peroxisomal OS=Arabidopsis thaliana GN=PED1 PE=1 SV=2
AT1G45201	A0A1P8AVY3	-0,62	0,023	Golgi	A0A1P8AVY3 A0A1P8AVY3_ARATH Triacylglycerol lipase-like 1 OS=Arabidopsis thaliana GN=TLL1 PE=4 SV=1
AT5G48880	Q570C8	-0,699	0,044	Peroxisome	Q570C8 THIK5_ARATH 3-ketoacyl-CoA thiolase 5, peroxisomal OS=Arabidopsis thaliana GN=KAT5 PE=1 SV=2
AT3G51840	Q96329	-1,185	0,001	Peroxisome	Q96329 ACOX4_ARATH Acyl-coenzyme A oxidase 4, peroxisomal OS=Arabidopsis thaliana GN=ACX4 PE=1 SV=1
AT4G16155	F4JLP5	-2,272	0,018	Plastid	F4JLP5 PLPD2_ARATH Dihydriolipoyl dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=LPD2 PE=2 SV=2
Major CHO metabolism					
AT1G62660	Q43348	-0,577	0,018	Vacuole	Q43348 INVA3_ARATH Acid beta-fructofuranosidase 3, vacuolar OS=Arabidopsis thaliana GN=BFRUCT3 PE=2 SV=1
AT1G12240	Q39041	-0,56	0,016	Vacuole	Q39041 INVA4_ARATH Acid beta-fructofuranosidase 4, vacuolar OS=Arabidopsis thaliana GN=BFRUCT4 PE=1 SV=2
Metal handling.binding					
AT3G56240	A0A1I9LNC0	0,678	0,004	Peroxisome	A0A1I9LNC0 A0A1I9LNC0_ARATH Copper chaperone OS=Arabidopsis thaliana GN=CCH PE=4 SV=1
Miscellaneous enzyme family					
AT4G16260	Q8VZJ2	1,053	0,001	Extracellular	Q8VZJ2 BGNEM_ARATH Probable glucan endo-1,3-beta-glucosidase At4g16260 OS=Arabidopsis thaliana GN=At4g16260 PE=1 SV=1
AT4G13180	Q9SVQ9	-0,578	0,039	Plastid	Q9SVQ9 Q9SVQ9_ARATH At4g13180/F17N18_70 OS=Arabidopsis thaliana GN=At4g13180 PE=1 SV=1
AT3G16420	O04314	-0,702	0,001	Cytosol	O04314 JAL30_ARATH PYK10-binding protein 1 OS=Arabidopsis thaliana GN=PBP1 PE=1 SV=1
AT1G78850	Q9ZVA4	-0,717	0,002	Extracellular	Q9ZVA4 EP1L3_ARATH EP1-like glycoprotein 3 OS=Arabidopsis thaliana GN=At1g78850 PE=1 SV=1
AT3G26720	P94078	-0,718	0,003	Extracellular	P94078 MANA1_ARATH Alpha-mannosidase At3g26720 OS=Arabidopsis thaliana GN=At3g26720 PE=1 SV=1
AT3G16410	O04316	-0,727	0,001	Cytosol	O04316 JAL29_ARATH Nitrile-specifier protein 4 OS=Arabidopsis thaliana GN=NSP4 PE=2 SV=1
AT3G16400	Q9SDM9	-0,782	0,023	Cytosol	Q9SDM9 JAL28_ARATH Nitrile-specifier protein 1 OS=Arabidopsis thaliana GN=NSP1 PE=1 SV=2
AT5G66920	Q8LPS9	-0,783	0,036	Extracellular	Q8LPS9 Q8LPS9_ARATH At5g66920/MUD21_18 OS=Arabidopsis thaliana GN=sk17 PE=2 SV=1
AT3G29250	F4JZ27	-0,84	0,011	Extracellular	F4JZ27 SDR4_ARATH Short-chain dehydrogenase reductase 4 OS=Arabidopsis thaliana GN=SDR4 PE=2 SV=1
AT4G34138	Q8VZE9	-0,902	0,011	Plasma membrane	Q8VZE9 U73B1_ARATH UDP-glycosyltransferase 73B1 OS=Arabidopsis thaliana GN=UGT73B1 PE=2 SV=1
AT4G21580	O65423	-0,918	0,003	Cytosol	O65423 O65423_ARATH At4g21580/F18E5_200 OS=Arabidopsis thaliana GN=F18E5.200 PE=2 SV=1
AT2G24180	O65787	-0,939	0,021	ER	O65787 C71B6_ARATH Cytochrome P450 71B6 OS=Arabidopsis thaliana GN=CYP71B6 PE=2 SV=1
AT4G12510	Q9S7U3	-1,086	0,001	Extracellular	Q9S7U3 Q9S7U3_ARATH At4g12520 OS=Arabidopsis thaliana GN=At4g12510 PE=2 SV=1
AT3G03980	Q9SQR4	-1,167	0,028	Plastid	Q9SQR4 ADRC3_ARATH NADPH-dependent aldehyde reductase-like protein, chloroplastic OS=Arabidopsis thaliana GN=At3g03980 PE=3 SV=1
AT2G44790	O80517	-1,195	0,006	Plasma membrane	O80517 BCB2_ARATH Uclacyanin-2 OS=Arabidopsis thaliana GN=At2g44790 PE=1 SV=1
AT4G09750	Q9SZ91	-1,321	0,001	Mitochondrion	Q9SZ91 Q9SZ91_ARATH NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At4g09750 PE=2 SV=1
AT1G10290	Q9SE83	-1,383	0,023	Golgi	Q9SE83 DRP2A_ARATH Dynamin-2A OS=Arabidopsis thaliana GN=DRP2A PE=1 SV=2
AT2G42250	O48532	-1,544	0,011	ER	O48532 O48532_ARATH Cytochrome P450, family 712, subfamily A, polypeptide 1 OS=Arabidopsis thaliana GN=CYP712A1 PE=3 SV=1
AT5G46900	Q39100	-2,265	0,001	Extracellular	Q39100 Q39100_ARATH Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=extA PE=2 SV=1
Nucleotide metabolism					
AT4G29630	Q9S847	-1,196	0,02	Cytosol	Q9S847 CDA3_ARATH Cytidine deaminase 3 OS=Arabidopsis thaliana GN=CDA3 PE=2 SV=1
Protein					
AT2G30050	O64740	0,9	0,016	Cytosol	O64740 SC13B_ARATH Protein transport protein SEC13 homolog B OS=Arabidopsis thaliana GN=SEC13B PE=1 SV=1
AT4G31700	O48549	0,859	0,013	Cytosol	O48549 R561_ARATH 40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2
AT5G47700	Q8LEQ0	0,836	0,046	Cytosol	Q8LEQ0 RLA13_ARATH 60S acidic ribosomal protein P1-3 OS=Arabidopsis thaliana GN=RPP1C PE=1 SV=2
AT3G07110	Q9SFU1	0,683	0,014	Cytosol	Q9SFU1 R13A1_ARATH 60S ribosomal protein L13a-1 OS=Arabidopsis thaliana GN=RPL13AA PE=2 SV=1
AT1G47128	P43297	-0,649	0,007	Extracellular	P43297 RD21A_ARATH Cysteine proteinase RD21A OS=Arabidopsis thaliana GN=RD21A PE=1 SV=1
AT1G03230	Q9ZV55	-0,696	0,005	Extracellular	Q9ZV55 Q9ZV55_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03230 PE=2 SV=1
AT4G20110	Q8L7E3	-0,744	0,027	Vacuole	Q8L7E3 VSR7_ARATH Vacuolar-sorting receptor 7 OS=Arabidopsis thaliana GN=VSR7 PE=2 SV=2
AT5G59090	Q8L7D2	-0,802	0,005	Extracellular	Q8L7D2 SBT4C_ARATH Subtilisin-like protease SBT4.12 OS=Arabidopsis thaliana GN=SBT4.12 PE=2 SV=1
AT3G50500	Q39192	-0,941	0,038	Cytosol	Q39192 SRK2D_ARATH Serine/threonine-protein kinase SRK2D OS=Arabidopsis thaliana GN=SRK2D PE=1 SV=1
AT1G04850	Q9MAT3	-1	0,029	Nucleus	Q9MAT3 Q9MAT3_ARATH F13M7.16 protein OS=Arabidopsis thaliana GN=At1g04850 PE=2 SV=1
AT1G11910	O65390	-1,016	0,005	Vacuole	O65390 APA1_ARATH Aspartic proteinase A1 OS=Arabidopsis thaliana GN=APA1 PE=1 SV=1
AT1G02305	Q93VC9	-1,023	0,001	Extracellular	Q93VC9 CATB2_ARATH Cathepsin B-like protease 2 OS=Arabidopsis thaliana GN=CATHB2 PE=2 SV=1
AT1G03220	Q9ZVS4	-1,158	0,001	Extracellular	Q9ZVS4 Q9ZVS4_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03220 PE=2 SV=1
AT1G14570	Q94JZ8	-1,517	0,019	Nucleus	Q94JZ8 PUX7_ARATH Plant UBX domain-containing protein 7 OS=Arabidopsis thaliana GN=PUX7 PE=1 SV=1
AT4G16190	Q9SUL1	-1,659	0,004	Vacuole	Q9SUL1 RD19C_ARATH Probable cysteine protease RD19C OS=Arabidopsis thaliana GN=RD19C PE=2 SV=1
AT5G14950	Q9LFR0	-2,042	0,029	Golgi	Q9LFR0 GMAN2_ARATH Alpha-mannosidase 2 OS=Arabidopsis thaliana GN=GMII PE=1 SV=1

AT1G30690	Q94C59	-2,067	0,001	Cytosol	Q94C59 PATL4_ARATH Patellin-4 OS=Arabidopsis thaliana GN=PATL4 PE=1 SV=2
Redox regulation					
AT2G16060	O24520	1,896	0,001	Cytosol	O24520 HBL1_ARATH Non-symbiotic hemoglobin 1 OS=Arabidopsis thaliana GN=AHB1 PE=1 SV=1
AT4G25100	P21276	0,888	0,004	Plastid	P21276 SODF1_ARATH Superoxide dismutase [Fe] 1, chloroplastic OS=Arabidopsis thaliana GN=FSD1 PE=1 SV=4
AT1G78370	Q8L7C9	0,829	0,021	Peroxisome	Q8L7C9 GSTUK_ARATH Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1
AT3G32980	Q9LHB9	-0,454	0,047	Extracellular	Q9LHB9 PER32_ARATH Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3
AT1G05260	Q23044	-0,539	0,024	Extracellular	Q23044 PER3_ARATH Peroxidase 3 OS=Arabidopsis thaliana GN=PER3 PE=2 SV=1
AT3G52880	Q9LFA3	-0,622	0,006	Peroxisome	Q9LFA3 MDAR1_ARATH Monodehydroascorbate reductase 1, peroxisomal OS=Arabidopsis thaliana GN=MDAR1 PE=1 SV=1
AT1G78380	Q9ZRW8	-0,8	0,001	Cytosol	Q9ZRW8 GSTUJ_ARATH Glutathione S-transferase U19 OS=Arabidopsis thaliana GN=GSTU19 PE=1 SV=1
AT5G28840	Q93VR3	-0,826	0,004	Cytosol	Q93VR3 GME_ARATH GDP-mannose 3,5-epimerase OS=Arabidopsis thaliana GN=At5g28840 PE=1 SV=1
AT3G49120	Q9SMU8	-1,009	0,001	Extracellular	Q9SMU8 PER34_ARATH Peroxidase 34 OS=Arabidopsis thaliana GN=PER34 PE=1 SV=1
AT2G28190	O78310	-1,105	0,009	Plastid	O78310 SODC2_ARATH Superoxide dismutase [Cu-Zn] 2, chloroplastic OS=Arabidopsis thaliana GN=CSD2 PE=1 SV=2
AT1G10370	Q9FUS8	-1,403	0,001	Cytosol	Q9FUS8 GSTUH_ARATH Glutathione S-transferase U17 OS=Arabidopsis thaliana GN=GSTU17 PE=2 SV=1
AT1G17170	Q9SHH6	-1,551	0,005	Cytosol	Q9SHH6 GSTUO_ARATH Glutathione S-transferase U24 OS=Arabidopsis thaliana GN=GSTU24 PE=2 SV=1
AT1G08830	P24704	-1,988	0,003	Cytosol	P24704 SODC1_ARATH Superoxide dismutase [Cu-Zn] 1 OS=Arabidopsis thaliana GN=CSD1 PE=1 SV=2
RNA					
AT2G02470	Q8S8M9	1,301	0,04	Nucleus	Q8S8M9 ALFL6_ARATH PHD finger protein ALFIN-LIKE 6 OS=Arabidopsis thaliana GN=AL6 PE=1 SV=1
AT2G21660	Q03250	0,615	0,017	Nucleus	Q03250 RBG7_ARATH Glycine-rich RNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1
Secondary metabolism					
AT4G34050	O49499	0,509	0,035	Cytosol	O49499 CAMT4_ARATH Caffeoyl-CoA O-methyltransferase 1 OS=Arabidopsis thaliana GN=CCOAMT1 PE=1 SV=1
AT1G74020	P94111	-0,717	0,023	Vacuole	P94111 SSL12_ARATH Protein STRICTOSIDINE SYNTHASE-LIKE 12 OS=Arabidopsis thaliana GN=SSL12 PE=2 SV=2
AT3G09220	Q9SR40	-0,757	0,007	Extracellular	Q9SR40 LAC7_ARATH Laccase-7 OS=Arabidopsis thaliana GN=LAC7 PE=2 SV=1
AT1G06000	Q9LNE6	-0,837	0,002	Cytosol	Q9LNE6 U89C1_ARATH UDP-glycosyltransferase 89C1 OS=Arabidopsis thaliana GN=UGT89C1 PE=2 SV=1
AT3G51240	Q9S818	-0,854	0,016	Cytosol	Q9S818 FL3H_ARATH Naringenin,2-oxoglutarate 3-dioxygenase OS=Arabidopsis thaliana GN=F3H PE=1 SV=1
AT1G51470	Q3ECS3	-0,937	0,001	Extracellular	Q3ECS3 BGL35_ARATH Myrosinase 5 OS=Arabidopsis thaliana GN=TGG5 PE=1 SV=1
AT5G13930	P13114	-0,98	0,001	ER	P13114 CHSY_ARATH Chalcone synthase OS=Arabidopsis thaliana GN=CHS PE=1 SV=1
AT3G55120	P41088	-1,4	0,001	ER	P41088 CFI1_ARATH Chalcone-flavanone isomerase 1 OS=Arabidopsis thaliana GN=CHI1 PE=1 SV=2
Signalling					
AT3G05490	Q9MA62	1,387	0,024	Extracellular	Q9MA62 RLF22_ARATH Protein RALF-like 22 OS=Arabidopsis thaliana GN=RALFL22 PE=3 SV=1
AT4G33240	Q0WUR5	1,201	0,046	Golgi	Q0WUR5 FAB1A_ARATH 1-phosphatidylinositol-3-phosphate 5-kinase FAB1A OS=Arabidopsis thaliana GN=FAB1A PE=2 SV=1
AT1G51840	F4IB68	-0,769	0,05	Extracellular	F4IB68 F4IB68_ARATH Kinase-like protein OS=Arabidopsis thaliana GN=At1g51840 PE=4 SV=2
AT5G16590	Q9FMD7	-0,94	0,039	Plasma membrane	Q9FMD7 Y5659_ARATH Probable inactive receptor kinase At5g16590 OS=Arabidopsis thaliana GN=At5g16590 PE=1 SV=1
AT4G20260	Q96262	-1,209	0,008	Plasma membrane	Q96262 PCAP1_ARATH Plasma membrane-associated cation-binding protein 1 OS=Arabidopsis thaliana GN=PCAP1 PE=1 SV=1
AT3G16570	Q9LUS7	-1,534	0,008	Extracellular	Q9LUS7 RLF23_ARATH Rapid alkalization factor 23 OS=Arabidopsis thaliana GN=RALF23 PE=1 SV=1
AT1G51820	COLGG3	-1,657	0,007	Plasma membrane	COLGG3 Y5182_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g51820 OS=Arabidopsis thaliana GN=At1g51820 PE=2 SV=1
AT5G41940	Q67YN2	-2,047	0,03	Mitochondrion	Q67YN2 Q67YN2_ARATH GTPase activator protein of Rab-like small GTPases-like protein OS=Arabidopsis thaliana GN=MJC20.4 PE=2 SV=1
Stress					
AT4G33720	O81888	2,748	0,001	Extracellular	O81888 O81888_ARATH AT4g33720 OS=Arabidopsis thaliana GN=T16L1.210 PE=2 SV=1
AT4G08780	Q9LDA4	1,605	0,002	Extracellular	Q9LDA4 PER38_ARATH Peroxidase 38 OS=Arabidopsis thaliana GN=PER38 PE=3 SV=1
AT5G38940	Q9FMA8	1,497	0,013	Extracellular	Q9FMA8 GL111_ARATH Germin-like protein subfamily 1 member 11 OS=Arabidopsis thaliana GN=At5g38940 PE=2 SV=1
AT4G02520	P46422	1,431	0,001	Cytosol	P46422 GSTF2_ARATH Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3
AT4G08770	Q9LDN9	1,427	0,002	Extracellular	Q9LDN9 PER37_ARATH Peroxidase 37 OS=Arabidopsis thaliana GN=PER37 PE=2 SV=1
AT2G43590	O24658	1,383	0,024	Extracellular	O24658 CHIS9_ARATH Endochitinase At2g43590 OS=Arabidopsis thaliana GN=At2g43590 PE=2 SV=1
AT1G52060	F4IB95	1,145	0,001	Extracellular	F4IB95 JAL9_ARATH Jacalin-related lectin 9 OS=Arabidopsis thaliana GN=JAL9 PE=3 SV=1
AT4G26010	Q93V93	1,099	0,002	Extracellular	Q93V93 PER44_ARATH Peroxidase 44 OS=Arabidopsis thaliana GN=PER44 PE=2 SV=1
AT1G05240	P0D110	1,069	0,012	Extracellular	P0D110 PER1_ARATH Peroxidase 1 OS=Arabidopsis thaliana GN=PER1 PE=1 SV=1
AT1G52070	Q8GW17	0,88	0,001	Extracellular	Q8GW17 JAL10_ARATH Jacalin-related lectin 10 OS=Arabidopsis thaliana GN=JAL10 PE=2 SV=1
AT3G12500	P19171	0,697	0,02	Extracellular	P19171 CHIB_ARATH Basic endochitinase B OS=Arabidopsis thaliana GN=CHI-B PE=1 SV=3
AT3G04720	P43082	0,672	0,023	Extracellular	P43082 HEVL_ARATH Hevein-like preproprotein OS=Arabidopsis thaliana GN=HEL PE=1 SV=1
AT2G39310	O80950	-0,499	0,023	Plasma membrane	O80950 JAL22_ARATH Jacalin-related lectin 22 OS=Arabidopsis thaliana GN=JAL22 PE=1 SV=1
At1g33590	F4HR88	-0,51	0,043	Extracellular	A0A1P8AWX3 A0A1P8AWX3_ARATH Leucine-rich repeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33590 PE=4 SV=1
AT3G16460	O04310	-0,533	0,006	Cytosol	O04310 JAL34_ARATH Jacalin-related lectin 34 OS=Arabidopsis thaliana GN=JAL34 PE=1 SV=1
AT3G12580	Q9LHA8	-0,613	0,039	Cytosol	Q9LHA8 MD37C_ARATH Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1
AT4G19880	Q8H121	-0,623	0,007	Plastid	Q8H121 Q8H121_ARATH Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=At4g19880 PE=1 SV=1
AT1G30360	Q9C8G5	-0,635	0,007	Plasma membrane	Q9C8G5 CSCLD_ARATH CSC1-like protein ERD4 OS=Arabidopsis thaliana GN=ERD4 PE=2 SV=1
AT2G02390	Q9ZVQ3	-0,639	0,026	Cytosol	Q9ZVQ3 GSTZ1_ARATH Glutathione S-transferase Z1 OS=Arabidopsis thaliana GN=GSTZ1 PE=1 SV=1
AT3G16470	O04309	-0,654	0,003	Cytosol	O04309 JAL35_ARATH Jacalin-related lectin 35 OS=Arabidopsis thaliana GN=JAL35 PE=1 SV=1
AT2G01520	Q9ZVF3	-0,71	0,002	Cytosol	Q9ZVF3 ML328_ARATH MLP-like protein 328 OS=Arabidopsis thaliana GN=MLP328 PE=2 SV=1

AT1G20440	P31168	-0,712	0,037	Nucleus	P31168 COR47_ARATH Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2
AT4G23670	Q9SUR0	-0,723	0,007	Cytosol	Q9SUR0 Q9SUR0_ARATH AT4G23670 protein OS=Arabidopsis thaliana GN=At4g23670 PE=2 SV=1
AT1G76690	Q8GYB8	-0,76	0,005	Cytosol	Q8GYB8 OPR2_ARATH 12-oxophytodienoate reductase 2 OS=Arabidopsis thaliana GN=OPR2 PE=1 SV=2
AT1G18970	P92995	-0,874	0,013	Extracellular	P92995 GLT1_ARATH Germin-like protein subfamily T member 1 OS=Arabidopsis thaliana GN=GLP1 PE=2 SV=2
AT1G70850	Q9SSK7	-0,88	0,001	Cytosol	Q9SSK7 MLP34_ARATH MLP-like protein 34 OS=Arabidopsis thaliana GN=MLP34 PE=2 SV=1
AT3G16450	O04311	-0,927	0,004	Cytosol	O04311 JAL33_ARATH Jacalin-related lectin 33 OS=Arabidopsis thaliana GN=JAL33 PE=1 SV=1
AT1G76680	Q8LAH7	-0,929	0,002	Cytosol	Q8LAH7 OPR1_ARATH 12-oxophytodienoate reductase 1 OS=Arabidopsis thaliana GN=OPR1 PE=1 SV=2
AT4G23690	Q9SUQ8	-0,954	0,014	Extracellular	Q9SUQ8 DIR6_ARATH Dirigent protein 6 OS=Arabidopsis thaliana GN=DIR6 PE=1 SV=1
AT2G01530	Q9ZVF2	-0,965	0,043	Cytosol	Q9ZVF2 ML329_ARATH MLP-like protein 329 OS=Arabidopsis thaliana GN=MLP329 PE=2 SV=1
AT1G17860	Q9LMU2	-1,029	0,001	Extracellular	Q9LMU2 KTI2_ARATH Kunitz trypsin inhibitor 2 OS=Arabidopsis thaliana GN=KTI2 PE=2 SV=1
AT3G01420	Q9SGH6	-1,067	0,001	Cytosol	Q9SGH6 DOX1_ARATH Alpha-dioxygenase 1 OS=Arabidopsis thaliana GN=DOX1 PE=1 SV=1
AT4G23680	Q9SUQ9	-1,068	0,016	Cytosol	Q9SUQ9 Q9SUQ9_ARATH AT4g23680/F9D16_150 OS=Arabidopsis thaliana GN=At4g23680 PE=2 SV=1
AT1G09560	P94014	-1,098	0,01	Extracellular	P94014 GL21_ARATH Germin-like protein subfamily 2 member 1 OS=Arabidopsis thaliana GN=GLP4 PE=2 SV=2
AT4G14060	O23267	-1,117	0,029	Cytosol	O23267 O23267_ARATH AT4g14060/dl3070w OS=Arabidopsis thaliana GN=dl3070w PE=2 SV=1
AT1G73260	Q8RXD5	-1,361	0,001	Extracellular	Q8RXD5 KTI1_ARATH Kunitz trypsin inhibitor 1 OS=Arabidopsis thaliana GN=KTI1 PE=2 SV=1
AT5G20970	F4K6X6	-1,492	0,02	Cytosol	F4K6X6 F4K6X6_ARATH HSP20-like chaperones superfamily protein OS=Arabidopsis thaliana GN=At5g20970 PE=3 SV=1
AT1G52100	Q5XF82	-1,703	0,008	Cytosol	Q5XF82 JAL11_ARATH Jacalin-related lectin 11 OS=Arabidopsis thaliana GN=JAL11 PE=2 SV=1
TCA/org transformation					
AT2G13560	Q9SIU0	-0,797	0,036	Mitochondrion	Q9SIU0 MAO1_ARATH NAD-dependent malic enzyme 1, mitochondrial OS=Arabidopsis thaliana GN=NAD-ME1 PE=1 SV=1
Transport					
AT5G43350	Q8VYM2	0,884	0,004	Plasma membrane	Q8VYM2 PHT11_ARATH Inorganic phosphate transporter 1-1 OS=Arabidopsis thaliana GN=PHT1-1 PE=1 SV=2
AT5G57110	Q9LF79	-0,549	0,038	Plasma membrane	Q9LF79 ACA8_ARATH Calcium-transporting ATPase 8, plasma membrane-type OS=Arabidopsis thaliana GN=ACA8 PE=1 SV=1
AT1G72150	Q56WK6	-0,762	0,004	Plasma membrane	Q56WK6 PATL1_ARATH Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2
AT2G37170	P43287	-0,842	0,006	Plasma membrane	P43287 PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2
AT3G26520	Q41963	-0,943	0,02	Vacuole	Q41963 TIP12_ARATH Aquaporin TIP1-2 OS=Arabidopsis thaliana GN=TIP1-2 PE=1 SV=2
AT5G58070	Q9FGT8	-1,003	0,002	ER	Q9FGT8 TIL_ARATH Temperature-induced lipocalin-1 OS=Arabidopsis thaliana GN=TIL PE=1 SV=1
AT2G36830	P25818	-1,132	0,005	Vacuole	P25818 TIP11_ARATH Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1
AT4G25640	F4JTB3	-1,207	0,048	Vacuole	F4JTB3 DTX35_ARATH Protein DETOXIFICATION 35 OS=Arabidopsis thaliana GN=DTX35 PE=1 SV=1
AT4G19690	Q38856	-1,264	0,02	Plasma membrane	Q38856 IRT1_ARATH Fe(2+) transport protein 1 OS=Arabidopsis thaliana GN=IRT1 PE=1 SV=2
AT4G35100	P93004	-1,399	0,01	Plasma membrane	P93004 PIP27_ARATH Aquaporin PIP2-7 OS=Arabidopsis thaliana GN=PIP2-7 PE=1 SV=2
AT1G61800	Q94B38	-1,454	0,023	Plastid	Q94B38 GPT2_ARATH Glucose-6-phosphate/phosphate translocator 2, chloroplastic OS=Arabidopsis thaliana GN=GPT2 PE=2 SV=2
AT3G61430	P61837	-1,465	0,008	Plasma membrane	P61837 PIP11_ARATH Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1
AT4G17340	Q41975	-1,606	0,05	Vacuole	Q41975 TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2
AT3G53420	P43286	-1,74	0,003	Plasma membrane	P43286 PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1
AT2G45960	Q06611	-1,747	0,002	Plasma membrane	Q06611 PIP12_ARATH Aquaporin PIP1-2 OS=Arabidopsis thaliana GN=PIP1-2 PE=1 SV=1
AT2G37180	P30302	-2,091	0,001	Plasma membrane	P30302 PIP23_ARATH Aquaporin PIP2-3 OS=Arabidopsis thaliana GN=PIP2-3 PE=1 SV=1

Table S3: List of proteins identified in the proteomic study

Description	num_peptides	Fold change (log2)	pvalue	evalue	qvalue (FDR)
O81888 O81888_ARATH AT4g33720 OS=Arabidopsis thaliana GN=T16L1.210 PE=2 SV=1	3	2,748	9,9999E-06	0,02	0,001
Q39100 Q39100_ARATH Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=extA PE=	1	-2,265	2,99997E-05	0,07	0,001
P30302 PIP23_ARATH Aquaporin PIP2-3 OS=Arabidopsis thaliana GN=PIP2-3 PE=1 SV=1	1	-2,091	2,99997E-05	0,07	0,001
Q94C59 PATL4_ARATH Patellin-4 OS=Arabidopsis thaliana GN=PATL4 PE=1 SV=2	1	-2,067	1,99998E-05	0,05	0,001
O24520 HBL1_ARATH Non-symbiotic hemoglobin 1 OS=Arabidopsis thaliana GN=AHB1 PE=1 SV=1	3	1,896	9,9999E-06	0,02	0,001
Q9FE29 CSPLM_ARATH CASP-like protein 1D1 OS=Arabidopsis thaliana GN=At4g15610 PE=2 SV=1	2	-1,583	9,9999E-06	0,02	0,001
P61837 PIP11_ARATH Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1	2	-1,505	9,9999E-06	0,02	0,001
P46422 GSTF2_ARATH Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3	12	1,431	9,9999E-06	0,02	0,001
Q9FUS8 GSTUH_ARATH Glutathione S-transferase U17 OS=Arabidopsis thaliana GN=GSTU17 PE=2 SV=1	2	-1,403	1,99998E-05	0,05	0,001
P41088 CFI1_ARATH Chalcone--flavonone isomerase 1 OS=Arabidopsis thaliana GN=CHI1 PE=1 SV=2	9	-1,4	9,9999E-06	0,02	0,001
Q8RXD5 KTI1_ARATH Kunitz trypsin inhibitor 1 OS=Arabidopsis thaliana GN=KTI1 PE=2 SV=1	7	-1,361	9,9999E-06	0,02	0,001
F4IRX7 F4IRX7_ARATH SOUL heme-binding family protein OS=Arabidopsis thaliana GN=SOUL-1 PE=1 SV=2	6	-1,336	9,9999E-06	0,02	0,001
Q9SZ91 Q9SZ91_ARATH NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At4g09750 PE=2 SV=1	3	-1,321	1,99998E-05	0,05	0,001
P06525 ADH1_ARATH Alcohol dehydrogenase class-P OS=Arabidopsis thaliana GN=ADH1 PE=1 SV=2	7	1,312	9,9999E-06	0,02	0,001
Q9C525 BGL21_ARATH Beta-glucosidase 21 OS=Arabidopsis thaliana GN=BGLU21 PE=1 SV=1	2	-1,265	9,9999E-06	0,02	0,001
Q9ZVF2 ML329_ARATH MLP-like protein 329 OS=Arabidopsis thaliana GN=MLP329 PE=2 SV=1	4	-1,248	9,9999E-06	0,02	0,001
Q6NQ66 GGLO2_ARATH L-gulonolactone oxidase 2 OS=Arabidopsis thaliana GN=GULLO2 PE=1 SV=1	7	-1,188	9,9999E-06	0,02	0,001
Q96329 ACOX4_ARATH Acyl-coenzyme A oxidase 4, peroxisomal OS=Arabidopsis thaliana GN=ACX4 PE=1 SV=1	6	-1,185	9,9999E-06	0,02	0,001
Q9ZVS4 Q9ZVS4_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03220 PE=2 SV=1	3	-1,158	9,9999E-06	0,02	0,001
Q9FPF0 DJ1A_ARATH Protein DJ-1 homolog A OS=Arabidopsis thaliana GN=DJ1A PE=1 SV=1	11	-1,147	9,9999E-06	0,02	0,001
F4IB95 JAL9_ARATH Jacalin-related lectin 9 OS=Arabidopsis thaliana GN=JAL9 PE=3 SV=1	4	1,145	9,9999E-06	0,02	0,001
Q9S7U3 Q9S7U3_ARATH AT4g12520 OS=Arabidopsis thaliana GN=At4g12510 PE=2 SV=1	3	-1,086	1,99998E-05	0,05	0,001
O23179 PLP1_ARATH Patatin-like protein 1 OS=Arabidopsis thaliana GN=PLP1 PE=1 SV=2	6	-1,076	9,9999E-06	0,02	0,001
Q9SGH6 DOX1_ARATH Alpha-dioxygenase 1 OS=Arabidopsis thaliana GN=DOX1 PE=1 SV=1	25	-1,067	9,9999E-06	0,02	0,001
Q9LTQ5 Q9LTQ5_ARATH AT3g20370/MQC12_13 OS=Arabidopsis thaliana GN=At3g20370 PE=2 SV=1	8	-1,058	9,9999E-06	0,02	0,001
Q8VZJ2 BGNEM_ARATH Probable glucan endo-1,3-beta-glucosidase At4g16260 OS=Arabidopsis thaliana GN=At4g16260 PE=1 SV=1	11	1,053	9,9999E-06	0,02	0,001
Q9FF98 ML3_ARATH MD-2-related lipid-recognition protein 3 OS=Arabidopsis thaliana GN=ML3 PE=1 SV=1	3	-1,032	1,99998E-05	0,05	0,001
Q9LMU2 KTI2_ARATH Kunitz trypsin inhibitor 2 OS=Arabidopsis thaliana GN=KTI2 PE=2 SV=1	8	-1,029	9,9999E-06	0,02	0,001
Q93VC9 CATB2_ARATH Cathepsin B-like protease 2 OS=Arabidopsis thaliana GN=CATHB2 PE=2 SV=1	4	-1,023	2,99997E-05	0,07	0,001
Q9SMU8 PER34_ARATH Peroxidase 34 OS=Arabidopsis thaliana GN=PER34 PE=1 SV=1	6	-1,009	9,9999E-06	0,02	0,001
P13114 CHSY_ARATH Chalcone synthase OS=Arabidopsis thaliana GN=CHS PE=1 SV=1	5	-0,98	1,99998E-05	0,05	0,001
Q9SLV3 Q9SLV3_ARATH At1g58270/F19C14_8 OS=Arabidopsis thaliana GN=ZW9 PE=2 SV=1	5	-0,967	1,99998E-05	0,05	0,001
A0A1P8BA53 A0A1P8BA53_ARATH TRAF-like family protein OS=Arabidopsis thaliana GN=At5g26280 PE=4 SV=1	15	-0,96	9,9999E-06	0,02	0,001
Q3ECS3 BGL35_ARATH Myrosinase 5 OS=Arabidopsis thaliana GN=TGG5 PE=1 SV=1	4	-0,937	9,9999E-06	0,02	0,001
Q9ZVS4 Q9ZVS4_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03220 PE=2 SV=1	10	-0,913	1,99998E-05	0,05	0,001
Q9SSK7 MLP34_ARATH MLP-like protein 34 OS=Arabidopsis thaliana GN=MLP34 PE=2 SV=1	17	-0,88	9,9999E-06	0,02	0,001
Q8GW17 JAL10_ARATH Jacalin-related lectin 10 OS=Arabidopsis thaliana GN=JAL10 PE=2 SV=1	8	0,88	9,9999E-06	0,02	0,001
P59259 H4_ARATH Histone H4 OS=Arabidopsis thaliana GN=At1g07660 PE=1 SV=2	7	-0,845	9,9999E-06	0,02	0,001
Q9ZRW8 GSTUJ_ARATH Glutathione S-transferase U19 OS=Arabidopsis thaliana GN=GSTU19 PE=1 SV=1	8	-0,8	2,99997E-05	0,07	0,001
O04316 JAL29_ARATH Nitrile-specifier protein 4 OS=Arabidopsis thaliana GN=NSP4 PE=2 SV=1	14	-0,727	9,9999E-06	0,02	0,001
O04314 JAL30_ARATH PYK10-binding protein 1 OS=Arabidopsis thaliana GN=PBP1 PE=1 SV=1	11	-0,702	9,9999E-06	0,02	0,001
Q9LSB4 NAI2_ARATH TSA1-like protein OS=Arabidopsis thaliana GN=NAI2 PE=1 SV=1	33	-0,691	9,9999E-06	0,02	0,001
Q06611 PIP12_ARATH Aquaporin PIP1-2 OS=Arabidopsis thaliana GN=PIP1-2 PE=1 SV=1	2	-1,747	9,9999E-06	0,02	0,002
Q9LDA4 PER38_ARATH Peroxidase 38 OS=Arabidopsis thaliana GN=PER38 PE=3 SV=1	2	1,605	9,9999E-06	0,02	0,002
Q9LDN9 PER37_ARATH Peroxidase 37 OS=Arabidopsis thaliana GN=PER37 PE=2 SV=1	5	1,427	9,9999E-06	0,02	0,002
Q93V93 PER44_ARATH Peroxidase 44 OS=Arabidopsis thaliana GN=PER44 PE=2 SV=1	9	1,099	9,9999E-06	0,02	0,002
Q41931 ACCO2_ARATH 1-aminocyclopropane-1-carboxylate oxidase 2 OS=Arabidopsis thaliana GN=ACO2 PE=1 SV=2	4	1,025	4,99995E-05	0,12	0,002

Q9FGT8 TIL_ARATH Temperature-induced lipocalin-1 OS=Arabidopsis thaliana GN=TIL PE=1 SV=1	6	-1,003	9,9999E-06	0,02	0,002
Q9SWG0 IVD_ARATH Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2	6	-0,942	3,99996E-05	0,09	0,002
Q8LAH7 OPR1_ARATH 12-oxophytodienoate reductase 1 OS=Arabidopsis thaliana GN=OPR1 PE=1 SV=2	9	-0,929	9,9999E-06	0,02	0,002
Q9LNE6 U89C1_ARATH UDP-glycosyltransferase 89C1 OS=Arabidopsis thaliana GN=UGT89C1 PE=2 SV=1	7	-0,837	4,99995E-05	0,12	0,002
Q9ZVA4 EP1L3_ARATH EP1-like glycoprotein 3 OS=Arabidopsis thaliana GN=At1g78850 PE=1 SV=1	7	-0,717	5,99994E-05	0,14	0,002
Q9ZVF3 ML328_ARATH MLP-like protein 328 OS=Arabidopsis thaliana GN=MLP328 PE=2 SV=1	7	-0,71	3,99996E-05	0,09	0,002
P24704 SODC1_ARATH Superoxide dismutase [Cu-Zn] 1 OS=Arabidopsis thaliana GN=CSD1 PE=1 SV=2	3	-1,988	9,9999E-06	0,02	0,003
P43286 PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1	1	-1,74	6,99993E-05	0,16	0,003
Q9SUQ9 Q9SUQ9_ARATH AT4g23680/F9D16_150 OS=Arabidopsis thaliana GN=At4g23680 PE=2 SV=1	2	-1,712	9,9999E-06	0,02	0,003
P32961 NRL1_ARATH Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	5	-1,114	9,9999E-06	0,02	0,003
O65423 O65423_ARATH AT4g21580/F18E5_200 OS=Arabidopsis thaliana GN=F18E5.200 PE=2 SV=1	4	-0,918	7,99992E-05	0,19	0,003
P94078 MANA1_ARATH Alpha-mannosidase At3g26720 OS=Arabidopsis thaliana GN=At3g26720 PE=1 SV=1	9	-0,718	8,99991E-05	0,21	0,003
Q8S8T4 UXS4_ARATH UDP-glucuronic acid decarboxylase 4 OS=Arabidopsis thaliana GN=UXS4 PE=2 SV=1	8	0,711	8,99991E-05	0,21	0,003
O04309 JAL35_ARATH Jacalin-related lectin 35 OS=Arabidopsis thaliana GN=JAL35 PE=1 SV=1	12	-0,654	9,9999E-05	0,23	0,003
Q9SUL1 RD19C_ARATH Probable cysteine protease RD19C OS=Arabidopsis thaliana GN=RD19C PE=2 SV=1	1	-1,659	0,000109999	0,26	0,004
O04311 JAL33_ARATH Jacalin-related lectin 33 OS=Arabidopsis thaliana GN=JAL33 PE=1 SV=1	10	-0,927	9,9999E-06	0,02	0,004
P21276 SODF1_ARATH Superoxide dismutase [Fe] 1, chloroplastic OS=Arabidopsis thaliana GN=FSD1 PE=1 SV=4	3	0,888	0,000129999	0,3	0,004
Q8VYM2 PHT11_ARATH Inorganic phosphate transporter 1-1 OS=Arabidopsis thaliana GN=PHT1-1 PE=1 SV=2	5	0,884	0,000129999	0,3	0,004
Q93VR3 GME_ARATH GDP-mannose 3,5-epimerase OS=Arabidopsis thaliana GN=At5g28840 PE=1 SV=1	5	-0,826	0,000109999	0,26	0,004
Q56WK6 PATL1_ARATH Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2	6	-0,762	0,000119999	0,28	0,004
Q9FM01 UGDH4_ARATH UDP-glucose 6-dehydrogenase 4 OS=Arabidopsis thaliana GN=UGD4 PE=1 SV=1	6	0,705	0,000109999	0,26	0,004
A0A19LNC0 A0A19LNC0_ARATH Copper chaperone OS=Arabidopsis thaliana GN=CCH PE=4 SV=1	8	0,678	0,000109999	0,26	0,004
Q84WV2 BGL20_ARATH Beta-glucosidase 20 OS=Arabidopsis thaliana GN=BGLU20 PE=2 SV=1	1	-1,834	0,000169998	0,39	0,005
Q9FF77 PME47_ARATH Probable pectinesterase/pectinesterase inhibitor 47 OS=Arabidopsis thaliana GN=PME47 PE=2 SV=1	1	-1,689	0,000169998	0,39	0,005
Q9SHH6 GSTUO_ARATH Glutathione S-transferase U24 OS=Arabidopsis thaliana GN=GSTU24 PE=2 SV=1	1	-1,551	0,000149999	0,35	0,005
Q8VZ21 Q8VZ21_ARATH Stress up-regulated Nod 19 protein OS=Arabidopsis thaliana GN=MAC9.6 PE=2 SV=1	4	-1,19	0,000169998	0,39	0,005
P25818 TIP11_ARATH Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1	2	-1,132	0,000189998	0,44	0,005
O65390 APA1_ARATH Aspartic proteinase A1 OS=Arabidopsis thaliana GN=APA1 PE=1 SV=1	16	-1,016	9,9999E-06	0,02	0,005
Q8L7D2 SBT4C_ARATH Subtilisin-like protease SBT4.12 OS=Arabidopsis thaliana GN=SBT4.12 PE=2 SV=1	5	-0,802	0,000169998	0,39	0,005
Q8GYB8 OPR2_ARATH 12-oxophytodienoate reductase 2 OS=Arabidopsis thaliana GN=OPR2 PE=1 SV=2	5	-0,76	0,000159998	0,37	0,005
Q9M5J9 PGIP1_ARATH Polygalacturonase inhibitor 1 OS=Arabidopsis thaliana GN=PGIP1 PE=1 SV=1	6	-0,744	0,000159998	0,37	0,005
Q9ZVS5 Q9ZVS5_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03230 PE=2 SV=1	9	-0,696	0,000149999	0,35	0,005
Q9SRH6 HIR3_ARATH Hypersensitive-induced response protein 3 OS=Arabidopsis thaliana GN=HIR3 PE=1 SV=1	11	-0,663	0,000189998	0,44	0,005
Q42406 CP18D_ARATH Peptidyl-prolyl cis-trans isomerase CYP18-4 OS=Arabidopsis thaliana GN=CYP18-4 PE=1 SV=1	8	0,609	0,000169998	0,39	0,005
Q80517 BCB2_ARATH Uclacyanin-2 OS=Arabidopsis thaliana GN=At2g44790 PE=1 SV=1	2	-1,195	0,000239998	0,56	0,006
Q9SR37 BGL23_ARATH Beta-glucosidase 23 OS=Arabidopsis thaliana GN=BGLU23 PE=1 SV=1	21	-0,857	9,9999E-06	0,02	0,006
P43287 PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2	4	-0,842	0,000249998	0,58	0,006
Q9LFA3 MDAR1_ARATH Monodehydroascorbate reductase 1, peroxisomal OS=Arabidopsis thaliana GN=MDAR1 PE=1 SV=1	13	-0,622	0,000239998	0,56	0,006
O04310 JAL34_ARATH Jacalin-related lectin 34 OS=Arabidopsis thaliana GN=JAL34 PE=1 SV=1	22	-0,533	0,000209998	0,49	0,006
COLGG3 Y5182_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g51820 OS=Arabidopsis thaliana GN=At1g51820 PE=2 SV=1	1	-1,657	0,000309997	0,72	0,007
Q9FM19 HIR1_ARATH Hypersensitive-induced response protein 1 OS=Arabidopsis thaliana GN=HIR1 PE=1 SV=1	3	-0,834	0,000289997	0,67	0,007
Q9SR40 LAC7_ARATH Laccase-7 OS=Arabidopsis thaliana GN=LAC7 PE=2 SV=1	6	-0,757	0,000299997	0,7	0,007
Q9SUR0 Q9SUR0_ARATH AT4G23670 protein OS=Arabidopsis thaliana GN=At4g23670 PE=2 SV=1	10	-0,723	0,000289997	0,67	0,007
P43297 RD21A_ARATH Cysteine proteinase RD21A OS=Arabidopsis thaliana GN=RD21A PE=1 SV=1	8	-0,649	0,000289997	0,67	0,007
Q9C8G5 CSCLD_ARATH CSC1-like protein ERD4 OS=Arabidopsis thaliana GN=ERD4 PE=2 SV=1	10	-0,635	0,000259997	0,6	0,007
Q8H121 Q8H121_ARATH Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=At4g19880 PE=1 SV=1	11	-0,623	0,000289997	0,67	0,007
Q5XF82 JAL11_ARATH Jacalin-related lectin 11 OS=Arabidopsis thaliana GN=JAL11 PE=2 SV=1	1	-1,703	0,000369996	0,86	0,008
Q8H1Q2 NBP35_ARATH Cytosolic Fe-S cluster assembly factor NBP35 OS=Arabidopsis thaliana GN=NBP35 PE=1 SV=1	1	-1,605	0,000349997	0,81	0,008
Q9LUS7 RLF23_ARATH Rapid alkalization factor 23 OS=Arabidopsis thaliana GN=RALF23 PE=1 SV=1	1	-1,534	0,000329997	0,77	0,008
P61837 PIP11_ARATH Aquaporin PIP1-1 OS=Arabidopsis thaliana GN=PIP1-1 PE=1 SV=1	1	-1,465	0,000339997	0,79	0,008
Q96262 PCAP1_ARATH Plasma membrane-associated cation-binding protein 1 OS=Arabidopsis thaliana GN=PCAP1 PE=1 SV=1	6	-1,209	9,9999E-06	0,02	0,008

Q9SYT0 ANXD1_ARATH Annexin D1 OS=Arabidopsis thaliana GN=ANN1 PE=1 SV=1	28	0,502	0,000349997	0,81	0,008
P43286 PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1	1	-1,325	0,000379996	0,88	0,009
O78310 SODC2_ARATH Superoxide dismutase [Cu-Zn] 2, chloroplastic OS=Arabidopsis thaliana GN=CSD2 PE=1 SV=2	3	-1,105	0,000419996	0,98	0,009
P93004 PIP27_ARATH Aquaporin PIP2-7 OS=Arabidopsis thaliana GN=PIP2-7 PE=1 SV=2	1	-1,399	0,000459995	1,07	0,01
P94014 GL21_ARATH Germin-like protein subfamily 2 member 1 OS=Arabidopsis thaliana GN=GLP4 PE=2 SV=2	2	-1,098	0,000469995	1,09	0,01
O48532 O48532_ARATH Cytochrome P450, family 712, subfamily A, polypeptide 1 OS=Arabidopsis thaliana GN=CYP712A1 PE=3 SV=1	1	-1,544	0,000509995	1,18	0,011
Q8VZE9 U73B1_ARATH UDP-glycosyltransferase 73B1 OS=Arabidopsis thaliana GN=UGT73B1 PE=2 SV=1	4	-0,902	0,000499995	1,16	0,011
F4J2Z7 SDR4_ARATH Short-chain dehydrogenase reductase 4 OS=Arabidopsis thaliana GN=SDR4 PE=2 SV=1	3	-0,84	0,000539995	1,25	0,011
F4JM51 F4JM51_ARATH Phosphorylase superfamily protein OS=Arabidopsis thaliana GN=At4g28940 PE=4 SV=1	5	-0,802	0,000509995	1,18	0,011
Q8LCE1 GLN12_ARATH Glutamine synthetase cytosolic isozyme 1-2 OS=Arabidopsis thaliana GN=GLN1-2 PE=1 SV=2	3	0,968	0,00096959	2,4	0,011
PODI10 PER1_ARATH Peroxidase 1 OS=Arabidopsis thaliana GN=PER1 PE=1 SV=1	9	1,069	9,9999E-06	0,02	0,012
Q9AST8 ROSY1_ARATH MD-2-related lipid-recognition protein ROSY1 OS=Arabidopsis thaliana GN=ROSY1 PE=1 SV=1	2	-0,976	0,000549995	1,28	0,012
Q9S7B5 THRC1_ARATH Threonine synthase 1, chloroplastic OS=Arabidopsis thaliana GN=TS1 PE=1 SV=1	1	-2,352	0,000699993	1,63	0,013
A0A19LRM4 A0A19LRM4_ARATH LUC7 related protein OS=Arabidopsis thaliana GN=UNE6 PE=4 SV=1	1	1,555	0,000679993	1,58	0,013
Q9FMA8 GL111_ARATH Germin-like protein subfamily 1 member 11 OS=Arabidopsis thaliana GN=At5g38940 PE=2 SV=1	1	1,497	0,000659993	1,53	0,013
Q9C525 BGL21_ARATH Beta-glucosidase 21 OS=Arabidopsis thaliana GN=BGLU21 PE=1 SV=1	1	-1,312	0,000609994	1,42	0,013
O81030 GGLO5_ARATH L-gulonolactone oxidase 5 OS=Arabidopsis thaliana GN=GULLO5 PE=1 SV=1	2	-1,243	0,000629994	1,46	0,013
O49636 MPC4_ARATH Mitochondrial pyruvate carrier 4 OS=Arabidopsis thaliana GN=MPC4 PE=3 SV=1	2	-1,069	0,000609994	1,42	0,013
P92995 GLT1_ARATH Germin-like protein subfamily T member 1 OS=Arabidopsis thaliana GN=GLP1 PE=2 SV=2	3	-0,874	0,000639994	1,49	0,013
Q9LR30 GGT1_ARATH Glutamate--glyoxylate aminotransferase 1 OS=Arabidopsis thaliana GN=GGAT1 PE=1 SV=1	3	-0,873	0,000639994	1,49	0,013
O48549 RS61_ARATH 40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2	3	0,859	0,000659993	1,53	0,013
Q9S7W4 Q9S7W4_ARATH At3g07720/F17A17_6 OS=Arabidopsis thaliana GN=F17A17.6 PE=2 SV=1	4	-0,781	0,000619994	1,44	0,013
A0A1P8BA53 A0A1P8BA53_ARATH TRAF-like family protein OS=Arabidopsis thaliana GN=At5g26280 PE=4 SV=1	1	-1,193	0,000789992	1,83	0,014
P46422 GSTF2_ARATH Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3	2	1,074	0,000779992	1,81	0,014
Q8W456 Q8W456_ARATH Thioredoxin superfamily protein OS=Arabidopsis thaliana GN=T20H2.2 PE=2 SV=1	2	-1,072	0,000759992	1,76	0,014
Q9SUQ8 DIR6_ARATH Dirigent protein 6 OS=Arabidopsis thaliana GN=DIR6 PE=1 SV=1	3	-0,954	0,000779992	1,81	0,014
P17562 METHK2_ARATH S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	3	0,896	0,000719993	1,67	0,014
Q9SFU1 R13A1_ARATH 60S ribosomal protein L13a-1 OS=Arabidopsis thaliana GN=RPL13AA PE=2 SV=1	4	0,683	0,000709993	1,65	0,014
O23628 H2AV1_ARATH Histone H2A variant 1 OS=Arabidopsis thaliana GN=H2AV PE=1 SV=1	4	-0,68	0,000769992	1,79	0,014
Q9C8Y9 BGL22_ARATH Beta-glucosidase 22 OS=Arabidopsis thaliana GN=BGLU22 PE=1 SV=1	6	-0,674	0,000729993	1,7	0,014
Q9LV03 GLUT1_ARATH Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana GN=GLT1 PE=1 SV=2	12	0,626	0,000759992	1,76	0,014
Q9FFQ7 FACT_ARATH Fatty alcohol:caffeoyl-CoA acyltransferase OS=Arabidopsis thaliana GN=FACT PE=2 SV=1	8	-0,659	0,000869991	2,02	0,015
Q0WP12-2 HOL1_ARATH Isoform 2 of Thiocyanate methyltransferase 1 OS=Arabidopsis thaliana GN=HOL1	10	-0,558	0,000839992	1,95	0,015
Q9SUQ9 Q9SUQ9_ARATH At4g23680/F9D16_150 OS=Arabidopsis thaliana GN=At4g23680 PE=2 SV=1	1	-1,068	0,000929991	2,16	0,016
Q8S8Q6 TET8_ARATH Tetraspanin-8 OS=Arabidopsis thaliana GN=TET8 PE=2 SV=1	2	-0,97	0,00095999	2,23	0,016
Q3EC53 BGL35_ARATH Myrosinase 5 OS=Arabidopsis thaliana GN=TGG5 PE=1 SV=1	4	-0,913	0,000929991	2,16	0,016
O64740 SC13B_ARATH Protein transport protein SEC13 homolog B OS=Arabidopsis thaliana GN=SEC13B PE=1 SV=1	3	0,9	0,000929991	2,16	0,016
Q9S818 FL3H_ARATH Naringenin,2-oxoglutarate 3-dioxygenase OS=Arabidopsis thaliana GN=F3H PE=1 SV=1	3	-0,854	0,000929991	2,16	0,016
Q39041 INVA4_ARATH Acid beta-fructofuranosidase 4, vacuolar OS=Arabidopsis thaliana GN=BFRUCT4 PE=1 SV=2	3	-0,56	0,001109756	2,55	0,016
O04848 H2AXA_ARATH Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1	1	-1,149	0,00101999	2,37	0,017
O81296 O81296_ARATH At4g02370 protein OS=Arabidopsis thaliana GN=At4g02370 PE=2 SV=1	2	-0,898	0,001059989	2,46	0,017
Q9S587 SEOB_ARATH Protein SIEVE ELEMENT OCCLUSION B OS=Arabidopsis thaliana GN=SEOB PE=1 SV=1	3	-0,837	0,00099999	2,32	0,017
Q03250 RBG7_ARATH Glycine-rich RNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1	8	0,615	0,00098999	2,3	0,017
F4JLP5 PLPD2_ARATH Dihydrolipoyl dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=LPD2 PE=2 SV=2	1	-2,272	0,001099989	2,55	0,018
Q43348 INVA3_ARATH Acid beta-fructofuranosidase 3, vacuolar OS=Arabidopsis thaliana GN=BFRUCT3 PE=2 SV=1	10	-0,577	0,001099989	2,55	0,018
Q94AE4 Q94AE4_ARATH At5g43400/MWF20_9 OS=Arabidopsis thaliana GN=MWF20.9 PE=2 SV=2	1	-2,264	0,001149989	2,67	0,019
Q94JZ8 PUX7_ARATH Plant UBX domain-containing protein 7 OS=Arabidopsis thaliana GN=PUX7 PE=1 SV=1	1	-1,517	0,001219988	2,83	0,019
Q9FPH3 THA2_ARATH Probable low-specificity L-threonine aldolase 2 OS=Arabidopsis thaliana GN=THA2 PE=1 SV=1	1	1,497	0,001189988	2,76	0,019
Q9FM01 UGDH4_ARATH UDP-glucose 6-dehydrogenase 4 OS=Arabidopsis thaliana GN=UGD4 PE=1 SV=1	3	1,144	0,001249988	2,9	0,019
O23298 O23298_ARATH At4g14420/dl3250c OS=Arabidopsis thaliana GN=dl3250c PE=2 SV=1	2	1,042	0,001219988	2,83	0,019
F4IAP5 F4IAP5_ARATH Ketose-bisphosphate aldolase class-II family protein OS=Arabidopsis thaliana GN=At1g18270 PE=4 SV=1	11	-0,576	0,001169988	2,72	0,019

F4K6X6 F4K6X6_ARATH HSP20-like chaperones superfamily protein OS=Arabidopsis thaliana GN=At5g20970 PE=3 SV=1	1	-1,492	0,001309987	3,04	0,02
Q9S847 CDA3_ARATH Cytidine deaminase 3 OS=Arabidopsis thaliana GN=CDA3 PE=2 SV=1	1	-1,196	0,001339987	3,11	0,02
Q41963 TIP12_ARATH Aquaporin TIP1-2 OS=Arabidopsis thaliana GN=TIP1-2 PE=1 SV=2	2	-0,943	0,001289987	3	0,02
P19171 CHIB_ARATH Basic endochitinase B OS=Arabidopsis thaliana GN=CHI-B PE=1 SV=3	5	0,697	0,001309987	3,04	0,02
Q9C8L4 ETHE1_ARATH Persulfide dioxygenase ETHE1 homolog, mitochondrial OS=Arabidopsis thaliana GN=GLY3 PE=1 SV=3	8	-0,633	0,001299987	3,02	0,02
Q38856 IRT1_ARATH Fe(2+) transport protein 1 OS=Arabidopsis thaliana GN=IRT1 PE=1 SV=2	1	-1,264	0,007032967	1,6	0,02
O80800 ACPM2_ARATH Acyl carrier protein 2, mitochondrial OS=Arabidopsis thaliana GN=MTACP2 PE=1 SV=1	1	1,298	0,001419986	3,3	0,021
P94014 GL21_ARATH Germin-like protein subfamily 2 member 1 OS=Arabidopsis thaliana GN=GLP4 PE=2 SV=2	1	-1,121	0,001449986	3,37	0,021
O65787 C71B6_ARATH Cytochrome P450 71B6 OS=Arabidopsis thaliana GN=CYP71B6 PE=2 SV=1	2	-0,939	0,001399986	3,25	0,021
Q8L7C9 GSTUK_ARATH Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1	3	0,829	0,001369986	3,18	0,021
Q9SG80 ASD1_ARATH Alpha-L-arabinofuranosidase 1 OS=Arabidopsis thaliana GN=ASD1 PE=1 SV=1	6	-0,621	0,001539985	3,58	0,022
Q94B38 GPT2_ARATH Glucose-6-phosphate/phosphate translocator 2, chloroplastic OS=Arabidopsis thaliana GN=GPT2 PE=2 SV=2	1	-1,454	0,001579984	3,67	0,023
Q9SE83 DRP2A_ARATH Dynamin-2A OS=Arabidopsis thaliana GN=DRP2A PE=1 SV=2	1	-1,383	0,001639984	3,81	0,023
Q9SDM9 JAL28_ARATH Nitrile-specifier protein 1 OS=Arabidopsis thaliana GN=NSP1 PE=1 SV=2	9	-0,782	9,9999E-06	0,02	0,023
P94111 SSL12_ARATH Protein STRICTOSIDINE SYNTHASE-LIKE 12 OS=Arabidopsis thaliana GN=SSL12 PE=2 SV=2	4	-0,717	0,001579984	3,67	0,023
P43082 HEVL_ARATH Hevein-like preproprotein OS=Arabidopsis thaliana GN=HEL PE=1 SV=1	5	0,672	0,001629984	3,78	0,023
A0A1P8AVY3 A0A1P8AVY3_ARATH Triacylglycerol lipase-like 1 OS=Arabidopsis thaliana GN=TLL1 PE=4 SV=1	6	-0,62	0,001699983	3,95	0,023
O80950 JAL22_ARATH Jacalin-related lectin 22 OS=Arabidopsis thaliana GN=JAL22 PE=1 SV=1	15	-0,499	0,001569984	3,65	0,023
Q9MA62 RLF22_ARATH Protein RALF-like 22 OS=Arabidopsis thaliana GN=RALFL22 PE=3 SV=1	1	1,387	0,001739983	4,04	0,024
O24658 CHI59_ARATH Endochitinase At2g43590 OS=Arabidopsis thaliana GN=At2g43590 PE=2 SV=1	1	1,383	0,001779982	4,13	0,024
Q9C827 COB22_ARATH Coatomer subunit beta'-2 OS=Arabidopsis thaliana GN=At1g52360 PE=1 SV=1	3	0,843	0,001759982	4,09	0,024
O23392 O23392_ARATH HSR201-like protein OS=Arabidopsis thaliana GN=dl3740c PE=2 SV=1	7	0,56	0,001719983	3,99	0,024
Q56WD9 THIK2_ARATH 3-ketoacyl-CoA thiolase 2, peroxisomal OS=Arabidopsis thaliana GN=PED1 PE=1 SV=2	14	-0,539	0,001689983	3,92	0,024
O23044 PER3_ARATH Peroxidase 3 OS=Arabidopsis thaliana GN=PER3 PE=2 SV=1	11	-0,539	0,001699983	3,95	0,024
Q9S757 CYSC1_ARATH Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial OS=Arabidopsis thaliana GN=CYSC1 PE=1 SV=1	11	0,52	0,001829982	4,25	0,025
Q9ZVQ3 GSTZ1_ARATH Glutathione S-transferase Z1 OS=Arabidopsis thaliana GN=GSTZ1 PE=1 SV=1	4	-0,639	0,001959576	4,55	0,026
Q9ZW34 ENO3_ARATH Cytosolic enolase 3 OS=Arabidopsis thaliana GN=ENO3 PE=1 SV=1	1	2,122	0,002098878	4,87	0,027
Q8L637 Q8L637_ARATH Pyridoxamine 5'-phosphate oxidase family protein OS=Arabidopsis thaliana GN=At3g21140 PE=2 SV=1	1	-2,089	0,002076064	4,82	0,027
Q8GX62 Q8GX62_ARATH At5g19920 OS=Arabidopsis thaliana GN=At5g19920 PE=2 SV=1	1	-1,437	0,002076064	4,82	0,027
P46010 NRL3_ARATH Nitrilase 3 OS=Arabidopsis thaliana GN=NIT3 PE=1 SV=1	4	-0,776	0,002065195	4,8	0,027
Q8L7E3 VSR7_ARATH Vacuolar-sorting receptor 7 OS=Arabidopsis thaliana GN=VSR7 PE=2 SV=2	4	-0,744	0,00205317	4,77	0,027
P93004 PIP27_ARATH Aquaporin PIP2-7 OS=Arabidopsis thaliana GN=PIP2-7 PE=1 SV=2	1	-1,953	0,00217043	5,04	0,028
Q9SQR4 ADRC3_ARATH NADPH-dependent aldehyde reductase-like protein, chloroplastic OS=Arabidopsis thaliana GN=At3g03980 PE=3 SV=1	1	-1,167	0,002195377	5,1	0,028
Q9LFR0 GMAN2_ARATH Alpha-mannosidase 2 OS=Arabidopsis thaliana GN=GMII PE=1 SV=1	1	-2,042	0,002289129	5,32	0,029
O23267 O23267_ARATH At4g14060/dl3070w OS=Arabidopsis thaliana GN=dl3070w PE=2 SV=1	1	-1,117	0,002270562	5,27	0,029
Q9MAT3 Q9MAT3_ARATH F13M7.16 protein OS=Arabidopsis thaliana GN=At1g04850 PE=2 SV=1	2	-1	0,002317045	5,38	0,029
Q9ZVA4 EP1L3_ARATH EP1-like glycoprotein 3 OS=Arabidopsis thaliana GN=At1g78850 PE=1 SV=1	7	-0,552	0,002289129	5,32	0,029
Q67YN2 Q67YN2_ARATH GTPase activator protein of Rab-like small GTPases-like protein OS=Arabidopsis thaliana GN=MJC20.4 PE=2 SV=1	1	-2,047	0,00239997	5,57	0,03
A0A1P8B128 A0A1P8B128_ARATH SKU5 similar 16 OS=Arabidopsis thaliana GN=sk516 PE=4 SV=1	1	-1,299	0,002435866	5,66	0,03
Q9LKU3 Q9LKU3_ARATH Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=T32B20.g PE=4 SV=1	1	-1,356	0,002526283	5,87	0,031
Q93208 E136_ARATH Glucan endo-1,3-beta-glucosidase 6 OS=Arabidopsis thaliana GN=At5g58090 PE=1 SV=2	2	-0,934	0,002782568	6,46	0,034
P43286 PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1	2	-1,014	0,002911722	6,76	0,035
O49499 CAMT4_ARATH Caffeoyl-CoA O-methyltransferase 1 OS=Arabidopsis thaliana GN=CCOAOMT1 PE=1 SV=1	12	0,509	0,002924198	6,79	0,035
Q9SIU0 MAO1_ARATH NAD-dependent malic enzyme 1, mitochondrial OS=Arabidopsis thaliana GN=NAD-ME1 PE=1 SV=1	4	-0,797	0,003031203	7,04	0,036
Q8LPS9 Q8LPS9_ARATH At5g66920/MUD21_18 OS=Arabidopsis thaliana GN=sk517 PE=2 SV=1	3	-0,783	0,003047571	7,08	0,036
P31168 COR47_ARATH Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2	3	-0,712	0,003128982	7,27	0,037
Q39192 SRK2D_ARATH Serine/threonine-protein kinase SRK2D OS=Arabidopsis thaliana GN=SRK2D PE=1 SV=1	2	-0,941	0,003199947	7,43	0,038
Q9LF79 ACA8_ARATH Calcium-transporting ATPase 8, plasma membrane-type OS=Arabidopsis thaliana GN=ACA8 PE=1 SV=1	7	-0,549	0,003249946	7,55	0,038
Q9FMD7 Y5659_ARATH Probable inactive receptor kinase At5g16590 OS=Arabidopsis thaliana GN=At5g16590 PE=1 SV=1	2	-0,94	0,003392797	7,88	0,039
Q9LHA8 MD37C_ARATH Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1	6	-0,613	0,003368362	7,82	0,039
Q9SVQ9 Q9SVQ9_ARATH At4g13180/F17N18_70 OS=Arabidopsis thaliana GN=At4g13180 PE=1 SV=1	7	-0,578	0,003310288	7,69	0,039

Q8S8M9 ALFL6_ARATH PHD finger protein ALFIN-LIKE 6 OS=Arabidopsis thaliana GN=AL6 PE=1 SV=1	1	1,301	0,003472664	8,06	0,04
Q9ZVF2 ML329_ARATH MLP-like protein 329 OS=Arabidopsis thaliana GN=MLP329 PE=2 SV=1	1	-0,965	0,003745025	8,7	0,043
A0A1P8AWX3 A0A1P8AWX3_ARATH Leucine-rich repeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33590 PE=4 SV=1	9	-0,51	0,003819924	8,87	0,043
O23654 VATA_ARATH V-type proton ATPase catalytic subunit A OS=Arabidopsis thaliana GN=VHA-A PE=1 SV=1	32	-0,398	0,003711467	8,62	0,043
Q9ZSU4 XTH14_ARATH Xyloglucan endotransglucosylase/hydrolase protein 14 OS=Arabidopsis thaliana GN=XTH14 PE=1 SV=1	1	1,857	0,003879922	9,01	0,044
Q570C8 THIK5_ARATH 3-ketoacyl-CoA thiolase 5, peroxisomal OS=Arabidopsis thaliana GN=KAT5 PE=1 SV=2	5	-0,699	0,003879922	9,01	0,044
Q9FFH6 FLA13_ARATH Fasciclin-like arabinogalactan protein 13 OS=Arabidopsis thaliana GN=FLA13 PE=1 SV=1	2	0,941	0,00402075	9,34	0,045
Q0WUR5 FAB1A_ARATH 1-phosphatidylinositol-3-phosphate 5-kinase FAB1A OS=Arabidopsis thaliana GN=FAB1A PE=2 SV=1	1	1,201	0,004085019	9,49	0,046
Q8LEQ0 RLA13_ARATH 60S acidic ribosomal protein P1-3 OS=Arabidopsis thaliana GN=RPP1C PE=1 SV=2	2	0,836	0,004152084	9,64	0,046
Q43729 PER57_ARATH Peroxidase 57 OS=Arabidopsis thaliana GN=PER57 PE=1 SV=1	12	0,45	0,004152084	9,64	0,046
Q9LHB9 PER32_ARATH Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3	9	-0,454	0,004311015	10,01	0,047
Q9SEL6 VTI11_ARATH Vesicle transport v-SNARE 11 OS=Arabidopsis thaliana GN=VTI11 PE=1 SV=2	1	1,218	0,004418502	10,26	0,048
F4JTB3 DTX35_ARATH Protein DETOXIFICATION 35 OS=Arabidopsis thaliana GN=DTX35 PE=1 SV=1	1	-1,207	0,004386264	10,18	0,048
O82230 EBFC2_ARATH Nucleoid-associated protein At2g24020, chloroplastic OS=Arabidopsis thaliana GN=At2g24020 PE=2 SV=2	1	-1,785	0,004651055	10,8	0,05
F4IB68 F4IB68_ARATH Kinase-like protein OS=Arabidopsis thaliana GN=At1g51840 PE=4 SV=2	3	-0,769	0,004658423	10,82	0,05
Q9M9P3 UGPA2_ARATH UTP--glucose-1-phosphate uridylyltransferase 2 OS=Arabidopsis thaliana GN=UGP2 PE=1 SV=1	19	0,414	0,004634033	10,76	0,05
Q41975 TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2	1	-1,606	0,004780371	11,1	0,05
Q9LS94 RAG3F_ARATH Ras-related protein RABG3f OS=Arabidopsis thaliana GN=RABG3F PE=1 SV=1	4	-0,618	0,004774881	11,09	0,051
O04313 JAL31_ARATH PYK10-binding protein 2 OS=Arabidopsis thaliana GN=PBP2 PE=1 SV=1	4	-0,59	0,004731592	10,99	0,051
Q42418 PROF2_ARATH Profilin-2 OS=Arabidopsis thaliana GN=PRO2 PE=2 SV=1	1	1,18	0,004999868	11,61	0,052
F4JTN1 F4JTN1_ARATH Patched family protein OS=Arabidopsis thaliana GN=At4g38350 PE=4 SV=1	4	-0,743	0,00489731	11,37	0,052
Q9FMG0 Q9FMG0_ARATH 2-nitropropane dioxygenase-like protein OS=Arabidopsis thaliana GN=MSJ1.9 PE=1 SV=1	4	-0,689	0,004974231	11,55	0,052
Q9M2D8 Y3126_ARATH Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1	3	-0,769	0,005189049	12,05	0,054
Q9SIJ8 Q9SIJ8_ARATH Adenine nucleotide alpha hydrolases-like superfamily protein OS=Arabidopsis thaliana GN=RD2 PE=1 SV=2	7	-0,55	0,005189049	12,05	0,054
Q8VX13 PDI13_ARATH Protein disulfide isomerase-like 1-3 OS=Arabidopsis thaliana GN=PDIL1-3 PE=2 SV=1	10	0,457	0,005456987	12,67	0,056
Q9SZJ5 GLYM1_ARATH Serine hydroxymethyltransferase 1, mitochondrial OS=Arabidopsis thaliana GN=SHM1 PE=1 SV=1	1	-1,165	0,005542699	12,87	0,057
Q940S3 UAP1_ARATH UDP-N-acetylglucosamine diphosphorylase 1 OS=Arabidopsis thaliana GN=GLCNAC1PUT1 PE=1 SV=1	2	1,008	0,005676304	13,18	0,058
Q9LXV3 DIT1_ARATH Dicarboxylate transporter 1, chloroplastic OS=Arabidopsis thaliana GN=DIT1 PE=1 SV=1	1	-1,236	0,005757401	13,37	0,059
Q9M8T0 Y3288_ARATH Probable inactive receptor kinase At3g02880 OS=Arabidopsis thaliana GN=At3g02880 PE=1 SV=1	9	-0,558	0,005787703	13,44	0,059
Q9FNH6 NHL3_ARATH NDR1/HIN1-like protein 3 OS=Arabidopsis thaliana GN=NHL3 PE=1 SV=1	2	-0,925	0,005937314	13,79	0,06
Q9M1J7 SSL8_ARATH Protein STRICTOSIDINE SYNTHASE-LIKE 8 OS=Arabidopsis thaliana GN=SSL8 PE=2 SV=1	5	-0,628	0,005999813	13,93	0,06
F4IBL0 F4IBL0_ARATH Microsomal glutathione s-transferase OS=Arabidopsis thaliana GN=At1g65820 PE=4 SV=1	2	-0,946	0,006187307	14,37	0,061
Q9SCT5 Q9SCT5_ARATH AT3g51730/T18N14_110 OS=Arabidopsis thaliana GN=T18N14.110 PE=2 SV=1	2	-0,76	0,006124809	14,22	0,061
P11574 VATB1_ARATH V-type proton ATPase subunit B1 OS=Arabidopsis thaliana GN=VHA-B1 PE=2 SV=2	17	-0,399	0,006128835	14,23	0,061
F4IW47 TKTC2_ARATH Transketolase-2, chloroplastic OS=Arabidopsis thaliana GN=TKL-2 PE=1 SV=1	2	-0,797	0,00629012	14,61	0,062
Q1H583 GDL18_ARATH GDSL esterase/lipase 22 OS=Arabidopsis thaliana GN=GLL22 PE=1 SV=1	12	-0,44	0,00629979	14,63	0,062
P46645 AAT2_ARATH Aspartate aminotransferase, cytoplasmic isozyme 1 OS=Arabidopsis thaliana GN=ASP2 PE=1 SV=2	13	0,419	0,00658598	15,29	0,05
F4HYQ1 F4HYQ1_ARATH WAS/WASL-interacting family protein OS=Arabidopsis thaliana GN=At1g55160 PE=4 SV=1	1	-1,141	0,006749759	15,67	0,066
Q9SIL7 FLA6_ARATH Fasciclin-like arabinogalactan protein 6 OS=Arabidopsis thaliana GN=FLA6 PE=2 SV=2	1	1,393	0,006856898	15,92	0,067
Q9LPU5 IGMT1_ARATH Indole glucosinolate O-methyltransferase 1 OS=Arabidopsis thaliana GN=IGMT1 PE=1 SV=1	1	-1,145	0,006892611	16	0,067
Q9SU83 Q9SU83_ARATH Alkaline-phosphatase-like family protein OS=Arabidopsis thaliana GN=At4g29680 PE=2 SV=1	4	-0,598	0,006964037	16,17	0,067
P32826 SCP49_ARATH Serine carboxypeptidase-like 49 OS=Arabidopsis thaliana GN=SCPL49 PE=2 SV=2	5	-0,539	0,006964037	16,17	0,067
Q9LQ4 H2B1_ARATH Histone H2B.1 OS=Arabidopsis thaliana GN=At1g07790 PE=1 SV=3	1	-1,218	0,007110848	16,51	0,068
Q93W34 RP45C_ARATH Polyadenylate-binding protein RBP45C OS=Arabidopsis thaliana GN=RBP45C PE=2 SV=1	2	0,947	0,007147883	16,6	0,068
Q39241 TRXH5_ARATH Thioredoxin H5 OS=Arabidopsis thaliana GN=TRX5 PE=1 SV=1	5	-0,589	0,007221955	16,77	0,068
Q9FJZ9 PER72_ARATH Peroxidase 72 OS=Arabidopsis thaliana GN=PER72 PE=1 SV=1	5	-0,584	0,00725899	16,86	0,068
P34788 RS18_ARATH 40S ribosomal protein S18 OS=Arabidopsis thaliana GN=RPS18A PE=1 SV=1	6	0,496	0,007345871	17,06	0,068
P46644 AAT3_ARATH Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1	8	-0,493	0,007307411	16,97	0,068
Q9SIL8 METK3_ARATH S-adenosylmethionine synthase 3 OS=Arabidopsis thaliana GN=METK3 PE=1 SV=1	10	0,435	0,007110848	16,51	0,049
Q43314 DHE1_ARATH Glutamate dehydrogenase 1 OS=Arabidopsis thaliana GN=GDH1 PE=2 SV=1	2	-0,74	0,007559698	17,55	0,069
P57691 RLA03_ARATH 60S acidic ribosomal protein P0-3 OS=Arabidopsis thaliana GN=RPP0C PE=1 SV=1	8	0,446	0,007461251	17,33	0,069

Q7XA63 Q7XA63_ARATH At5g19860 OS=Arabidopsis thaliana GN=At5g19860 PE=2 SV=1	2	-0,802	0,007559698	17,55	0,07
Q9FMN0 Q9FMN0_ARATH Sterol carrier protein 2 OS=Arabidopsis thaliana GN=SCP2 PE=2 SV=1	4	-0,624	0,007639694	17,74	0,07
Q42533 BCCP1_ARATH Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=BCCP1 PE=1 SV=2	4	-0,591	0,007719691	17,93	0,07
P28186 RAE1C_ARATH Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	2	0,872	0,007874672	18,28	0,071
Q9FE06 EXOL2_ARATH Protein EXORDIUM-like 2 OS=Arabidopsis thaliana GN=EXL2 PE=2 SV=1	1	-0,932	0,007999667	18,58	0,072
Q9FK25 OMT1_ARATH Flavone 3'-O-methyltransferase 1 OS=Arabidopsis thaliana GN=OMT1 PE=1 SV=1	16	0,407	0,007919683	18,39	0,072
Q9SRZ4 PRX2C_ARATH Peroxiredoxin-2C OS=Arabidopsis thaliana GN=PRXIIC PE=1 SV=1	2	-0,862	0,008166326	18,96	0,073
Q8VYI3 ECH2_ARATH Enoyl-CoA hydratase 2, peroxisomal OS=Arabidopsis thaliana GN=ECH2 PE=1 SV=1	1	-1,164	0,008374651	19,45	0,075
Q9SGY2 ACLA1_ARATH ATP-citrate synthase alpha chain protein 1 OS=Arabidopsis thaliana GN=ACLA-1 PE=1 SV=1	5	0,598	0,008434416	19,58	0,05
Q7Y175 PUX5_ARATH Plant UBX domain-containing protein 5 OS=Arabidopsis thaliana GN=PUX5 PE=1 SV=1	1	-1,179	0,008695274	20,19	0,076
Q9SY97 LHCA3_ARATH Photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic OS=Arabidopsis thaliana GN=LHCA3 PE=1 SV=1	2	0,941	0,008521369	19,79	0,076
P49690 RL23_ARATH 60S ribosomal protein L23 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=3	10	0,427	0,008590519	19,95	0,076
P32962 NRL2_ARATH Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1	1	-1,03	0,008999571	20,9	0,078
Q9LHB9 PER32_ARATH Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3	3	-0,613	0,008999571	20,9	0,078
Q8W4S4 VHAA3_ARATH V-type proton ATPase subunit a3 OS=Arabidopsis thaliana GN=VHA-a3 PE=1 SV=1	6	-0,552	0,008954138	20,79	0,078
O80576 O80576_ARATH At2g44060 OS=Arabidopsis thaliana GN=late embryogenesis abundant 26 PE=2 SV=1	14	0,416	0,008908686	20,69	0,078
O48788 Y2267_ARATH Probable inactive receptor kinase At2g26730 OS=Arabidopsis thaliana GN=At2g26730 PE=1 SV=1	1	-1,161	0,009142422	21,23	0,079
O49195 VSP1_ARATH Vegetative storage protein 1 OS=Arabidopsis thaliana GN=VSP1 PE=1 SV=2	4	-0,612	0,009237655	21,45	0,079
Q9LSY7 PER30_ARATH Peroxidase 30 OS=Arabidopsis thaliana GN=PER30 PE=1 SV=1	7	-0,467	0,009237655	21,45	0,079
Q9M0F4 Q9M0F4_ARATH Acid phosphatase-like protein OS=Arabidopsis thaliana GN=At4g29270 PE=2 SV=1	3	-0,66	0,009499525	22,06	0,081
Q9LVM1 AB25B_ARATH ABC transporter B family member 25, mitochondrial OS=Arabidopsis thaliana GN=ABCB25 PE=1 SV=1	1	-1,672	0,00979951	22,75	0,083
P24806 XTH24_ARATH Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2	2	-0,884	0,009949503	23,1	0,084
Q5XEP2 HSOP2_ARATH Hsp70-Hsp90 organizing protein 2 OS=Arabidopsis thaliana GN=HOP2 PE=1 SV=1	2	-0,746	0,009946845	23,1	0,084
Q8GW48 Q8GW48_ARATH At4g15810 OS=Arabidopsis thaliana GN=HSBP PE=2 SV=1	2	0,742	0,009999474	23,22	0,084
Q9FH82 PAE11_ARATH Pectin acetylesterase 11 OS=Arabidopsis thaliana GN=PAE11 PE=2 SV=1	4	0,598	0,009899505	22,99	0,084
Q9LIN0 Q9LIN0_ARATH Major latex protein, putative OS=Arabidopsis thaliana GN=At3g26450 PE=1 SV=1	3	-0,717	0,01015736	23,59	0,085
P42798 R15A1_ARATH 40S ribosomal protein S15a-1 OS=Arabidopsis thaliana GN=RPS15AA PE=2 SV=2	6	0,469	0,010262618	23,83	0,085
F4JL11 IMPA2_ARATH Importin subunit alpha-2 OS=Arabidopsis thaliana GN=IMPA2 PE=1 SV=1	3	-0,963	0,010525762	24,44	0,086
P23686 METK1_ARATH S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2	1	0,902	0,010420504	24,2	0,086
O80837 REMO_ARATH Remorin OS=Arabidopsis thaliana GN=DBP PE=1 SV=1	3	-0,752	0,010420504	24,2	0,086
Q56WK6 PATL1_ARATH Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2	2	-0,645	0,010420504	24,2	0,086
Q9FKK7 XYLA_ARATH Xylose isomerase OS=Arabidopsis thaliana GN=XYLA PE=2 SV=2	10	-0,435	0,010499417	24,38	0,086
O80925 AGD7_ARATH ADP-ribosylation factor GTPase-activating protein AGD7 OS=Arabidopsis thaliana GN=AGD7 PE=1 SV=1	1	1,687	0,010777179	25,02	0,087
Q9FF87 Q9FF87_ARATH reversed Mitochondrial transcription termination factor family protein OS=Arabidopsis thaliana GN=MRO11.3 PE=1 SV=1	1	-1,603	0,010666074	24,77	0,087
P51430 RS62_ARATH 40S ribosomal protein S6-2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=3	3	0,631	0,010721627	24,9	0,087
Q9LFY3 Q9LFY3_ARATH At1g27030/T7N9_9 OS=Arabidopsis thaliana GN=At1g27030 PE=2 SV=1	5	-0,539	0,010999389	25,54	0,089
F4JVN6 TPPII_ARATH Tripeptidyl-peptidase 2 OS=Arabidopsis thaliana GN=TPP2 PE=1 SV=1	27	-0,358	0,011587554	26,91	0,092
Q06588 ACCO4_ARATH 1-aminocyclopropane-1-carboxylate oxidase 4 OS=Arabidopsis thaliana GN=ACO4 PE=1 SV=2	1	1,114	0,011587554	26,91	0,093
Q9LJR2 LECT2_ARATH Lectin-like protein LEC OS=Arabidopsis thaliana GN=LEC PE=1 SV=1	1	1,083	0,011587554	26,91	0,093
Q570Y6 ADF8_ARATH Actin-depolymerizing factor 8 OS=Arabidopsis thaliana GN=ADF8 PE=2 SV=2	1	1,028	0,011705194	27,18	0,093
Q9C829 NU50A_ARATH Nuclear pore complex protein NUP50A OS=Arabidopsis thaliana GN=NUP50A PE=1 SV=1	1	-1,14	0,011881654	27,59	0,094
Q8W491 U73B3_ARATH UDP-glycosyltransferase 73B3 OS=Arabidopsis thaliana GN=UGT73B3 PE=2 SV=1	2	-0,76	0,011999294	27,86	0,095
P48578 PP2A4_ARATH Serine/threonine-protein phosphatase PP2A-4 catalytic subunit OS=Arabidopsis thaliana GN=PP2A4 PE=1 SV=1	1	1,089	0,012732485	29,56	0,1
Q42580 PER21_ARATH Peroxidase 21 OS=Arabidopsis thaliana GN=PER21 PE=1 SV=1	5	-0,654	0,012732485	29,56	0,1
Q9M156 U72B1_ARATH UDP-glycosyltransferase 72B1 OS=Arabidopsis thaliana GN=UGT72B1 PE=1 SV=1	1	-1,109	0,012932471	30,03	0,101
A0A1I9LQ94 A0A1I9LQ94_ARATH PAR1 protein OS=Arabidopsis thaliana GN=At3g54040 PE=4 SV=1	1	-1,087	0,013132458	30,49	0,102
P46645 AAT2_ARATH Aspartate aminotransferase, cytoplasmic isozyme 1 OS=Arabidopsis thaliana GN=ASP2 PE=1 SV=2	1	0,852	0,013265782	30,8	0,102
A0A1P8BA53 A0A1P8BA53_ARATH TRAF-like family protein OS=Arabidopsis thaliana GN=At5g26280 PE=4 SV=1	2	-0,84	0,013132458	30,49	0,102
P49201 RS232_ARATH 40S ribosomal protein S23-2 OS=Arabidopsis thaliana GN=RPS23B PE=2 SV=2	3	0,553	0,013132458	30,49	0,102
P23321 PSBO1_ARATH Oxygen-evolving enhancer protein 1-1, chloroplastic OS=Arabidopsis thaliana GN=PSBO1 PE=1 SV=2	1	-1,105	0,013465769	31,27	0,104
Q9C8X4 Q9C8X4_ARATH reversed GrpE protein homolog OS=Arabidopsis thaliana GN=At1g36390 PE=2 SV=1	1	-1,005	0,013713306	31,84	0,105

Q9SUR3 RTNLA_ARATH Reticulon-like protein B1 OS=Arabidopsis thaliana GN=RTNLB1 PE=1 SV=1	1	1,083	0,013856153	32,17	0,106
Q29Q26 AKR2B_ARATH Ankyrin repeat domain-containing protein 2B OS=Arabidopsis thaliana GN=AKR2B PE=1 SV=1	1	0,946	0,013999	32,51	0,107
P18612 KIN1_ARATH Stress-induced protein KIN1 OS=Arabidopsis thaliana GN=KIN1 PE=2 SV=1	2	-0,741	0,014070424	32,67	0,107
Q9M9R9 NDB3B_ARATH NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B OS=Arabidopsis thaliana GN=At1g14450 PE=3 SV=1	1	1,505	0,01421327	33	0,108
A0A1P8B8B4 A0A1P8B8B4_ARATH reversed TolB protein-like protein OS=Arabidopsis thaliana GN=At4g01870 PE=4 SV=1	1	-1,101	0,014460426	33,58	0,108
Q8GWE1 UCH3_ARATH Ubiquitin carboxyl-terminal hydrolase 3 OS=Arabidopsis thaliana GN=UCH3 PE=2 SV=1	1	-1,056	0,014570388	33,83	0,108
Q39152 FACR1_ARATH reversed Fatty acyl-CoA reductase 1 OS=Arabidopsis thaliana GN=FAR1 PE=1 SV=1	1	-1,05	0,01461426	33,93	0,108
Q9T052 PLDG3_ARATH Phospholipase D gamma 3 OS=Arabidopsis thaliana GN=PLDGAMMA3 PE=1 SV=1	1	-0,91	0,014284694	33,17	0,108
P32962 NRL2_ARATH Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1	3	-0,809	0,014460426	33,58	0,108
F4IN63 F4IN63_ARATH Oxidoreductase, 2OG-Fe(II) oxygenase family protein OS=Arabidopsis thaliana GN=At2g48080 PE=4 SV=1	1	-0,79	0,014427541	33,5	0,108
F4K1D3 F4K1D3_ARATH Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=MXH1.2 PE=3 SV=1	2	-0,739	0,014921929	34,65	0,108
P42825 DNAJ2_ARATH Chaperone protein dnaJ 2 OS=Arabidopsis thaliana GN=ATJ2 PE=1 SV=2	3	-0,585	0,014498964	33,67	0,108
Q9C5Z3 EIF3E_ARATH Eukaryotic translation initiation factor 3 subunit E OS=Arabidopsis thaliana GN=TIF3E1 PE=1 SV=1	8	0,466	0,014356117	33,33	0,108
O64628 TXND9_ARATH Thioredoxin domain-containing protein 9 homolog OS=Arabidopsis thaliana GN=At2g18990 PE=2 SV=1	1	1,57	0,015152681	35,18	0,109
Q84WL9 AP25_ARATH AP-2 complex subunit sigma OS=Arabidopsis thaliana GN=AP17 PE=2 SV=1	1	1,105	0,014845012	34,47	0,109
Q8VZP1 GPP2_ARATH (DL)-glycerol-3-phosphatase 2 OS=Arabidopsis thaliana GN=GPP2 PE=1 SV=1	1	1,083	0,014921929	34,65	0,109
O04209 CLC2_ARATH Clathrin light chain 2 OS=Arabidopsis thaliana GN=CLC2 PE=1 SV=1	2	-0,902	0,014921929	34,65	0,109
Q1H583 GDL18_ARATH GDSL esterase/lipase 22 OS=Arabidopsis thaliana GN=GLL22 PE=1 SV=1	1	-0,73	0,014768095	34,29	0,109
O81493 O81493_ARATH F9D12.8 protein OS=Arabidopsis thaliana GN=F9D12.8 PE=2 SV=1	15	-0,383	0,015075763	35,01	0,109
Q9ZUX4 UMP2_ARATH Uncharacterized protein At2g27730, mitochondrial OS=Arabidopsis thaliana GN=At2g27730 PE=1 SV=1	3	0,537	0,015614184	36,26	0,112
O81862 O81862_ARATH At4g19810 OS=Arabidopsis thaliana GN=Chc1 PE=1 SV=1	6	-0,485	0,015665361	36,37	0,112
F4JKZ9 F4JKZ9_ARATH Uncharacterized protein OS=Arabidopsis thaliana GN=At4g16060 PE=1 SV=1	1	-1,088	0,016081993	37,34	0,113
Q9SRZ4 PRX2C_ARATH Peroxiredoxin-2C OS=Arabidopsis thaliana GN=PRXIIC PE=1 SV=1	2	-0,841	0,01591534	36,96	0,113
P25819 CATA2_ARATH Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3	2	-0,672	0,015998667	37,15	0,113
Q9SUC6 BBE22_ARATH Berberine bridge enzyme-like 22 OS=Arabidopsis thaliana GN=FAD-OXR PE=2 SV=1	6	-0,543	0,015748688	36,57	0,113
Q8VXZ7 AGAL3_ARATH Alpha-galactosidase 3 OS=Arabidopsis thaliana GN=AGAL3 PE=1 SV=1	4	-0,516	0,015832014	36,76	0,113
Q9LIM9 Q9LIM9_ARATH Major latex protein-like OS=Arabidopsis thaliana GN=At3g26460 PE=4 SV=1	4	-0,611	0,016081993	37,34	0,114
F4JTK8 F4JTK8_ARATH Peptidase M20/M25/M40 family protein OS=Arabidopsis thaliana GN=AQI PE=4 SV=1	12	-0,383	0,016248646	37,73	0,114
Q9FIU6 ORRM2_ARATH Organelle RRM domain-containing protein 2, mitochondrial OS=Arabidopsis thaliana GN=ORRM2 PE=1 SV=1	2	-0,874	0,016581952	38,5	0,115
O23267 O23267_ARATH At4g14060/dl3070w OS=Arabidopsis thaliana GN=dl3070w PE=2 SV=1	1	-0,694	0,016498625	38,31	0,115
O04905 KCY3_ARATH UMP-CMP kinase 3 OS=Arabidopsis thaliana GN=UMK3 PE=1 SV=1	4	0,597	0,016498625	38,31	0,115
Q9LSQ5 FQR1_ARATH NAD(P)H dehydrogenase (quinone) FQR1 OS=Arabidopsis thaliana GN=FQR1 PE=1 SV=1	7	-0,463	0,016748604	38,89	0,116
Q9LVJ1 SBT14_ARATH Subtilisin-like protease SBT1.4 OS=Arabidopsis thaliana GN=SBT1.4 PE=2 SV=1	9	-0,443	0,016915257	39,28	0,117
O04130 SERA2_ARATH D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2	2	0,743	0,017165236	39,86	0,118
O65572 CCD1_ARATH Carotenoid 9,10(9',10')-cleavage dioxygenase 1 OS=Arabidopsis thaliana GN=CCD1 PE=1 SV=2	1	-1,033	0,017331889	40,24	0,119
P93829 PRA1D_ARATH PRA1 family protein D OS=Arabidopsis thaliana GN=PRA1D PE=1 SV=1	1	0,971	0,017362058	40,31	0,119
Q9T043 RL142_ARATH 60S ribosomal protein L14-2 OS=Arabidopsis thaliana GN=RPL14B PE=1 SV=1	5	0,458	0,017271157	40,1	0,119
P48641 GSHRC_ARATH Glutathione reductase, cytosolic OS=Arabidopsis thaliana GN=At3g24170 PE=1 SV=1	10	-0,409	0,01754386	40,74	0,119
Q9XF89 CB5_ARATH Chlorophyll a-b binding protein CP26, chloroplastic OS=Arabidopsis thaliana GN=LHCB5 PE=1 SV=1	1	1,054	0,017816562	41,37	0,121
Q9SUT5 SGT1B_ARATH Protein SGT1 homolog B OS=Arabidopsis thaliana GN=SGT1B PE=1 SV=1	5	-0,511	0,017816562	41,37	0,121
A0A1P8BG25 A0A1P8BG25_ARATH Glycosyl hydrolase family protein OS=Arabidopsis thaliana GN=At5g20950 PE=1 SV=1	6	0,509	0,017998364	41,79	0,121
O22715 AP1M2_ARATH AP-1 complex subunit mu-2 OS=Arabidopsis thaliana GN=AP1M2 PE=1 SV=1	2	0,782	0,018180165	42,21	0,122
Q9FZ76 RL61_ARATH 60S ribosomal protein L6-1 OS=Arabidopsis thaliana GN=RPL6A PE=2 SV=1	5	0,484	0,018089265	42	0,122
Q9CAN8 MBOA2_ARATH Lysophospholipid acyltransferase 2 OS=Arabidopsis thaliana GN=LPLAT2 PE=1 SV=1	1	-1,516	0,018361967	42,64	0,123
Q9FH04 ADHL7_ARATH Alcohol dehydrogenase-like 7 OS=Arabidopsis thaliana GN=At5g42250 PE=2 SV=1	1	-0,951	0,018452868	42,85	0,123
Q43873 PER73_ARATH Peroxidase 73 OS=Arabidopsis thaliana GN=PER73 PE=1 SV=1	3	0,675	0,018452868	42,85	0,123
Q38924 PPA12_ARATH Fe(3+)-Zn(2+) purple acid phosphatase 12 OS=Arabidopsis thaliana GN=PAP12 PE=2 SV=3	1	1,046	0,0189981	44,11	0,125
Q42553 IDI2_ARATH Isopentenyl-diphosphate Delta-isomerase II, chloroplastic OS=Arabidopsis thaliana GN=IPP2 PE=1 SV=1	5	0,466	0,01889811	43,88	0,125
P42794 RL112_ARATH 60S ribosomal protein L11-2 OS=Arabidopsis thaliana GN=RPL11B PE=2 SV=2	7	0,391	0,01879812	43,65	0,125
Q0WW84 RB47B_ARATH Polyadenylate-binding protein RBP47B OS=Arabidopsis thaliana GN=RBP47B PE=2 SV=1	2	0,826	0,01919808	44,58	0,126
Q9SKZ3 RS122_ARATH 40S ribosomal protein S12-2 OS=Arabidopsis thaliana GN=RPS12C PE=1 SV=1	2	0,597	0,01949805	45,27	0,127

O22842 CHI61_ARATH Endochitinase At2g43610 OS=Arabidopsis thaliana GN=At2g43610 PE=2 SV=1	5	-0,57	0,01929807	44,81	0,127
O48646 GPX6_ARATH Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial OS=Arabidopsis thaliana GN=GPX6 PE=2 SV=2	3	-0,496	0,01939806	45,04	0,127
Q9ZW95 C7352_ARATH reversed Cytokinin hydroxylase OS=Arabidopsis thaliana GN=CYP735A2 PE=1 SV=1	1	-0,963	0,01989801	46,2	0,129
Q38970 ACC1_ARATH Acetyl-CoA carboxylase 1 OS=Arabidopsis thaliana GN=ACC1 PE=1 SV=1	10	-0,405	0,01979802	45,97	0,129
O49597 HMGB5_ARATH High mobility group B protein 5 OS=Arabidopsis thaliana GN=HMGB5 PE=2 SV=1	1	-0,981	0,02009799	46,67	0,13
O22832 STAD7_ARATH Stearoyl-[acyl-carrier-protein] 9-desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1	1	1,487	0,02029797	47,13	0,131
Q9SU81 Q9SU81_ARATH Alkaline-phosphatase-like family protein OS=Arabidopsis thaliana GN=At4g29700 PE=2 SV=1	1	-0,961	0,02049795	47,6	0,131
Q8VZC3 AL121_ARATH Delta-1-pyrroline-5-carboxylate dehydrogenase 12A1, mitochondrial OS=Arabidopsis thaliana GN=ALDH12A1 PE=2 SV=1	5	-0,493	0,02059794	47,83	0,131
O80725 AB4B_ARATH ABC transporter B family member 4 OS=Arabidopsis thaliana GN=ABCB4 PE=1 SV=1	11	-0,42	0,02039796	47,36	0,131
Q9LX13 Q9LX13_ARATH (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-like protein OS=Arabidopsis thaliana GN=At5g10160 PE=2 SV=1	4	-0,474	0,02059794	47,83	0,132
Q96266 GSTF8_ARATH Glutathione S-transferase F8, chloroplastic OS=Arabidopsis thaliana GN=GSTF8 PE=1 SV=3	10	-0,388	0,020997667	48,76	0,133
Q9FKV0 BBE24_ARATH Berberine bridge enzyme-like 24 OS=Arabidopsis thaliana GN=At5g44380 PE=2 SV=1	6	-0,451	0,020997667	48,76	0,134
O04373 ILL4_ARATH IAA-amino acid hydrolase ILR1-like 4 OS=Arabidopsis thaliana GN=ILL4 PE=1 SV=2	1	-0,907	0,021553161	50,05	0,136
Q96510 PER35_ARATH Peroxidase 35 OS=Arabidopsis thaliana GN=PER35 PE=1 SV=1	2	0,665	0,021997556	51,08	0,137
Q9M1J6 SSL9_ARATH Protein STRICTOSIDINE SYNTHASE-LIKE 9 OS=Arabidopsis thaliana GN=SSL9 PE=2 SV=1	4	-0,645	0,021775358	50,56	0,137
Q9STE8 TC753_ARATH Protein TOC75-3, chloroplastic OS=Arabidopsis thaliana GN=TOC75-3 PE=1 SV=1	4	-0,581	0,021775358	50,56	0,137
Q9ZW24 GSTU7_ARATH Glutathione S-transferase U7 OS=Arabidopsis thaliana GN=GSTU7 PE=2 SV=1	6	-0,492	0,021886457	50,82	0,137
P59223 RS131_ARATH 40S ribosomal protein S13-1 OS=Arabidopsis thaliana GN=RPS13A PE=2 SV=1	6	0,421	0,021775358	50,56	0,137
O23629 H2B6_ARATH Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	1	-0,699	0,022219753	51,59	0,138
Q84M97 MSL9_ARATH Mechanosensitive ion channel protein 9 OS=Arabidopsis thaliana GN=MSL9 PE=1 SV=1	1	-1,445	0,022330852	51,85	0,139
Q9LZ06 GSTL3_ARATH Glutathione S-transferase L3 OS=Arabidopsis thaliana GN=GSTL3 PE=2 SV=1	1	1,056	0,02255305	52,37	0,139
Q8H104 SYDC1_ARATH Aspartate--tRNA ligase 1, cytoplasmic OS=Arabidopsis thaliana GN=At4g26870 PE=2 SV=1	1	-0,942	0,022441951	52,11	0,139
Q8VZS8 PYL1_ARATH Absciscic acid receptor PYL1 OS=Arabidopsis thaliana GN=PYL1 PE=1 SV=1	2	-0,705	0,022886346	53,14	0,141
Q9LMQ2 Q9LMQ2_ARATH Chlorophyll a-b binding protein, chloroplastic OS=Arabidopsis thaliana GN=CHLOROPHYLL PROTEIN 24 PE=1 SV=1	1	-1,016	0,023372078	54,27	0,143
Q9M0F5 Q9M0F5_ARATH Acid phosphatase-like protein OS=Arabidopsis thaliana GN=At4g29260 PE=2 SV=1	2	-0,866	0,023372078	54,27	0,143
Q42064 RL83_ARATH 60S ribosomal protein L8-3 OS=Arabidopsis thaliana GN=RPL8C PE=2 SV=2	2	-0,78	0,023330741	54,17	0,143
Q94CD1 HHT1_ARATH Omega-hydroxypalmitate O-feruloyl transferase OS=Arabidopsis thaliana GN=HHT1 PE=1 SV=1	2	-0,668	0,023497063	54,56	0,143
Q43387 PER71_ARATH Peroxidase 71 OS=Arabidopsis thaliana GN=PER71 PE=1 SV=1	5	-0,499	0,023552939	54,69	0,143
Q8H0S9 PSA_ARATH Puromycin-sensitive aminopeptidase OS=Arabidopsis thaliana GN=MPA1 PE=2 SV=1	6	0,473	0,023552939	54,69	0,143
O23629 H2B6_ARATH Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	1	-0,7	0,023997334	55,72	0,145
Q8LDP4 CP19D_ARATH Peptidyl-prolyl cis-trans isomerase CYP19-4 OS=Arabidopsis thaliana GN=CYP19-4 PE=1 SV=2	3	0,536	0,024246969	56,3	0,146
Q9LNP3 Q9LNP3_ARATH At1g17620/F11A6_23 OS=Arabidopsis thaliana GN=At1g17620 PE=2 SV=1	1	0,989	0,024496938	56,88	0,147
Q8LFL5 Q8LFL5_ARATH reversed At1g49975 OS=Arabidopsis thaliana GN=At1g49975 PE=2 SV=1	1	0,937	0,024621922	57,17	0,147
F4JRE0 TMN12_ARATH Transmembrane 9 superfamily member 12 OS=Arabidopsis thaliana GN=TMN12 PE=2 SV=1	2	0,705	0,024621922	57,17	0,147
Q8L828 COB23_ARATH Coatomer subunit beta'-3 OS=Arabidopsis thaliana GN=At3g15980 PE=2 SV=1	3	0,578	0,024371954	56,59	0,147
Q93VG5 RS81_ARATH 40S ribosomal protein S8-1 OS=Arabidopsis thaliana GN=RPS8A PE=1 SV=1	8	0,387	0,024496938	56,88	0,147
F4I420 F4I420_ARATH Eukaryotic translation initiation factor 2 (eIF-2) family protein OS=Arabidopsis thaliana GN=At1g76810 PE=1 SV=1	1	-0,933	0,02512186	58,33	0,148
F4JFN3 HS906_ARATH Heat shock protein 90-6, mitochondrial OS=Arabidopsis thaliana GN=HSP90-6 PE=2 SV=1	1	0,717	0,024871891	57,75	0,148
P92935 TLC2_ARATH ADP,ATP carrier protein 2, chloroplastic OS=Arabidopsis thaliana GN=AATP2 PE=1 SV=2	4	-0,593	0,025246844	58,62	0,148
Q681Q7 Y1390_ARATH Uncharacterized protein At1g03900 OS=Arabidopsis thaliana GN=At1g03900 PE=2 SV=1	1	1,392	0,02512186	58,33	0,149
Q84TF0 AKRCA_ARATH Aldo-keto reductase family 4 member C10 OS=Arabidopsis thaliana GN=AKR4C10 PE=1 SV=1	1	0,961	0,025496813	59,2	0,149
Q9ZVA2 EP1L2_ARATH EP1-like glycoprotein 2 OS=Arabidopsis thaliana GN=At1g78830 PE=1 SV=1	2	-0,661	0,025246844	58,62	0,149
Q9FHM7 HIR4_ARATH Hypersensitive-induced response protein 4 OS=Arabidopsis thaliana GN=HIR4 PE=1 SV=1	4	-0,567	0,025621797	59,49	0,149
Q84VZ6 Q84VZ6_ARATH At2g31140 OS=Arabidopsis thaliana GN=At2g31140 PE=2 SV=1	1	-1,024	0,025496813	59,2	0,15
Q944B6 TYRA1_ARATH Arogenate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=TYRAAT1 PE=1 SV=1	1	1,417	0,025871766	60,07	0,151
Q8W4E6 HPAT1_ARATH Hydroxyproline O-arabinosyltransferase 1 OS=Arabidopsis thaliana GN=HPAT1 PE=1 SV=1	1	-1,366	0,026246719	60,94	0,152
P31168 COR47_ARATH Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2	1	-0,67	0,026496688	61,53	0,152
P59169 H33_ARATH Histone H3.3 OS=Arabidopsis thaliana GN=HTR4 PE=1 SV=2	2	-0,635	0,026567633	61,69	0,152
Q94AR8 LEUC_ARATH 3-isopropylmalate dehydratase large subunit, chloroplastic OS=Arabidopsis thaliana GN=IIL1 PE=1 SV=1	13	0,354	0,026121735	60,65	0,152
F4JNE0 F4JNE0_ARATH Poly(U)-specific endoribonuclease-B protein OS=Arabidopsis thaliana GN=At4g17100 PE=4 SV=1	15	0,347	0,026246719	60,94	0,152
Q9SID0 SCRK1_ARATH Probable fructokinase-1 OS=Arabidopsis thaliana GN=At2g31390 PE=2 SV=1	17	0,331	0,026496688	61,53	0,152

Q2HIM5 MMGT_ARATH Membrane magnesium transporter OS=Arabidopsis thaliana GN=At5g03345 PE=3 SV=1	1	-1,011	0,026496688	61,53	0,153
Q9FIK7 THIC2_ARATH Probable acetyl-CoA acetyltransferase, cytosolic 2 OS=Arabidopsis thaliana GN=At5g47720 PE=2 SV=1	2	-1,037	0,02713898	63,02	0,154
Q9FJS1 Q9FJS1_ARATH Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=MQD22.2	1	-0,961	0,026996143	62,69	0,154
Q05763 DRTS2_ARATH Bifunctional dihydrofolate reductase-thymidylate synthase 2 OS=Arabidopsis thaliana GN=THY-2 PE=2 SV=2	1	-0,96	0,02713898	63,02	0,154
Q82355 LEA2R_ARATH Desiccation-related protein At2g46140 OS=Arabidopsis thaliana GN=At2g46140 PE=1 SV=1	6	0,483	0,027424654	63,68	0,155
P92974 UBE12_ARATH Ubiquitin-activating enzyme E1 2 OS=Arabidopsis thaliana GN=UBA2 PE=1 SV=1	2	0,671	0,027710327	64,34	0,157
F4I448 F4I448_ARATH Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=PRP39 PE=1 SV=1	3	0,633	0,027853164	64,68	0,157
Q9M2F1 RS272_ARATH 40S ribosomal protein S27-2 OS=Arabidopsis thaliana GN=RPS27B PE=2 SV=2	2	0,585	0,027996001	65,01	0,157
Q8LGG0 FKB12_ARATH Peptidyl-prolyl cis-trans isomerase FKBP12 OS=Arabidopsis thaliana GN=FKBP12 PE=1 SV=2	1	1,02	0,028567348	66,33	0,16
P17562 METK2_ARATH S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	3	0,549	0,028710184	66,67	0,161
P0DKL4 S130A_ARATH Spliceosome-associated protein 130 A OS=Arabidopsis thaliana GN=SAP130A PE=2 SV=1	4	-0,546	0,028853021	67	0,161
Q9SGZ5 BXL7_ARATH Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2	6	-0,472	0,028853021	67	0,161
Q9LF68 BOLA4_ARATH Protein BOLA4, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=BOLA4 PE=1 SV=1	1	-0,952	0,029281531	67,99	0,163
Q9SAR5 AKR2A_ARATH Ankyrin repeat domain-containing protein 2A OS=Arabidopsis thaliana GN=AKR2A PE=1 SV=2	1	0,888	0,029567205	68,66	0,163
Q944S8 Q944S8_ARATH At4g21108/At4g21108 OS=Arabidopsis thaliana GN=At4g21105 PE=2 SV=1	1	0,887	0,029424368	68,32	0,163
P27323 HS901_ARATH Heat shock protein 90-1 OS=Arabidopsis thaliana GN=HSP90-1 PE=1 SV=3	2	-0,676	0,029424368	68,32	0,163
Q9LE06 BCAT4_ARATH Methionine aminotransferase BCAT4 OS=Arabidopsis thaliana GN=BCAT4 PE=1 SV=1	4	0,561	0,029567205	68,66	0,163
Q9XI05 PSB3A_ARATH Proteasome subunit beta type-3-A OS=Arabidopsis thaliana GN=PBC1 PE=1 SV=2	4	-0,555	0,029852878	69,32	0,163
Q9FNN1 Q9FNN1_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=MAH20.13 PE=2 SV=1	1	1,309	0,029852878	69,32	0,164
O65202 ACOX1_ARATH Peroxisomal acyl-coenzyme A oxidase 1 OS=Arabidopsis thaliana GN=ACX1 PE=1 SV=1	12	-0,349	0,030138552	69,98	0,165
Q96330 FLS1_ARATH Flavonol synthase/flavanone 3-hydroxylase OS=Arabidopsis thaliana GN=FLS1 PE=1 SV=1	3	-0,593	0,030567062	70,98	0,166
P46644 AAT3_ARATH Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1	2	0,553	0,030424225	70,65	0,166
O80565 OEP37_ARATH Outer envelope pore protein 37, chloroplastic OS=Arabidopsis thaliana GN=OEP37 PE=2 SV=2	1	-1,338	0,030994834	71,97	0,167
Q8LB47 MGE2_ARATH GrpE protein homolog 2, mitochondrial OS=Arabidopsis thaliana GN=Mge2 PE=1 SV=1	2	0,697	0,030994834	71,97	0,167
Q8W454 VHAA3_ARATH V-type proton ATPase subunit a3 OS=Arabidopsis thaliana GN=VHA-a3 PE=1 SV=1	10	-0,396	0,030852735	71,64	0,167
F4JYH0 F4JYH0_ARATH Transmembrane protein OS=Arabidopsis thaliana GN=MBK23.19 PE=4 SV=1	1	0,987	0,031328112	72,74	0,168
Q9LEZ4 MBP2C_ARATH reversed Protein MICROTUBULE BINDING PROTEIN 2C OS=Arabidopsis thaliana GN=MBP2C PE=1 SV=1	1	-0,851	0,030994834	71,97	0,168
Q9T017 DIR13_ARATH Dirigent protein 13 OS=Arabidopsis thaliana GN=DIR13 PE=2 SV=1	3	-0,603	0,031328112	72,74	0,168
P31169 KIN2_ARATH Stress-induced protein KIN2 OS=Arabidopsis thaliana GN=KIN2 PE=2 SV=1	2	-0,572	0,031828029	73,9	0,168
Q9FMT1 LEU33_ARATH 3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMDH3 PE=1 SV=1	4	0,558	0,031994668	74,29	0,168
O22941 IDE1_ARATH Insulin-degrading enzyme-like 1, peroxisomal OS=Arabidopsis thaliana GN=PX16 PE=2 SV=1	4	-0,522	0,031828029	73,9	0,168
Q940S0 TMN2_ARATH Transmembrane 9 superfamily member 2 OS=Arabidopsis thaliana GN=TMN2 PE=2 SV=1	4	0,5	0,031494751	73,13	0,168
Q9ZS51 PMP22_ARATH Peroxisomal membrane protein PMP22 OS=Arabidopsis thaliana GN=PMP22 PE=1 SV=1	1	-1,353	0,032161306	74,68	0,169
Q9LZS7 GDL71_ARATH GDSL esterase/lipase At5g03610 OS=Arabidopsis thaliana GN=At5g03610 PE=2 SV=1	1	-0,905	0,032161306	74,68	0,169
Q9LEV2 Q9LEV2_ARATH reversed Uncharacterized protein T30N20_150 OS=Arabidopsis thaliana GN=At5g10880 PE=4 SV=1	1	0,742	0,032994501	76,61	0,169
Q9ZW30 GSTU1_ARATH Glutathione S-transferase U1 OS=Arabidopsis thaliana GN=GSTU1 PE=2 SV=1	4	-0,622	0,032994501	76,61	0,169
P46286 RL81_ARATH 60S ribosomal protein L8-1 OS=Arabidopsis thaliana GN=RPL8A PE=1 SV=2	3	0,6	0,031828029	73,9	0,169
Q9SF29 SYP71_ARATH Syntaxin-71 OS=Arabidopsis thaliana GN=SYP71 PE=1 SV=1	4	-0,506	0,03166139	73,52	0,169
P22953 MD37E_ARATH Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	7	0,421	0,031494751	73,13	0,169
Q9MAX3 SUT12_ARATH Sulfate transporter 1.2 OS=Arabidopsis thaliana GN=SULTR1;2 PE=1 SV=1	1	-1,318	0,032661223	75,84	0,17
Q9FVE6 HDT1_ARATH Histone deacetylase HDT1 OS=Arabidopsis thaliana GN=HDT1 PE=1 SV=1	1	-0,963	0,033994334	78,93	0,17
Q80845 PX11D_ARATH Peroxisomal membrane protein 11D OS=Arabidopsis thaliana GN=PEX11D PE=1 SV=2	1	-0,866	0,03466089	80,48	0,17
P54967 BIOB_ARATH Biotin synthase, mitochondrial OS=Arabidopsis thaliana GN=BIO2 PE=1 SV=1	1	-0,854	0,032494584	75,45	0,17
Q9ZQ80 NDRP1_ARATH Nodulin-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=1 SV=1	2	-0,727	0,033994334	78,93	0,17
Q9LNI3 APF2_ARATH Aspartyl protease family protein 2 OS=Arabidopsis thaliana GN=APF2 PE=2 SV=1	2	-0,683	0,033327779	77,39	0,17
Q93XM7 MCAT_ARATH Mitochondrial carnitine/acylcarnitine carrier-like protein OS=Arabidopsis thaliana GN=BOU PE=1 SV=1	2	0,651	0,032994501	76,61	0,17
Q80626 RL352_ARATH 60S ribosomal protein L35-2 OS=Arabidopsis thaliana GN=RPL35B PE=2 SV=1	2	0,555	0,03316114	77	0,17
Q9SVN5 SYMC_ARATH Methionine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At4g13780 PE=2 SV=1	3	-0,537	0,033827695	78,55	0,17
Q9M2E2 SDR1_ARATH (+)-neomenthol dehydrogenase OS=Arabidopsis thaliana GN=SDR1 PE=1 SV=1	4	-0,499	0,032827862	76,23	0,17
Q9LK36 SAHH2_ARATH Adenosylhomocysteinase 2 OS=Arabidopsis thaliana GN=SAHH2 PE=2 SV=1	4	-0,467	0,033327779	77,39	0,17
Q42449 PROF1_ARATH Profilin-1 OS=Arabidopsis thaliana GN=PRO1 PE=1 SV=1	3	0,447	0,032994501	76,61	0,17

Q9FFR3 6PGD2_ARATH 6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV=1	9	-0,361	0,033827695	78,55	0,17
P42761 GSTFA_ARATH Glutathione S-transferase F10 OS=Arabidopsis thaliana GN=GSTF10 PE=1 SV=3	11	0,352	0,033494418	77,77	0,17
Q9FMP4 SF3B6_ARATH Splicing factor 3B subunit 6-like protein OS=Arabidopsis thaliana GN=At5g12190 PE=2 SV=1	1	-1,358	0,032994501	76,61	0,171
Q9M9W8 PLDZ2_ARATH reversed Phospholipase D zeta 2 OS=Arabidopsis thaliana GN=PLPZETA2 PE=1 SV=2	1	-0,916	0,03466089	80,48	0,171
A7WM73 HEXO1_ARATH Beta-hexosaminidase 1 OS=Arabidopsis thaliana GN=HEXO1 PE=1 SV=1	1	-0,792	0,033661056	78,16	0,171
A8MS32 A8MS32_ARATH AT5G64130 protein OS=Arabidopsis thaliana GN=MHJ24.11 PE=1 SV=1	2	0,776	0,033827695	78,55	0,171
Q9C5C8-2 MSRB2_ARATH reversed Isoform 2 of Peptide methionine sulfoxide reductase B2, chloroplastic OS=Arabidopsis thaliana GN=MSRB2	1	-0,73	0,03466089	80,48	0,171
Q9LQU4 PCR2_ARATH Protein PLANT CADMIUM RESISTANCE 2 OS=Arabidopsis thaliana GN=PCR2 PE=1 SV=1	2	-0,627	0,034494251	80,1	0,171
Q9SU81 Q9SU81_ARATH Alkaline-phosphatase-like family protein OS=Arabidopsis thaliana GN=At4g29700 PE=2 SV=1	3	-0,615	0,032827862	76,23	0,171
F4IWW2 F4IWW2_ARATH 2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=At3g55410 PE=1 SV=1	5	0,491	0,034827529	80,87	0,171
P42763 ERD14_ARATH Dehydrin ERD14 OS=Arabidopsis thaliana GN=ERD14 PE=1 SV=1	5	-0,457	0,03466089	80,48	0,171
Q9LUT2 METF4_ARATH S-adenosylmethionine synthase 4 OS=Arabidopsis thaliana GN=METF4 PE=1 SV=1	7	0,367	0,034327612	79,71	0,171
Q9FLT0 TSN2_ARATH Ribonuclease TUDOR 2 OS=Arabidopsis thaliana GN=TSN2 PE=1 SV=1	10	0,361	0,032827862	76,23	0,171
P51427 RS52_ARATH 40S ribosomal protein S5-2 OS=Arabidopsis thaliana GN=RPS5B PE=1 SV=2	9	0,359	0,033827695	78,55	0,171
P0DH91 ARF2B_ARATH ADP-ribosylation factor 2-B OS=Arabidopsis thaliana GN=ARF2-B PE=2 SV=1	9	0,351	0,034327612	79,71	0,171
O49006 PME3_ARATH Pectinesterase/pectinesterase inhibitor 3 OS=Arabidopsis thaliana GN=PME3 PE=1 SV=2	11	-0,35	0,034160973	79,32	0,171
Q38946 DHE2_ARATH Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1	13	-0,335	0,034494251	80,1	0,171
Q8RWC3 Q8RWC3_ARATH Aminopeptidase (DUF3754) OS=Arabidopsis thaliana GN=At3g19340 PE=2 SV=1	1	0,914	0,035327445	82,03	0,172
Q9LIS3 GAE6_ARATH UDP-glucuronate 4-epimerase 6 OS=Arabidopsis thaliana GN=GAE6 PE=1 SV=1	1	0,903	0,035327445	82,03	0,172
Q9LVW7 CARA_ARATH Carbamoyl-phosphate synthase small chain, chloroplastic OS=Arabidopsis thaliana GN=CARA PE=1 SV=1	4	-0,475	0,035327445	82,03	0,172
Q8W108 MTND3_ARATH 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 3 OS=Arabidopsis thaliana GN=ARD3 PE=2 SV=1	5	-0,42	0,035160807	81,64	0,172
Q570Y6 ADF8_ARATH Actin-depolymerizing factor 8 OS=Arabidopsis thaliana GN=ADF8 PE=2 SV=2	1	0,941	0,035994001	83,58	0,174
F4K2J2 F4K2J2_ARATH Auxin-responsive GH3 family protein OS=Arabidopsis thaliana GN=At5g13360 PE=4 SV=1	1	1,282	0,03616064	83,97	0,175
Q9M2U7 Q9M2U7_ARATH AT3g54400/T12E18_90 OS=Arabidopsis thaliana GN=T12E18_90 PE=2 SV=1	6	-0,427	0,036327279	84,35	0,175
Q9LXQ2 Q9LXQ2_ARATH At3g44100 OS=Arabidopsis thaliana GN=F26G5_50 PE=2 SV=1	2	-0,613	0,036992601	85,9	0,178
Q94CD1 HHT1_ARATH Omega-hydroxypalmitate O-feruloyl transferase OS=Arabidopsis thaliana GN=HHT1 PE=1 SV=1	2	-0,592	0,036993834	85,9	0,178
Q8VYN6 PFKA5_ARATH ATP-dependent 6-phosphofructokinase 5, chloroplastic OS=Arabidopsis thaliana GN=PFK5 PE=1 SV=1	3	-0,636	0,037327112	86,67	0,179
Q41932 PSBQ2_ARATH Oxygen-evolving enhancer protein 3-2, chloroplastic OS=Arabidopsis thaliana GN=PSBQ2 PE=1 SV=2	1	1,312	0,037592482	87,29	0,18
O80504 CH102_ARATH 10 kDa chaperonin 2, chloroplastic OS=Arabidopsis thaliana GN=CPN10-2 PE=2 SV=1	2	0,662	0,03766039	87,45	0,18
Q9SVM8 RBG2_ARATH Glycine-rich RNA-binding protein 2, mitochondrial OS=Arabidopsis thaliana GN=RBG2 PE=1 SV=1	5	0,421	0,037792442	87,75	0,18
O23171 MES9_ARATH Methyltransferase 9 OS=Arabidopsis thaliana GN=MES9 PE=1 SV=1	1	-0,895	0,038192362	88,68	0,181
Q39033 PLCD2_ARATH Phosphoinositide phospholipase C 2 OS=Arabidopsis thaliana GN=PLC2 PE=1 SV=1	2	-0,615	0,037992402	88,22	0,181
Q9LPC3 BBE1_ARATH Berberine bridge enzyme-like 1 OS=Arabidopsis thaliana GN=SEC1A PE=2 SV=1	1	-0,875	0,038592282	89,61	0,182
P92985 RBP1C_ARATH Ran-binding protein 1 homolog c OS=Arabidopsis thaliana GN=RANBP1C PE=2 SV=1	1	0,814	0,038592282	89,61	0,182
O22126 FLA8_ARATH Fasciclin-like arabinogalactan protein 8 OS=Arabidopsis thaliana GN=FLA8 PE=1 SV=1	3	-0,543	0,038392322	89,15	0,182
O22797 GLTP1_ARATH Glycolipid transfer protein 1 OS=Arabidopsis thaliana GN=GLTP1 PE=2 SV=1	4	0,522	0,038392322	89,15	0,182
O23144 PPI1_ARATH Proton pump-interactor 1 OS=Arabidopsis thaliana GN=PPI1 PE=1 SV=2	8	0,364	0,038792242	90,08	0,182
Q9SA85 BBE8_ARATH Berberine bridge enzyme-like 8 OS=Arabidopsis thaliana GN=At1g30700 PE=2 SV=1	3	-0,56	0,039392122	91,47	0,184
Q9C9C9 SOT18_ARATH Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1	1	-1,339	0,039592082	91,93	0,185
Q9XGX9 TIM9_ARATH Mitochondrial import inner membrane translocase subunit TIM9 OS=Arabidopsis thaliana GN=TIM9 PE=1 SV=2	2	0,672	0,039592082	91,93	0,185
Q9SRX2 RL191_ARATH 60S ribosomal protein L19-1 OS=Arabidopsis thaliana GN=RPL19A PE=2 SV=1	4	0,448	0,039392122	91,47	0,185
P30184 AMPL1_ARATH Leucine aminopeptidase 1 OS=Arabidopsis thaliana GN=LAP1 PE=1 SV=1	15	-0,324	0,039792042	92,4	0,185
A0A1P8B5A6 A0A1P8B5A6_ARATH Ribosomal protein S24/S35 OS=Arabidopsis thaliana GN=At4g21460 PE=1 SV=1	1	-0,85	0,040191962	93,33	0,186
P49209 RL91_ARATH 60S ribosomal protein L9-1 OS=Arabidopsis thaliana GN=RPL9B PE=1 SV=3	8	0,347	0,039992002	92,86	0,186
Q944A6 SNF4_ARATH Sucrose nonfermenting 4-like protein OS=Arabidopsis thaliana GN=SNF4 PE=1 SV=1	1	-1,292	0,040791842	94,72	0,188
Q9FKA3 Q9FKA3_ARATH TLD-domain containing nucleolar protein OS=Arabidopsis thaliana GN=MIJ24.8 PE=4 SV=1	1	-0,833	0,040991802	95,18	0,188
Q9M329 Q9M329_ARATH At3g53980 OS=Arabidopsis thaliana GN=F5K20_280 PE=2 SV=1	1	-0,888	0,040791842	94,72	0,189
Q9FL54 DNAJ6_ARATH reversed Chaperone protein dnaJ 6 OS=Arabidopsis thaliana GN=ATJ6 PE=2 SV=1	1	0,865	0,040991802	95,18	0,189
Q9FLQ4 ODO2A_ARATH Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1, mitochondrial OS=Ara	2	-0,641	0,041391722	96,11	0,19
O24456 GBLPA_ARATH Receptor for activated C kinase 1A OS=Arabidopsis thaliana GN=RACK1A PE=1 SV=2	13	0,331	0,041391722	96,11	0,19
Q9LN62 RRA3_ARATH Arabinosyltransferase RRA3 OS=Arabidopsis thaliana GN=RRA3 PE=2 SV=1	2	-0,662	0,041991602	97,5	0,192

F4KG14 F4KG14_ARATH Guanylate-binding family protein OS=Arabidopsis thaliana GN=MCL19.12 PE=4 SV=1	3	-0,529	0,041991602	97,5	0,192
Q9LF98 ALFC8_ARATH Fructose-bisphosphate aldolase 8, cytosolic OS=Arabidopsis thaliana GN=FBA8 PE=1 SV=1	12	0,313	0,042191562	97,97	0,192
Q8L7U3 Q8L7U3_ARATH reversed At1g14620/T5E21_15 OS=Arabidopsis thaliana GN=DECOY PE=2 SV=1	1	-0,89	0,042591482	98,9	0,193
Q9LRN8 RK3B_ARATH 50S ribosomal protein L3-2, chloroplastic OS=Arabidopsis thaliana GN=RPL3B PE=2 SV=1	1	0,853	0,042791442	99,36	0,193
Q8VYC9 Q8VYC9_ARATH Coiled-coil protein OS=Arabidopsis thaliana GN=At1g16210 PE=2 SV=1	1	-0,852	0,042591482	98,9	0,193
Q9SH69 6PGD1_ARATH 6-phosphogluconate dehydrogenase, decarboxylating 1, chloroplastic OS=Arabidopsis thaliana GN=At1g64190 PE=1 SV=1	6	-0,414	0,042391522	98,43	0,193
P49209 RL91_ARATH 60S ribosomal protein L9-1 OS=Arabidopsis thaliana GN=RPL9B PE=1 SV=3	4	0,395	0,042791442	99,36	0,193
O50039 OTC_ARATH Ornithine carbamoyltransferase, chloroplastic OS=Arabidopsis thaliana GN=OTC PE=1 SV=2	4	0,487	0,043191362	100,29	0,194
P42643 14331_ARATH 14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	2	-0,523	0,043391322	100,75	0,195
Q0WM29 MMSA_ARATH Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Arabidopsis thaliana GN=ALDH6B2 PE=1 SV=2	6	-0,393	0,043591282	101,22	0,195
Q93ZN5 Q93ZN5_ARATH At4g00090/F6N15_8 OS=Arabidopsis thaliana GN=At4g00090 PE=2 SV=1	1	1,277	0,043791242	101,68	0,196
P41127 RL131_ARATH 60S ribosomal protein L13-1 OS=Arabidopsis thaliana GN=RPL13B PE=1 SV=1	3	0,44	0,044391122	103,08	0,198
O80912 PER23_ARATH Peroxidase 23 OS=Arabidopsis thaliana GN=PER23 PE=2 SV=1	3	-0,537	0,044991002	104,47	0,2
Q9FLH8 SCRK7_ARATH Probable fructokinase-7 OS=Arabidopsis thaliana GN=At5g51830 PE=1 SV=1	1	0,513	0,044791042	104	0,2
Q9CAI1 DRG2_ARATH Developmentally-regulated G-protein 2 OS=Arabidopsis thaliana GN=DRG2 PE=2 SV=1	1	-0,904	0,045790842	106,33	0,203
Q93YP9 ERDL4_ARATH Sugar transporter ERD6-like 4 OS=Arabidopsis thaliana GN=At1g19450 PE=2 SV=1	1	-0,877	0,046488378	107,95	0,203
O81147 PSA6B_ARATH Proteasome subunit alpha type-6-B OS=Arabidopsis thaliana GN=PAA2 PE=1 SV=1	2	-0,762	0,045790842	106,33	0,203
Q9LIA8 UGDH2_ARATH UDP-glucose 6-dehydrogenase 2 OS=Arabidopsis thaliana GN=UGD2 PE=1 SV=1	3	0,707	0,045990802	106,79	0,203
Q8RWT5 Q8RWT5_ARATH AICARFT/IMPCHase bienzyme family protein OS=Arabidopsis thaliana GN=At2g35040 PE=1 SV=1	3	0,63	0,04623844	107,37	0,203
P46644 AAT3_ARATH Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1	2	0,545	0,04623844	107,37	0,203
Q39041 INVA4_ARATH Acid beta-fructofuranosidase 4, vacuolar OS=Arabidopsis thaliana GN=BFRUCT4 PE=1 SV=2	2	-0,525	0,045738565	106,2	0,203
Q9ZW84 LEUD1_ARATH 3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1	5	0,468	0,045988503	106,79	0,203
Q96251 ATPO_ARATH ATP synthase subunit O, mitochondrial OS=Arabidopsis thaliana GN=At5g13450 PE=1 SV=2	8	-0,359	0,046488378	107,95	0,203
Q8GY61 BH063_ARATH reversed Transcription factor bHLH63 OS=Arabidopsis thaliana GN=BHLH63 PE=1 SV=1	1	-1,271	0,046488378	107,95	0,204
Q9CAB7 PXG4_ARATH Probable peroxxygenase 4 OS=Arabidopsis thaliana GN=PXG4 PE=1 SV=1	1	-0,855	0,046988253	109,11	0,204
Q93W03 Q93W03_ARATH AT3g56130/F18O21_90 OS=Arabidopsis thaliana GN=At3g56130 PE=2 SV=1	2	-0,607	0,04723819	109,69	0,204
P41376 IF4A1_ARATH Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	1	0,558	0,046988253	109,11	0,204
Q9FMH8 RD21B_ARATH Probable cysteine protease RD21B OS=Arabidopsis thaliana GN=RD21B PE=1 SV=1	7	-0,355	0,046738315	108,53	0,204
Q9S791 Q9S791_ARATH AT1G70770 protein OS=Arabidopsis thaliana GN=F15H11.2 PE=1 SV=1	12	0,337	0,04723819	109,69	0,205
O23657 RABC1_ARATH Ras-related protein RABC1 OS=Arabidopsis thaliana GN=RABC1 PE=1 SV=1	1	0,812	0,047738065	110,85	0,206
Q9LFD5 BPA1_ARATH Binding partner of ACD11 1 OS=Arabidopsis thaliana GN=BPA1 PE=1 SV=1	2	0,565	0,047738065	110,85	0,206
Q8W4H8 GDL19_ARATH Inactive GDSL esterase/lipase-like protein 23 OS=Arabidopsis thaliana GN=GLL23 PE=1 SV=1	8	-0,343	0,048237941	112,01	0,207
Q8VZG7 TSN1_ARATH Ribonuclease TUDOR 1 OS=Arabidopsis thaliana GN=TSN1 PE=1 SV=1	7	0,354	0,048737816	113,17	0,209
Q9LZX8 BIG2_ARATH Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Arabidopsis thaliana GN=BIG2 PE=2 SV=1	1	1,204	0,049987503	116,07	0,211
Q9ZSD4 SY121_ARATH Syntaxin-121 OS=Arabidopsis thaliana GN=SYP121 PE=1 SV=1	1	0,875	0,050487378	117,23	0,211
O65639 CSP1_ARATH Cold shock protein 1 OS=Arabidopsis thaliana GN=CSP1 PE=1 SV=1	1	-0,835	0,050487378	117,23	0,211
Q9LZM6 Q9LZM6_ARATH At5g02050 OS=Arabidopsis thaliana GN=At5g02050 PE=2 SV=1	1	0,774	0,049737566	115,49	0,211
Q9LF33 UGDH3_ARATH UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1	2	0,588	0,049237691	114,33	0,211
Q9STS1 BADH2_ARATH Betaine aldehyde dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=ALDH10A9 PE=1 SV=1	3	-0,508	0,050237441	116,65	0,211
P46286 RL81_ARATH 60S ribosomal protein L8-1 OS=Arabidopsis thaliana GN=RPL8A PE=1 SV=2	6	0,385	0,049237691	114,33	0,211
Q42547 CATA3_ARATH Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3	7	-0,345	0,049487628	114,91	0,211
Q9FNA9 PDAT1_ARATH Phospholipid:diacylglycerol acyltransferase 1 OS=Arabidopsis thaliana GN=PDAT1 PE=2 SV=1	1	0,859	0,050487378	117,23	0,212
F4J4N3 DIR17_ARATH Dirigent protein 17 OS=Arabidopsis thaliana GN=DIR17 PE=2 SV=1	1	-0,836	0,050487378	117,23	0,212
Q8W4D0 CPY71_ARATH Peptidyl-prolyl cis-trans isomerase CYP71 OS=Arabidopsis thaliana GN=CYP71 PE=1 SV=1	1	-0,824	0,049987503	116,07	0,212
Q9SIV0 SUR1_ARATH S-alkyl-thiohydroximate lyase SUR1 OS=Arabidopsis thaliana GN=SUR1 PE=1 SV=1	4	0,526	0,050237441	116,65	0,212
P59232 R27AB_ARATH Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=2 SV=2	2	0,509	0,050737316	117,81	0,212
Q9ZPI1 SYK_ARATH Lysine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At3g11710 PE=1 SV=1	6	0,402	0,050237441	116,65	0,212
Q949Y3 PPA26_ARATH Bifunctional purple acid phosphatase 26 OS=Arabidopsis thaliana GN=PAP26 PE=1 SV=1	7	-0,382	0,049737566	115,49	0,212
Q9ASR1 EF2_ARATH Elongation factor 2 OS=Arabidopsis thaliana GN=LOS1 PE=1 SV=1	25	0,276	0,049737566	115,49	0,212
Q9LFF6 H2B8_ARATH Histone H2B.8 OS=Arabidopsis thaliana GN=At3g53650 PE=1 SV=3	1	0,753	0,051737066	120,13	0,215
Q3EAF8 PP294_ARATH reversed Pentatricopeptide repeat-containing protein At3g62540, mitochondrial OS=Arabidopsis thaliana GN=At3g62540 PE=2 SV=1	1	-1,23	0,051987003	120,71	0,216

P25819 CATA2_ARATH Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3	5	-0,381	0,052236941	121,29	0,216
Q94CC6 Q94CC6_ARATH Prolyl carboxypeptidase like protein OS=Arabidopsis thaliana GN=At4g36195 PE=2 SV=1	5	-0,457	0,052736816	122,45	0,217
P49692 RL7A1_ARATH 60S ribosomal protein L7a-1 OS=Arabidopsis thaliana GN=RPL7AA PE=2 SV=2	8	0,347	0,052236941	121,29	0,217
Q9LG23 PPR82_ARATH Pentatricopeptide repeat-containing protein At1g55890, mitochondrial OS=Arabidopsis thaliana GN=At1g55890 PE=1 SV=1	2	-0,689	0,052736816	122,45	0,218
F4J7G5 F4J7G5_ARATH MD-2-related lipid recognition domain-containing protein / ML domain-containing protein OS=Arabidopsis thaliana GN=At3g117	2	-0,506	0,052736816	122,45	0,218
Q9C835 CP21D_ARATH Peptidyl-prolyl cis-trans isomerase CYP21-4 OS=Arabidopsis thaliana GN=CYP21-4 PE=2 SV=1	2	-0,624	0,053986503	125,36	0,221
P42036 RS143_ARATH 40S ribosomal protein S14-3 OS=Arabidopsis thaliana GN=RPS14C PE=2 SV=2	2	0,564	0,053986503	125,36	0,221
P11574 VATB1_ARATH V-type proton ATPase subunit B1 OS=Arabidopsis thaliana GN=VHA-B1 PE=2 SV=2	3	-0,462	0,053736566	124,78	0,221
Q9ZJW3 U85A2_ARATH UDP-glycosyltransferase 85A2 OS=Arabidopsis thaliana GN=UGT85A2 PE=2 SV=1	1	-0,876	0,054486378	126,52	0,222
A0A1P8BG17 A0A1P8BG17_ARATH Phosphoglucosamine mutase family protein OS=Arabidopsis thaliana GN=At5g17530 PE=4 SV=1	3	-0,554	0,054486378	126,52	0,222
O48549 RS61_ARATH 40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2	4	0,383	0,054236441	125,94	0,222
Q9SK84 Q9SK84_ARATH Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Arabidopsis thaliana GN=At1g22410 PE=3 SV=1	7	0,363	0,055236191	128,26	0,225
Q9SCZ4 FERON_ARATH Receptor-like protein kinase FERONIA OS=Arabidopsis thaliana GN=FER PE=1 SV=1	1	-0,81	0,055736066	129,42	0,226
Q42599 NDS8A_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial OS=Arabidopsis thaliana GN=At1g79010 PE=1 SV=1	1	-0,717	0,056235941	130,58	0,227
B9DFI7 PMT2_ARATH Probable methyltransferase PMT2 OS=Arabidopsis thaliana GN=At1g26850 PE=2 SV=2	2	0,626	0,056235941	130,58	0,227
Q94BT2 AIR12_ARATH Auxin-induced in root cultures protein 12 OS=Arabidopsis thaliana GN=AIR12 PE=1 SV=3	1	-1,187	0,057235691	132,9	0,228
Q93VI4 PABN1_ARATH Polyadenylate-binding protein 1 OS=Arabidopsis thaliana GN=PABN1 PE=1 SV=1	1	-0,827	0,056735816	131,74	0,228
Q9SA87 BBE10_ARATH Berberine bridge enzyme-like 10 OS=Arabidopsis thaliana GN=At1g30720 PE=2 SV=1	2	-0,677	0,056985754	132,32	0,228
Q56YT0 LAC3_ARATH Laccase-3 OS=Arabidopsis thaliana GN=LAC3 PE=2 SV=2	2	-0,606	0,056235941	130,58	0,228
Q9FMC7 Q9FMC7_ARATH Nuclear transport factor 2 (NTF2) family protein OS=Arabidopsis thaliana GN=MUK11.15 PE=2 SV=1	3	-0,501	0,056735816	131,74	0,228
Q43735 PER27_ARATH Peroxidase 27 OS=Arabidopsis thaliana GN=PER27 PE=1 SV=1	4	-0,448	0,056485879	131,16	0,228
P57752 ACBP6_ARATH Acyl-CoA-binding domain-containing protein 6 OS=Arabidopsis thaliana GN=ACBP6 PE=1 SV=1	3	0,394	0,056735816	131,74	0,228
Q9LNL0 PER8_ARATH Peroxidase 8 OS=Arabidopsis thaliana GN=PER8 PE=2 SV=1	1	1,131	0,057235691	132,9	0,229
Q9M3A8 PP273_ARATH Pentatricopeptide repeat-containing protein At3g49240, mitochondrial OS=Arabidopsis thaliana GN=EMB1796 PE=1 SV=1	1	-1,206	0,057735566	134,06	0,23
O23523 RGGA_ARATH RGG repeats nuclear RNA binding protein A OS=Arabidopsis thaliana GN=RGGA PE=1 SV=1	1	0,824	0,058985254	136,96	0,235
Q9LPC7 CP18A_ARATH Peptidyl-prolyl cis-trans isomerase CYP18-1 OS=Arabidopsis thaliana GN=CYP18-1 PE=2 SV=1	1	-1,192	0,060646451	140,82	0,239
F4KIH8 F4KIH8_ARATH Transducin/WD40 repeat-like superfamily protein OS=Arabidopsis thaliana GN=MXC17.10 PE=4 SV=1	2	0,664	0,060313229	140,05	0,239
Q56Z12 PATL2_ARATH Patellin-2 OS=Arabidopsis thaliana GN=PATL2 PE=1 SV=2	20	0,27	0,060234941	139,87	0,239
Q9FGY1 BXL1_ARATH Beta-D-xylosidase 1 OS=Arabidopsis thaliana GN=BXL1 PE=1 SV=1	1	-1,176	0,060979673	141,59	0,24
P21240 CPNB1_ARATH Chaperonin 60 subunit beta 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60B1 PE=1 SV=3	6	-0,372	0,060646451	140,82	0,24
Q9SIY3 TTM3_ARATH reversed Triphosphate tunnel metalloenzyme 3 OS=Arabidopsis thaliana GN=TTM3 PE=1 SV=1	1	0,666	0,06197934	143,92	0,243
Q84WT8 CYT4_ARATH Cysteine proteinase inhibitor 4 OS=Arabidopsis thaliana GN=CYS4 PE=3 SV=2	2	-0,495	0,06197934	143,92	0,243
Q9LNB6 HSOP1_ARATH Hsp70-Hsp90 organizing protein 1 OS=Arabidopsis thaliana GN=HOP1 PE=2 SV=1	3	0,48	0,061646118	143,14	0,243
Q9SHL8 PILS5_ARATH Protein PIN-LIKES 5 OS=Arabidopsis thaliana GN=PILS5 PE=2 SV=1	1	-0,763	0,06197934	143,92	0,244
Q6NLB0 GSTL1_ARATH Glutathione S-transferase L1 OS=Arabidopsis thaliana GN=GSTL1 PE=2 SV=1	1	-0,798	0,062645785	145,46	0,245
Q9ZPI5 MFP2_ARATH Peroxisomal fatty acid beta-oxidation multifunctional protein MFP2 OS=Arabidopsis thaliana GN=MFP2 PE=1 SV=1	10	-0,343	0,063312229	147,01	0,247
P42798 R15A1_ARATH 40S ribosomal protein S15a-1 OS=Arabidopsis thaliana GN=RPS15AA PE=2 SV=2	3	0,441	0,063645452	147,78	0,248
Q9M1H3 AB4F_ARATH ABC transporter F family member 4 OS=Arabidopsis thaliana GN=ABCF4 PE=2 SV=1	2	-0,573	0,064311896	149,33	0,249
Q9FF97 Q9FF97_ARATH MD-2-related lipid recognition domain-containing protein OS=Arabidopsis thaliana GN=MRO11.13 PE=2 SV=1	3	-0,481	0,063978674	148,56	0,249
O23593 RGGB_ARATH RGG repeats nuclear RNA binding protein B OS=Arabidopsis thaliana GN=RGGB PE=1 SV=1	3	0,44	0,064645118	150,11	0,249
Q9SZB9 PER47_ARATH Peroxidase 47 OS=Arabidopsis thaliana GN=PER47 PE=2 SV=2	2	-0,836	0,064645118	150,11	0,25
P47998 CYSK1_ARATH Cysteine synthase 1 OS=Arabidopsis thaliana GN=OASA1 PE=1 SV=2	1	-0,715	0,064978341	150,88	0,25
B9DGT7 TBA2_ARATH Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	1	0,602	0,064645118	150,11	0,25
Q94AU7 GCA3_ARATH Gamma carbonic anhydrase 3, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA3 PE=1 SV=1	2	-0,528	0,064311896	149,33	0,25
Q56Z59 PATL3_ARATH Patellin-3 OS=Arabidopsis thaliana GN=PATL3 PE=1 SV=2	5	-0,435	0,065644785	152,43	0,252
Q9M0F9 PFKA1_ARATH ATP-dependent 6-phosphofructokinase 1 OS=Arabidopsis thaliana GN=PFK1 PE=1 SV=1	1	-1,118	0,06631123	153,97	0,253
Q94K30 Q94K30_ARATH AT1G01800 protein OS=Arabidopsis thaliana GN=At1g01800 PE=2 SV=1	1	-0,69	0,065978007	153,2	0,253
Q9ASS2 FREE1_ARATH Protein FREE1 OS=Arabidopsis thaliana GN=FREE1 PE=1 SV=1	3	-0,47	0,06631123	153,97	0,253
Q8GYZ3 Q8GYZ3_ARATH RmlC-like jelly roll fold protein OS=Arabidopsis thaliana GN=At1g19130 PE=2 SV=1	1	1,121	0,06631123	153,97	0,254
O23006 LYM2_ARATH LysM domain-containing GPI-anchored protein 2 OS=Arabidopsis thaliana GN=LYM2 PE=1 SV=1	2	-0,516	0,06631123	153,97	0,254
O65570 VIL4_ARATH Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1	1	0,592	0,067644119	157,07	0,255

O82204 RL281_ARATH 60S ribosomal protein L28-1 OS=Arabidopsis thaliana GN=RPL28A PE=1 SV=1	1	0,582	0,067310896	156,3	0,255
P93017 DRMH1_ARATH Dormancy-associated protein homolog 1 OS=Arabidopsis thaliana GN=DRMH1 PE=1 SV=1	2	-0,518	0,067310896	156,3	0,255
Q94AI7 TPL_ARATH Protein TOPLESS OS=Arabidopsis thaliana GN=TPL PE=1 SV=1	6	-0,382	0,066977674	155,52	0,255
O80858 O80858_ARATH Expressed protein OS=Arabidopsis thaliana GN=At2g30930 PE=1 SV=1	7	0,338	0,067310896	156,3	0,255
Q8RUF8 NILP3_ARATH Omega-amidase, chloroplastic OS=Arabidopsis thaliana GN=NLP3 PE=1 SV=1	2	-0,866	0,067310896	156,3	0,256
Q09152 FPPS1_ARATH Farnesyl pyrophosphate synthase 1, mitochondrial OS=Arabidopsis thaliana GN=FPS1 PE=2 SV=2	5	-0,414	0,067977341	157,84	0,256
Q9SR36 GSTU8_ARATH Glutathione S-transferase U8 OS=Arabidopsis thaliana GN=GSTU8 PE=2 SV=1	5	-0,372	0,067977341	157,84	0,256
O49377 VA711_ARATH Vesicle-associated membrane protein 711 OS=Arabidopsis thaliana GN=VAMP711 PE=1 SV=2	1	-1,067	0,068310563	158,62	0,257
F4IB95 JAL9_ARATH Jacalin-related lectin 9 OS=Arabidopsis thaliana GN=JAL9 PE=3 SV=1	2	0,65	0,069643452	161,71	0,261
O65271 FOLD4_ARATH Bifunctional protein FoId 4, chloroplastic OS=Arabidopsis thaliana GN=FOLD4 PE=1 SV=1	2	0,573	0,069643452	161,71	0,261
Q9C4Z6 GPLPB_ARATH Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1	7	0,338	0,069976674	162,49	0,261
Q9C8X4 Q9C8X4_ARATH GrpE protein homolog OS=Arabidopsis thaliana GN=At1g36390 PE=2 SV=1	1	0,789	0,069976674	162,49	0,262
Q94BR1 Q94BR1_ARATH MA3 domain-containing protein OS=Arabidopsis thaliana GN=MDC12.16 PE=1 SV=1	2	-0,812	0,071309563	165,58	0,265
Q38905 PROF4_ARATH Profilin-4 OS=Arabidopsis thaliana GN=PRO4 PE=2 SV=1	1	-0,754	0,071309563	165,58	0,265
Q9C907 GDPD5_ARATH Glycerophosphodiester phosphodiesterase GDPD5 OS=Arabidopsis thaliana GN=GDPD5 PE=2 SV=1	2	-0,536	0,071642786	166,35	0,265
Q8LEJ7 Q8LEJ7_ARATH At1g55265 OS=Arabidopsis thaliana GN=At1g55265 PE=2 SV=1	1	0,803	0,071309563	165,58	0,266
Q949R9 MPC1_ARATH Mitochondrial pyruvate carrier 1 OS=Arabidopsis thaliana GN=MPC1 PE=3 SV=1	2	-0,617	0,071976008	167,13	0,266
Q9STX2 VEP1_ARATH 3-oxo-Delta(4,5)-steroid 5-beta-reductase OS=Arabidopsis thaliana GN=VEP1 PE=1 SV=1	5	-0,442	0,071642786	166,35	0,266
Q9S7E4 FDH_ARATH Formate dehydrogenase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=FDH1 PE=1 SV=1	2	-0,537	0,07230923	167,9	0,267
F4JY76 F4JY76_ARATH Eukaryotic translation initiation factor 3 subunit L OS=Arabidopsis thaliana GN=At5g25754 PE=1 SV=1	4	-0,4	0,072975675	169,45	0,269
Q9LZG0 ADK2_ARATH Adenosine kinase 2 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	9	0,319	0,073308897	170,22	0,27
Q9M879 STAD5_ARATH Stearoyl-[acyl-carrier-protein] 9-desaturase 5, chloroplastic OS=Arabidopsis thaliana GN=S-ACP-DESS PE=1 SV=1	1	1,108	0,073975342	171,77	0,271
P16181 RS111_ARATH 40S ribosomal protein S11-1 OS=Arabidopsis thaliana GN=RPS11A PE=2 SV=1	3	0,391	0,073642119	171	0,271
P59229 VATL4_ARATH V-type proton ATPase subunit c4 OS=Arabidopsis thaliana GN=VHA-c4 PE=2 SV=1	1	-0,495	0,074308564	172,54	0,272
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	4	0,373	0,074641786	173,32	0,272
O22263 PDI21_ARATH Protein disulfide-isomerase like 2-1 OS=Arabidopsis thaliana GN=PDIL2-1 PE=2 SV=1	1	-0,746	0,074641786	173,32	0,273
Q9M2N5 DSLE_ARATH Zinc finger BED domain-containing protein DAYSLLEEPER OS=Arabidopsis thaliana GN=HAT PE=1 SV=1	2	-0,668	0,074641786	173,32	0,273
Q9ZNW0 MOC53_ARATH Adenylyltransferase and sulfurtransferase MOC53 OS=Arabidopsis thaliana GN=MOC53 PE=2 SV=1	1	-1,136	0,075308231	174,87	0,274
Q9FF75 SUN1_ARATH SUN domain-containing protein 1 OS=Arabidopsis thaliana GN=SUN1 PE=1 SV=1	1	1,112	0,075308231	174,87	0,274
Q9FE06 EXOL2_ARATH Protein EXORDIUM-like 2 OS=Arabidopsis thaliana GN=EXL2 PE=2 SV=1	2	-0,802	0,075974675	176,41	0,274
Q8RV68 Q8RV68_ARATH Expressed protein OS=Arabidopsis thaliana GN=At2g31725 PE=2 SV=1	1	-0,797	0,075641453	175,64	0,274
O65041 UBA3_ARATH NEDD8-activating enzyme E1 catalytic subunit OS=Arabidopsis thaliana GN=ECR1 PE=1 SV=2	1	0,653	0,075641453	175,64	0,274
F4HZS8 F4HZS8_ARATH reversed Sporulation-specific protein OS=Arabidopsis thaliana GN=At1g22060 PE=4 SV=1	1	-0,627	0,075641453	175,64	0,274
Q8LF21 DRP1C_ARATH Dynamin-related protein 1C OS=Arabidopsis thaliana GN=DRP1C PE=1 SV=2	3	-0,517	0,076307897	177,19	0,274
Q9C6B3 GCA2_ARATH Gamma carbonic anhydrase 2, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA2 PE=1 SV=1	7	-0,331	0,075974675	176,41	0,274
Q8GYM1 GSTUM_ARATH Glutathione S-transferase U22 OS=Arabidopsis thaliana GN=GSTU22 PE=1 SV=1	2	-0,571	0,076974342	178,73	0,275
Q9SIB9 ACO3M_ARATH Aconitate hydratase 3, mitochondrial OS=Arabidopsis thaliana GN=ACO3 PE=1 SV=2	16	-0,254	0,076307897	177,19	0,275
O04486 RAA2A_ARATH Ras-related protein RABA2a OS=Arabidopsis thaliana GN=RABA2A PE=2 SV=1	1	0,674	0,077307564	179,51	0,276
Q39131 LAML_ARATH Lamin-like protein OS=Arabidopsis thaliana GN=At5g15350 PE=1 SV=1	1	-0,662	0,076974342	178,73	0,276
Q94CE4-2 BCA4_ARATH Isoform 2 of Beta carbonic anhydrase 4 OS=Arabidopsis thaliana GN=BCA4	2	0,591	0,077307564	179,51	0,276
Q9XIE2 AB36G_ARATH ABC transporter G family member 36 OS=Arabidopsis thaliana GN=ABCG36 PE=1 SV=1	7	-0,352	0,076974342	178,73	0,276
Q9M2Y6 Y3972_ARATH Uncharacterized protein At3g49720 OS=Arabidopsis thaliana GN=At3g49720 PE=2 SV=1	2	0,633	0,077640786	180,28	0,277
O04486 RAA2A_ARATH Ras-related protein RABA2a OS=Arabidopsis thaliana GN=RABA2A PE=2 SV=1	1	0,577	0,077974009	181,06	0,277
Q42540 UBC7_ARATH Ubiquitin-conjugating enzyme E2 7 OS=Arabidopsis thaliana GN=UBC7 PE=1 SV=1	1	0,711	0,078307231	181,83	0,278
Q9C901 Q9C901_ARATH DNA-binding enhancer protein-like protein OS=Arabidopsis thaliana GN=At3g06610 PE=1 SV=1	1	-0,745	0,079306898	184,15	0,281
O04619 ADNT1_ARATH Mitochondrial adenine nucleotide transporter ADNT1 OS=Arabidopsis thaliana GN=ADNT1 PE=1 SV=1	5	0,419	0,07964012	184,92	0,281
Q9FRL8 DHAR2_ARATH Glutathione S-transferase DHAR2 OS=Arabidopsis thaliana GN=DHAR2 PE=1 SV=1	8	-0,33	0,079306898	184,15	0,281
F4JRE0 TMN12_ARATH Transmembrane 9 superfamily member 12 OS=Arabidopsis thaliana GN=TMN12 PE=2 SV=1	1	0,737	0,080639787	187,25	0,283
Q9SYA9 STKLD_ARATH Probable transcription factor At1g61730 OS=Arabidopsis thaliana GN=At1g61730 PE=1 SV=1	3	-0,455	0,080306564	186,47	0,283
Q8L831 NUDT3_ARATH Nudix hydrolase 3 OS=Arabidopsis thaliana GN=NUDT3 PE=1 SV=1	5	-0,372	0,080306564	186,47	0,283
POCAN7 VATE3_ARATH V-type proton ATPase subunit E3 OS=Arabidopsis thaliana GN=VHA-E3 PE=2 SV=1	5	-0,323	0,080306564	186,47	0,283

Q43316 HEM3_ARATH Porphobilinogen deaminase, chloroplastic OS=Arabidopsis thaliana GN=HEMC PE=1 SV=1	1	0,698	0,081306231	188,79	0,284
P51419 RL273_ARATH 60S ribosomal protein L27-3 OS=Arabidopsis thaliana GN=RPL27C PE=2 SV=2	3	0,371	0,080973009	188,02	0,284
O04486 RAA2A_ARATH Ras-related protein RABA2a OS=Arabidopsis thaliana GN=RABA2A PE=2 SV=1	1	0,643	0,081972676	190,34	0,285
Q93ZG7 RH38_ARATH DEAD-box ATP-dependent RNA helicase 38 OS=Arabidopsis thaliana GN=RH38 PE=1 SV=2	3	0,511	0,081306231	188,79	0,285
Q9LKA3 MDHM2_ARATH Malate dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=At3g15020 PE=1 SV=1	6	0,347	0,081972676	190,34	0,285
Q9ZVN2 Y1457_ARATH Acyltransferase-like protein At1g54570, chloroplastic OS=Arabidopsis thaliana GN=At1g54570 PE=1 SV=1	1	0,768	0,082305898	191,11	0,286
P48006 EF1D1_ARATH Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2	2	0,601	0,081972676	190,34	0,286
Q39043 MD37F_ARATH Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	18	0,258	0,081972676	190,34	0,286
O49343 PP177_ARATH Pentatricopeptide repeat-containing protein At2g30780 OS=Arabidopsis thaliana GN=At2g30780 PE=2 SV=1	1	-0,649	0,082972343	192,66	0,288
Q56WH4 HDT2_ARATH Histone deacetylase HDT2 OS=Arabidopsis thaliana GN=HDT2 PE=1 SV=2	2	-0,54	0,084305232	195,76	0,291
Q9ZUC2 BCA3_ARATH Beta carbonic anhydrase 3 OS=Arabidopsis thaliana GN=BCA3 PE=2 SV=1	2	0,526	0,084638454	196,53	0,291
Q8L6Y1 UBP14_ARATH Ubiquitin carboxyl-terminal hydrolase 14 OS=Arabidopsis thaliana GN=UBP14 PE=1 SV=1	4	-0,469	0,083972009	194,98	0,291
Q8VYJ6 Q8VYJ6_ARATH At2g30880/F7F1.9 OS=Arabidopsis thaliana GN=SWAP70 PE=2 SV=1	1	-1,071	0,084638454	196,53	0,292
Q9LYF8 Q9LYF8_ARATH Alpha-glucosidase 1 OS=Arabidopsis thaliana GN=At5g11720 PE=2 SV=1	2	-0,652	0,084638454	196,53	0,292
P52901 ODPA1_ARATH Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=E1 ALPHA PE=1 SV=2	2	0,47	0,085304898	198,08	0,293
O48802 PHOX2_ARATH Protein CLMP1 OS=Arabidopsis thaliana GN=CLMP1 PE=1 SV=1	1	0,702	0,085638121	198,85	0,294
Q940M2 AGT21_ARATH Alanine-glyoxylate aminotransferase 2 homolog 1, mitochondrial OS=Arabidopsis thaliana GN=AGT2 PE=1 SV=1	4	-0,441	0,086304565	200,4	0,296
Q93VH2 BBD2_ARATH Bifunctional nuclease 2 OS=Arabidopsis thaliana GN=BBD2 PE=2 SV=1	1	1,062	0,086971101	201,95	0,297
Q9T076 ENL2_ARATH Early nodulin-like protein 2 OS=Arabidopsis thaliana GN=At4g27520 PE=1 SV=1	2	-0,523	0,086971101	201,95	0,297
Q9SYP1 DEXHC_ARATH DEXH-box ATP-dependent RNA helicase DEXH12 OS=Arabidopsis thaliana GN=BRR2A PE=1 SV=1	6	-0,367	0,086971101	201,95	0,297
Q9SA78 COPE1_ARATH Coatomer subunit epsilon-1 OS=Arabidopsis thaliana GN=At1g30630 PE=2 SV=1	3	0,492	0,087637454	203,49	0,298
Q8S9J6 ASPA_ARATH Aspartyl protease family protein At5g10770 OS=Arabidopsis thaliana GN=At5g10770 PE=2 SV=1	1	-1,094	0,091454273	212,36	0,299
Q9LKB2 Q9LKB2_ARATH Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein OS=Arabidopsis thaliana GN=At3g14920 PE=4 SV=1	1	-0,732	0,088955522	206,55	0,299
Q8L7W0 SH3P3_ARATH SH3 domain-containing protein 3 OS=Arabidopsis thaliana GN=SH3P3 PE=1 SV=1	1	0,718	0,090454773	210,04	0,299
Q9SBB2 ABC1_ARATH Protein ABC transporter 1, mitochondrial OS=Arabidopsis thaliana GN=ABC1 PE=2 SV=1	1	-0,713	0,091454273	212,36	0,299
Q9CAT7 BTF3L_ARATH Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=At1g73230 PE=2 SV=1	2	0,598	0,091302899	212,01	0,299
Q8GXU7 Q8GXU7_ARATH At4g13612 OS=Arabidopsis thaliana GN=At4g13615 PE=2 SV=1	2	-0,566	0,090969677	211,23	0,299
A0A1I9LN21 A0A1I9LN21_ARATH Phosphoglycerate mutase family protein OS=Arabidopsis thaliana GN=At3g60450 PE=4 SV=1	4	-0,413	0,090969677	211,23	0,299
Q9SGT7 Q9SGT7_ARATH At1g56110/T6H22_9 OS=Arabidopsis thaliana GN=NOP56 PE=2 SV=1	7	0,328	0,087970676	204,27	0,299
Q39258 VATE1_ARATH V-type proton ATPase subunit E1 OS=Arabidopsis thaliana GN=VHA-E1 PE=1 SV=2	6	-0,31	0,090636455	210,46	0,299
Q56YU0 AL2C4_ARATH Aldehyde dehydrogenase family 2 member C4 OS=Arabidopsis thaliana GN=ALDH2C4 PE=1 SV=2	15	-0,257	0,091954023	213,52	0,299
Q9C7C3 C3H36_ARATH Zinc finger CCH domain-containing protein 36 OS=Arabidopsis thaliana GN=At3g12130 PE=2 SV=1	1	-1,063	0,089636788	208,14	0,3
O04379 AGO1_ARATH Protein argonaute 1 OS=Arabidopsis thaliana GN=AGO1 PE=1 SV=1	1	-1,048	0,090454773	210,04	0,3
Q8GWC7 Q8GWC7_ARATH MICOS complex subunit, putative (DUF543) OS=Arabidopsis thaliana GN=At1g72165/T9N14_2 PE=2 SV=1	1	-1,04	0,088955522	206,55	0,3
O23252 IF4E1_ARATH Eukaryotic translation initiation factor 4E-1 OS=Arabidopsis thaliana GN=EIF4E1 PE=1 SV=1	1	0,969	0,092953523	215,84	0,3
Q9LIS2 RBG4_ARATH Glycine-rich RNA-binding protein 4, mitochondrial OS=Arabidopsis thaliana GN=RBG4 PE=2 SV=1	1	0,754	0,088955522	206,55	0,3
Q6NQD2 Q6NQD2_ARATH At5g12240 OS=Arabidopsis thaliana GN=MXC9.20 PE=2 SV=1	1	0,736	0,088455772	205,39	0,3
Q94K30 Q94K30_ARATH AT1G01800 protein OS=Arabidopsis thaliana GN=At1g01800 PE=2 SV=1	1	-0,71	0,091454273	212,36	0,3
Q93W05 Q93W05_ARATH At1g10590/F20B24_1 OS=Arabidopsis thaliana GN=At1g10590 PE=1 SV=1	1	-0,693	0,091954023	213,52	0,3
Q9SEU4 SRC33_ARATH Serine/arginine-rich SC35-like splicing factor SCL33 OS=Arabidopsis thaliana GN=SCL33 PE=1 SV=1	1	-0,689	0,092453773	214,68	0,3
Q84Y95 GRS14_ARATH Monothiol glutaredoxin-S14, chloroplastic OS=Arabidopsis thaliana GN=GRXS14 PE=1 SV=2	2	-0,629	0,088637121	205,82	0,3
Q81645 VIL13_ARATH Villin-3 OS=Arabidopsis thaliana GN=VLN3 PE=1 SV=2	2	-0,615	0,092953523	215,84	0,3
Q9LX07 ANXD7_ARATH Annexin D7 OS=Arabidopsis thaliana GN=ANNAT7 PE=2 SV=1	2	-0,533	0,090454773	210,04	0,3
Q8L7S6 HEX03_ARATH Beta-hexosaminidase 3 OS=Arabidopsis thaliana GN=HEX03 PE=1 SV=1	2	-0,524	0,090954523	211,2	0,3
O04265 O04265_ARATH AT5g08160 OS=Arabidopsis thaliana GN=PK3 PE=2 SV=1	3	0,523	0,090954523	211,2	0,3
Q08112 RS151_ARATH 40S ribosomal protein S15-1 OS=Arabidopsis thaliana GN=RP515A PE=2 SV=1	1	0,515	0,092453773	214,68	0,3
A0A1P8BDM1 A0A1P8BDM1_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At5g19110 PE=3 SV=1	2	0,504	0,089455272	207,72	0,3
F4K1U5 F4K1U5_ARATH Trafficking protein particle complex subunit OS=Arabidopsis thaliana GN=MBG8.1 PE=3 SV=1	3	0,472	0,088455772	205,39	0,3
Q93Z70 ARGC_ARATH Probable N-acetyl-gamma-glutamyl-phosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=At2g19940 PE=1 SV=2	4	-0,406	0,08997001	208,91	0,3
Q9LF98 ALFC8_ARATH Fructose-bisphosphate aldolase 8, cytosolic OS=Arabidopsis thaliana GN=FBA8 PE=1 SV=1	9	0,27	0,090454773	210,04	0,3
Q9LVA5 Q9LVA5_ARATH At5g62340 OS=Arabidopsis thaliana GN=MMI9.17 PE=2 SV=1	1	-0,769	0,088955522	206,55	0,301

Q9C920 KDSB_ARATH 3-deoxy-manno-octulosonate cytidyltransferase, mitochondrial OS=Arabidopsis thaliana GN=KDSB PE=1 SV=1	1	-0,739	0,092453773	214,68	0,301
Q93Z17 HLP_ARATH 50S ribosomal protein HLP, mitochondrial OS=Arabidopsis thaliana GN=HLP PE=2 SV=1	1	-0,693	0,089955022	208,88	0,301
Q93ZC5 AOC4_ARATH Allene oxide cyclase 4, chloroplastic OS=Arabidopsis thaliana GN=AOC4 PE=2 SV=1	1	-0,674	0,089955022	208,88	0,301
Q42546 DPNP1_ARATH SAL1 phosphatase OS=Arabidopsis thaliana GN=SAL1 PE=1 SV=1	2	-0,501	0,092953523	215,84	0,301
Q39043 MD37F_ARATH Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	2	0,464	0,090303232	209,68	0,301
Q9S7L9 CX6B1_ARATH Cytochrome c oxidase subunit 6b-1 OS=Arabidopsis thaliana GN=COX6B-1 PE=1 SV=1	2	0,441	0,090454773	210,04	0,301
O49506 GLO5_ARATH Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 OS=Arabidopsis thaliana GN=GLO5 PE=1 SV=1	4	-0,427	0,089455272	207,72	0,301
O23714 PSB2A_ARATH Proteasome subunit beta type-2-A OS=Arabidopsis thaliana GN=PBD1 PE=1 SV=1	5	-0,37	0,093453273	217	0,301
Q9SKP6 TPIC_ARATH Triosephosphate isomerase, chloroplastic OS=Arabidopsis thaliana GN=TIM PE=1 SV=1	7	0,287	0,093453273	217	0,301
Q9LDZ0 HSP7J_ARATH Heat shock 70 kDa protein 10, mitochondrial OS=Arabidopsis thaliana GN=HSP70-10 PE=1 SV=1	13	-0,264	0,092953523	215,84	0,301
Q9FID5 Y5393_ARATH Probable receptor-like protein kinase At5g39030 OS=Arabidopsis thaliana GN=At5g39030 PE=2 SV=1	1	0,492	0,093953023	218,16	0,302
Q93VB0 Q93VB0_ARATH Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=At2g40660 PE=2 SV=1	3	0,393	0,094452774	219,32	0,303
P22953 MD37E_ARATH Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	2	0,528	0,094952524	220,48	0,304
Q9S2N1 VATB2_ARATH V-type proton ATPase subunit B2 OS=Arabidopsis thaliana GN=VHA-B2 PE=1 SV=1	2	-0,483	0,095952024	222,8	0,304
P50318 PGKH2_ARATH Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=1 SV=3	5	-0,356	0,095452274	221,64	0,304
Q8LC12 Q8LC12_ARATH At4g01897 OS=Arabidopsis thaliana GN=At4g01897 PE=1 SV=1	1	-1,034	0,095952024	222,8	0,305
P29402 CALX1_ARATH Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1	1	0,627	0,095952024	222,8	0,305
Q9SRR8 Q9SRR8_ARATH 2Fe-2S ferredoxin-like superfamily protein OS=Arabidopsis thaliana GN=F2I03.19 PE=2 SV=1	3	0,394	0,095452274	221,64	0,305
Q680A5 KPRS4_ARATH Ribose-phosphate pyrophosphokinase 4 OS=Arabidopsis thaliana GN=PRS4 PE=1 SV=2	5	0,356	0,095452274	221,64	0,305
Q9LEV3 CBSX3_ARATH CBS domain-containing protein CBSX3, mitochondrial OS=Arabidopsis thaliana GN=CBSX3 PE=1 SV=1	7	-0,307	0,096451774	223,96	0,305
O80575 RISB_ARATH 6,7-dimethyl-8-ribityllumazine synthase, chloroplastic OS=Arabidopsis thaliana GN=At2g44050 PE=2 SV=1	1	-1,049	0,096951524	225,12	0,306
P23586 STP1_ARATH Sugar transport protein 1 OS=Arabidopsis thaliana GN=STP1 PE=1 SV=2	1	-0,978	0,096951524	225,12	0,306
F4J8D3 TPLAT_ARATH Protein TPLATE OS=Arabidopsis thaliana GN=TPLATE PE=1 SV=1	2	0,595	0,096451774	223,96	0,306
Q9CAI3 CADH1_ARATH Probable cinnamyl alcohol dehydrogenase 1 OS=Arabidopsis thaliana GN=CAD1 PE=2 SV=1	2	-0,574	0,095952024	222,8	0,306
Q9SIV2 PSD2A_ARATH 26S proteasome non-ATPase regulatory subunit 2 homolog A OS=Arabidopsis thaliana GN=RPN1A PE=1 SV=2	14	-0,271	0,097451274	226,28	0,306
Q94C86 Q94C86_ARATH Pectin lyase-like superfamily protein OS=Arabidopsis thaliana GN=At3g16850 PE=2 SV=1	2	-0,696	0,097451274	226,28	0,307
Q9SI22 IF2AH_ARATH Eukaryotic translation initiation factor 2 subunit alpha homolog OS=Arabidopsis thaliana GN=At2g40290 PE=1 SV=2	2	-0,533	0,097951024	227,44	0,307
Q948K8 RAG3A_ARATH Ras-related protein RABG3a OS=Arabidopsis thaliana GN=RABG3A PE=2 SV=1	3	0,437	0,097451274	226,28	0,307
Q9FX54 G3PC2_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPC2, cytosolic OS=Arabidopsis thaliana GN=GAPC2 PE=1 SV=1	3	0,387	0,098450775	228,6	0,308
Q9LHE7 FYPP3_ARATH Phytochrome-associated serine/threonine-protein phosphatase 3 OS=Arabidopsis thaliana GN=FYPP3 PE=1 SV=1	3	-0,479	0,099450275	230,92	0,309
Q8LPR9 TI110_ARATH Protein TIC110, chloroplastic OS=Arabidopsis thaliana GN=TIC110 PE=1 SV=1	5	0,358	0,098450775	228,6	0,309
O04487 EF1G1_ARATH Probable elongation factor 1-gamma 1 OS=Arabidopsis thaliana GN=At1g09640 PE=1 SV=1	6	0,324	0,098950525	229,76	0,309
P25819 CATA2_ARATH Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3	1	-0,632	0,100449775	233,24	0,31
Q9SE50 BGL18_ARATH Beta-D-glucopyranosyl abscisate beta-glucosidase OS=Arabidopsis thaliana GN=BGLU18 PE=1 SV=2	1	-0,621	0,099450275	230,92	0,31
Q9SI61 ASE1_ARATH Amidophosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=ASE1 PE=2 SV=1	3	-0,46	0,100949525	234,4	0,31
Q9S9P1 RS121_ARATH 40S ribosomal protein S12-1 OS=Arabidopsis thaliana GN=RPS12A PE=2 SV=1	3	0,446	0,100949525	234,4	0,31
Q9LMK7 RBP1A_ARATH Ran-binding protein 1 homolog a OS=Arabidopsis thaliana GN=RANBP1A PE=1 SV=1	2	0,425	0,099450275	230,92	0,31
O65396 GCST_ARATH Aminomethyltransferase, mitochondrial OS=Arabidopsis thaliana GN=GDCST PE=2 SV=1	4	-0,384	0,101449275	235,57	0,31
Q96518 PER16_ARATH Peroxidase 16 OS=Arabidopsis thaliana GN=PER16 PE=1 SV=2	4	-0,372	0,099950025	232,08	0,31
P49243 FABH_ARATH 3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic OS=Arabidopsis thaliana GN=At1g62640 PE=2 SV=2	6	-0,348	0,100449775	233,24	0,31
Q8LPJ3 MANA2_ARATH Probable alpha-mannosidase At5g13980 OS=Arabidopsis thaliana GN=At5g13980 PE=2 SV=1	8	-0,338	0,099450275	230,92	0,31
Q8W4M5 PFPB1_ARATH Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 1 OS=Arabidopsis thaliana GN=PFP-BETA1 PE=1 SV=:	10	0,301	0,100949525	234,4	0,31
Q84M92 ARP4_ARATH Actin-related protein 4 OS=Arabidopsis thaliana GN=ARP4 PE=1 SV=1	1	-1,008	0,100449775	233,24	0,311
Q9LHQ5 H2A2_ARATH Probable histone H2A.2 OS=Arabidopsis thaliana GN=At3g20670 PE=1 SV=1	1	-0,758	0,101949025	236,73	0,311
Q38922 RAB1B_ARATH Ras-related protein RABB1b OS=Arabidopsis thaliana GN=RABB1B PE=2 SV=1	2	0,603	0,102448776	237,89	0,311
P46421 GSTU5_ARATH Glutathione S-transferase U5 OS=Arabidopsis thaliana GN=GSTU5 PE=2 SV=1	2	-0,599	0,102448776	237,89	0,311
Q9LME8 U85A7_ARATH reversed UDP-glycosyltransferase 85A7 OS=Arabidopsis thaliana GN=UGT85A7 PE=2 SV=1	1	0,547	0,100949525	234,4	0,311
Q9FN52 MAM3_ARATH Methylthioalkylmalate synthase 3, chloroplastic OS=Arabidopsis thaliana GN=MAM3 PE=1 SV=1	2	0,498	0,101949025	236,73	0,311
Q93XZ7 Q93XZ7_ARATH At5g42570 OS=Arabidopsis thaliana GN=At5g42570 PE=1 SV=1	2	-0,487	0,100449775	233,24	0,311
Q0WPPW4 ACCO5_ARATH 1-aminocyclopropane-1-carboxylate oxidase 5 OS=Arabidopsis thaliana GN=At1g77330 PE=2 SV=1	3	0,44	0,100449775	233,24	0,311
P48348 14338_ARATH 14-3-3-like protein GF14 kappa OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=2	4	-0,385	0,102448776	237,89	0,311

P54873 HMCS_ARATH Hydroxymethylglutaryl-CoA synthase OS=Arabidopsis thaliana GN=HMGS PE=1 SV=2	5	0,357	0,101449275	235,57	0,311
P49204 RS42_ARATH 40S ribosomal protein S4-2 OS=Arabidopsis thaliana GN=RPS4B PE=2 SV=4	13	0,25	0,101949025	236,73	0,311
B3LFA4 SYCC2_ARATH Cysteine--tRNA ligase 2, cytoplasmic OS=Arabidopsis thaliana GN=At5g38830 PE=2 SV=1	2	-0,483	0,102448776	237,89	0,312
Q8VZG7 TSN1_ARATH Ribonuclease TUDOR 1 OS=Arabidopsis thaliana GN=TSN1 PE=1 SV=1	16	0,249	0,102948526	239,05	0,312
F4J5S1 CLU_ARATH Clustered mitochondria protein OS=Arabidopsis thaliana GN=FMT PE=2 SV=1	4	0,411	0,103448276	240,21	0,313
P42792 CYB_ARATH Cytochrome b OS=Arabidopsis thaliana GN=MT-CYB PE=2 SV=2	2	0,434	0,104447776	242,53	0,315
Q9FIK1 AIGLB_ARATH AIG2-like protein B OS=Arabidopsis thaliana GN=AIG2LB PE=1 SV=1	2	0,575	0,104947526	243,69	0,316
Q7Y232 U73B4_ARATH UDP-glycosyltransferase 73B4 OS=Arabidopsis thaliana GN=UGT73B4 PE=2 SV=1	3	-0,442	0,104947526	243,69	0,316
Q9FMP3 DPYS_ARATH reversed Dihydropyrimidinase OS=Arabidopsis thaliana GN=PYD2 PE=1 SV=1	1	-1,016	0,105947026	246,01	0,317
Q9M2T6 Q9M2T6_ARATH Beta-1, 3-glucanase-like protein OS=Arabidopsis thaliana GN=T22E16.90 PE=2 SV=1	1	-0,658	0,105447276	244,85	0,317
F4IPW5 F4IPW5_ARATH Elongation factor family protein OS=Arabidopsis thaliana GN=EMB2785 PE=4 SV=1	2	0,566	0,105947026	246,01	0,317
O50008 METE1_ARATH 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV=1	21	0,238	0,105947026	246,01	0,317
O49460 PHB1_ARATH Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1	2	0,465	0,106946527	248,33	0,318
Q42342 CYB5E_ARATH Cytochrome b5 isoform E OS=Arabidopsis thaliana GN=CYTB5-E PE=1 SV=2	6	-0,348	0,105947026	246,01	0,318
Q65TH5 HF101_ARATH Fe-S cluster assembly factor HCF101, chloroplastic OS=Arabidopsis thaliana GN=HCF101 PE=1 SV=1	1	-0,656	0,106946527	248,33	0,319
Q9ZW33 TIM10_ARATH Mitochondrial import inner membrane translocase subunit TIM10 OS=Arabidopsis thaliana GN=TIM10 PE=1 SV=1	2	-0,481	0,107446277	249,49	0,319
Q9FKC0 R13A4_ARATH 60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	2	0,429	0,107446277	249,49	0,319
P49040 SUS1_ARATH Sucrose synthase 1 OS=Arabidopsis thaliana GN=SUS1 PE=1 SV=3	5	0,337	0,106946527	248,33	0,319
Q96282 CLCC_ARATH Chloride channel protein CLC-c OS=Arabidopsis thaliana GN=CLC-C PE=1 SV=1	1	-0,704	0,107946027	250,65	0,32
Q7PC86 AB35G_ARATH ABC transporter G family member 35 OS=Arabidopsis thaliana GN=ABCG35 PE=2 SV=1	3	-0,512	0,107946027	250,65	0,32
Q9ASP6 HNRPQ_ARATH Heterogeneous nuclear ribonucleoprotein Q OS=Arabidopsis thaliana GN=LIF2 PE=1 SV=1	1	0,66	0,108445777	251,81	0,321
Q949P3 Y2734_ARATH Uncharacterized protein At2g17340 OS=Arabidopsis thaliana GN=At2g17340 PE=1 SV=1	1	0,708	0,109945027	255,29	0,322
Q9FM47 Q9FM47_ARATH RNA-binding (RRM/RBD/RNP motifs) family protein OS=Arabidopsis thaliana GN=MNF13.1 PE=2 SV=1	2	0,506	0,110944528	257,61	0,322
Q9FX94 CXE5_ARATH Probable carboxylesterase 5 OS=Arabidopsis thaliana GN=CXE5 PE=2 SV=1	3	0,443	0,110444778	256,45	0,322
Q84VW9 CAPP3_ARATH Phosphoenolpyruvate carboxylase 3 OS=Arabidopsis thaliana GN=PPC3 PE=1 SV=2	19	0,235	0,110444778	256,45	0,322
Q9ZR03 UCRIA_ARATH Cytochrome b6-f complex iron-sulfur subunit, chloroplastic OS=Arabidopsis thaliana GN=petC PE=1 SV=1	1	-1,003	0,111444278	258,77	0,323
Q9FF52 RL123_ARATH 60S ribosomal protein L12-3 OS=Arabidopsis thaliana GN=RPL12C PE=2 SV=1	1	-0,943	0,110444778	256,45	0,323
Q9LJ86 Q9LJ86_ARATH AT3g22600/F16J14_17 OS=Arabidopsis thaliana GN=LTPG5 PE=2 SV=1	1	0,612	0,109445277	254,13	0,323
Q7DM58 AB4C_ARATH ABC transporter C family member 4 OS=Arabidopsis thaliana GN=ABCC4 PE=1 SV=2	2	0,584	0,110444778	256,45	0,323
Q9FLH8 SCRK7_ARATH Probable fructokinase-7 OS=Arabidopsis thaliana GN=At5g51830 PE=1 SV=1	2	0,501	0,109445277	254,13	0,323
Q94K85 CATB3_ARATH Cathepsin B-like protease 3 OS=Arabidopsis thaliana GN=CATHB3 PE=1 SV=1	2	-0,463	0,110444778	256,45	0,323
O80763 NRX1_ARATH Probable nucleoredoxin 1 OS=Arabidopsis thaliana GN=At1g60420 PE=1 SV=1	4	-0,41	0,111444278	258,77	0,323
Q9SA18 AKH1_ARATH Bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH1 PE=1 SV=1	4	0,41	0,109445277	254,13	0,323
O22940 O22940_ARATH At2g41800/T11A7.10 OS=Arabidopsis thaliana GN=At2g41800 PE=2 SV=1	4	-0,368	0,109945027	255,29	0,323
P25858 G3PC1_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	2	0,335	0,109945027	255,29	0,323
Q43291 RL211_ARATH 60S ribosomal protein L21-1 OS=Arabidopsis thaliana GN=RPL21A PE=2 SV=2	4	0,303	0,110944528	257,61	0,323
O22149 PME17_ARATH Probable pectinesterase/pectinesterase inhibitor 17 OS=Arabidopsis thaliana GN=PME17 PE=2 SV=2	8	-0,293	0,111444278	258,77	0,323
Q9LS94 RAG3F_ARATH Ras-related protein RABG3f OS=Arabidopsis thaliana GN=RABG3F PE=1 SV=1	1	-0,975	0,109945027	255,29	0,324
Q9LIK1 Q9LIK1_ARATH ADP-ribosylation factor C1 OS=Arabidopsis thaliana GN=ARFC1 PE=2 SV=1	1	0,974	0,112443778	261,09	0,325
Q9SX78 CXE2_ARATH Probable carboxylesterase 2 OS=Arabidopsis thaliana GN=CXE2 PE=2 SV=1	1	-0,739	0,112443778	261,09	0,325
Q9ZQX4 VATF_ARATH V-type proton ATPase subunit F OS=Arabidopsis thaliana GN=VHA-F PE=2 SV=1	3	-0,378	0,112943528	262,25	0,325
Q39239 TRXH4_ARATH Thioredoxin H4 OS=Arabidopsis thaliana GN=TRX4 PE=3 SV=2	1	-1,042	0,112943528	262,25	0,326
Q8H103 G6PIP_ARATH Glucose-6-phosphate isomerase 1, chloroplastic OS=Arabidopsis thaliana GN=PGI1 PE=1 SV=1	13	-0,263	0,113943028	264,58	0,327
O65660 PLAT1_ARATH PLAT domain-containing protein 1 OS=Arabidopsis thaliana GN=PLAT1 PE=1 SV=1	2	-0,509	0,113943028	264,58	0,328
Q8LL04 CPL3_ARATH RNA polymerase II C-terminal domain phosphatase-like 3 OS=Arabidopsis thaliana GN=CPL3 PE=1 SV=2	1	-0,647	0,114942529	266,9	0,33
Q66GK1 Q66GK1_ARATH At3g26990 OS=Arabidopsis thaliana GN=At3g26990 PE=2 SV=1	1	0,616	0,114942529	266,9	0,33
Q9SLF7 RLA22_ARATH 60S acidic ribosomal protein P2-2 OS=Arabidopsis thaliana GN=RPP2B PE=1 SV=1	5	0,321	0,115442279	268,06	0,33
P0DH95 CALM1_ARATH Calmodulin-1 OS=Arabidopsis thaliana GN=CAM1 PE=1 SV=1	1	0,689	0,115942029	269,22	0,331
A0A1P8B068 A0A1P8B068_ARATH Pathogenesis-related thaumatin superfamily protein OS=Arabidopsis thaliana GN=At2g28790 PE=4 SV=1	1	0,688	0,116941529	271,54	0,331
Q9LZD4 RAE1D_ARATH Ras-related protein RABE1d OS=Arabidopsis thaliana GN=RAE1D PE=1 SV=1	1	0,679	0,117441279	272,7	0,331
Q9ZU32 NADC_ARATH Nicotinate-nucleotide pyrophosphorylase [carboxylating], chloroplastic OS=Arabidopsis thaliana GN=QPT PE=2 SV=2	1	0,671	0,116441779	270,38	0,331

Q9LW34 Q9LW34_ARATH Alcohol dehydrogenase-like protein OS=Arabidopsis thaliana GN=At3g26770 PE=2 SV=1	2	-0,569	0,116441779	270,38	0,331
Q38900 CP19A_ARATH Peptidyl-prolyl cis-trans isomerase CYP19-1 OS=Arabidopsis thaliana GN=CYP19-1 PE=1 SV=1	1	0,498	0,116441779	270,38	0,331
O80912 PER23_ARATH Peroxidase 23 OS=Arabidopsis thaliana GN=PER23 PE=2 SV=1	2	-0,353	0,115942029	269,22	0,331
Q9SE60 MTHR1_ARATH Methylenetetrahydrofolate reductase 1 OS=Arabidopsis thaliana GN=MTHFR1 PE=1 SV=1	9	0,271	0,115442279	268,06	0,331
Q42560 ACO1_ARATH Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2	12	0,242	0,117441279	272,7	0,331
F4IA30 F4IA30_ARATH WD repeat protein OS=Arabidopsis thaliana GN=At1g71780 PE=4 SV=1	1	-0,958	0,117441279	272,7	0,332
Q6ICZ8 NACA3_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 3 OS=Arabidopsis thaliana GN=At5g13850 PE=1 SV=1	2	-0,467	0,116441779	270,38	0,332
Q9SHH6 GSTUO_ARATH Glutathione S-transferase U24 OS=Arabidopsis thaliana GN=GSTU24 PE=2 SV=1	2	-0,441	0,117941029	273,86	0,332
Q84WU2 UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana GN=UBP13 PE=1 SV=1	6	-0,36	0,116941529	271,54	0,332
Q08682 RSSA1_ARATH 40S ribosomal protein Sa-1 OS=Arabidopsis thaliana GN=RPSaA PE=1 SV=3	11	0,26	0,117441279	272,7	0,332
Q9LUQ6 RL192_ARATH 60S ribosomal protein L19-2 OS=Arabidopsis thaliana GN=RPL19B PE=2 SV=1	1	-0,534	0,11844078	275,02	0,333
Q9SK27 ENL1_ARATH Early nodulin-like protein 1 OS=Arabidopsis thaliana GN=At2g25060 PE=1 SV=2	1	0,627	0,11894053	276,18	0,334
O04904 PYRC_ARATH Dihydroorotase, mitochondrial OS=Arabidopsis thaliana GN=PYR4 PE=1 SV=1	4	0,41	0,11944028	277,34	0,335
Q9MAB3 NOP5B_ARATH Probable nucleolar protein 5-2 OS=Arabidopsis thaliana GN=NOP5-2 PE=1 SV=1	4	0,377	0,11944028	277,34	0,335
Q6Q4D0 TONS_ARATH Protein TONSOKU OS=Arabidopsis thaliana GN=TSK PE=1 SV=2	1	-0,638	0,12043978	279,66	0,336
Q9ASW5 Q9ASW5_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g18360 PE=2 SV=1	1	0,879	0,12093953	280,82	0,337
P34789 RS282_ARATH 40S ribosomal protein S28-2 OS=Arabidopsis thaliana GN=RPS28C PE=3 SV=1	1	0,613	0,12043978	279,66	0,337
O82487 O82487_ARATH Phosphoenolpyruvate carboxylase family protein OS=Arabidopsis thaliana GN=T12H20.10 PE=1 SV=1	2	-0,473	0,12093953	280,82	0,337
P0DH99 EF1A1_ARATH Elongation factor 1-alpha 1 OS=Arabidopsis thaliana GN=A1 PE=1 SV=1	20	0,218	0,12043978	279,66	0,337
Q9LE82 RAGP1_ARATH RAN GTPase-activating protein 1 OS=Arabidopsis thaliana GN=RANGAP1 PE=1 SV=1	1	-0,643	0,12193903	283,14	0,338
Q96299 14339_ARATH 14-3-3-like protein GF14 mu OS=Arabidopsis thaliana GN=GRF9 PE=1 SV=2	4	-0,332	0,12143928	281,98	0,338
Q9S9W2 SDRA_ARATH Short-chain dehydrogenase/reductase SDRA OS=Arabidopsis thaliana GN=SDRA PE=1 SV=1	5	-0,319	0,12193903	283,14	0,338
Q9C5Y0 PLDD1_ARATH Phospholipase D delta OS=Arabidopsis thaliana GN=PLDDELTA PE=1 SV=2	2	-0,478	0,12193903	283,14	0,339
F4I116 SYLC_ARATH Leucine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At1g09620 PE=1 SV=1	5	-0,373	0,122438781	284,3	0,339
Q8VZV7 PMT9_ARATH Probable methyltransferase PMT9 OS=Arabidopsis thaliana GN=At5g14430 PE=2 SV=1	1	0,954	0,123438281	286,62	0,34
A3KPF5 PDI15_ARATH Protein disulfide isomerase-like 1-5 OS=Arabidopsis thaliana GN=PDIL1-5 PE=2 SV=1	1	-0,63	0,123438281	286,62	0,34
P10795 RBS1A_ARATH Ribulose biphosphate carboxylase small chain 1A, chloroplastic OS=Arabidopsis thaliana GN=RBSCS-1A PE=1 SV=2	2	-0,615	0,123938031	287,78	0,34
Q9M291 SC24C_ARATH Protein transport protein Sec24-like CEF OS=Arabidopsis thaliana GN=CEF PE=2 SV=3	3	0,471	0,122938531	285,46	0,34
A8MS68 PLPD1_ARATH Dihydrolipoyl dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=LPD1 PE=2 SV=1	5	-0,349	0,123438281	286,62	0,34
Q6AWX0 XYLL2_ARATH D-xylose-proton symporter-like 2 OS=Arabidopsis thaliana GN=At5g17010 PE=1 SV=1	1	-0,648	0,123438281	286,62	0,341
Q9FNJ8 AROD5_ARATH Arogenate dehydratase 5, chloroplastic OS=Arabidopsis thaliana GN=ADT5 PE=1 SV=1	3	0,4	0,123938031	287,78	0,341
Q0WVZ7 Q0WVZ7_ARATH 24 kDa vacuolar protein-like OS=Arabidopsis thaliana GN=At5g20655 PE=2 SV=1	1	-0,951	0,125437281	291,27	0,343
Q9SLJ2 HRD11_ARATH Dehydrin HIRD11 OS=Arabidopsis thaliana GN=HIRD11 PE=1 SV=1	2	0,344	0,125437281	291,27	0,343
P30184 AMPL1_ARATH Leucine aminopeptidase 1 OS=Arabidopsis thaliana GN=LAP1 PE=1 SV=1	6	-0,298	0,124937531	290,1	0,343
Q944L8 Q944L8_ARATH At1g11930/F12F1_20 OS=Arabidopsis thaliana GN=At1g11930 PE=1 SV=1	1	0,941	0,125937031	292,43	0,344
Q8VXX5 SKS1_ARATH Monocopper oxidase-like protein SKS1 OS=Arabidopsis thaliana GN=SKS1 PE=1 SV=1	1	-0,638	0,126436782	293,59	0,344
Q9SB42 STKLS_ARATH GLABROUS1 enhancer-binding protein-like OS=Arabidopsis thaliana GN=GEBPL PE=1 SV=1	1	0,547	0,126936532	294,75	0,344
Q9LV09 BOB1_ARATH Protein BOBBER 1 OS=Arabidopsis thaliana GN=BOB1 PE=1 SV=1	2	-0,498	0,125937031	292,43	0,344
Q9FMP3 DPYS_ARATH Dihydropyrimidinase OS=Arabidopsis thaliana GN=PYD2 PE=1 SV=1	2	-0,455	0,127436282	295,91	0,344
P41376 IF4A1_ARATH Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	2	-0,41	0,126936532	294,75	0,344
O64700 UREG_ARATH Urease accessory protein G OS=Arabidopsis thaliana GN=UREG PE=2 SV=1	2	0,68	0,126436782	293,59	0,345
O04486 RAA2A_ARATH Ras-related protein RABA2a OS=Arabidopsis thaliana GN=RABA2A PE=2 SV=1	1	0,571	0,126936532	294,75	0,345
Q9C8D8 Q9C8D8_ARATH Eukaryotic translation initiation factor 3 subunit J OS=Arabidopsis thaliana GN=At1g66070 PE=2 SV=1	2	0,484	0,126936532	294,75	0,345
F4JXP5 F4JXP5_ARATH ACT domain-containing protein OS=Arabidopsis thaliana GN=ACR12 PE=4 SV=1	3	0,456	0,127436282	295,91	0,345
Q43866 INV1_ARATH Beta-fructofuranosidase, insoluble isoenzyme CWINV1 OS=Arabidopsis thaliana GN=CWINV1 PE=1 SV=1	6	-0,307	0,128435782	298,23	0,346
A0A1P8B1C9 A0A1P8B1C9_ARATH reversed Uncharacterized protein OS=Arabidopsis thaliana GN=At2g39690 PE=4 SV=1	1	0,661	0,128935532	299,39	0,347
Q94JS4 SMT3B_ARATH 24-methylenesterol C-methyltransferase 3 OS=Arabidopsis thaliana GN=SMT3 PE=2 SV=1	2	-0,56	0,128435782	298,23	0,347
Q949Y0 UBP6_ARATH Ubiquitin carboxyl-terminal hydrolase 6 OS=Arabidopsis thaliana GN=UBP6 PE=1 SV=1	5	0,297	0,128935532	299,39	0,347
Q9LNN2 LECT3_ARATH Lectin-like protein At1g53070 OS=Arabidopsis thaliana GN=At1g53070 PE=2 SV=1	2	-0,471	0,129435282	300,55	0,348
O49460 PHB1_ARATH Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1	5	-0,341	0,129935032	301,71	0,348
Q7PC87 AB34G_ARATH ABC transporter G family member 34 OS=Arabidopsis thaliana GN=ABCG34 PE=2 SV=1	6	-0,322	0,129935032	301,71	0,348

Q9LVA4 Q9LVA4_ARATH Plant invertase/pectin methylesterase inhibitor superfamily protein OS=Arabidopsis thaliana GN=MMI9.18 PE=2 SV=1	1	0,686	0,130434783	302,87	0,349
Q9SQZ9 PITH1_ARATH PITH domain-containing protein At3g04780 OS=Arabidopsis thaliana GN=At3g04780 PE=1 SV=2	1	-0,581	0,130934533	304,03	0,349
Q9FZ48 UBC36_ARATH Ubiquitin-conjugating enzyme E2 36 OS=Arabidopsis thaliana GN=UBC36 PE=1 SV=1	2	-0,56	0,130934533	304,03	0,349
P46643 AAT1_ARATH Aspartate aminotransferase, mitochondrial OS=Arabidopsis thaliana GN=ASP1 PE=1 SV=1	5	-0,385	0,130934533	304,03	0,349
Q93ZE8 SDF2_ARATH Stromal cell-derived factor 2-like protein OS=Arabidopsis thaliana GN=SDF2 PE=1 SV=1	3	0,369	0,130434783	302,87	0,349
Q9LZ57 RL363_ARATH 60S ribosomal protein L36-3 OS=Arabidopsis thaliana GN=RPL36C PE=3 SV=1	4	0,306	0,129935032	301,71	0,349
Q9LVI8 GLN13_ARATH Glutamine synthetase cytosolic isozyme 1-3 OS=Arabidopsis thaliana GN=GLN1-3 PE=1 SV=1	2	-0,406	0,131434283	305,19	0,35
Q43315 FPPS2_ARATH Farnesyl pyrophosphate synthase 2 OS=Arabidopsis thaliana GN=FPS2 PE=2 SV=1	2	-0,57	0,132433783	307,51	0,351
Q9SQR3 D14_ARATH Strigolactone esterase D14 OS=Arabidopsis thaliana GN=D14 PE=1 SV=1	1	-0,929	0,132933533	308,67	0,352
P32961 NRL1_ARATH Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	1	-0,53	0,132933533	308,67	0,352
P17562 METHK2_ARATH S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	4	0,358	0,132433783	307,51	0,352
Q9FE58 RL223_ARATH 60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1	4	0,307	0,132933533	308,67	0,352
Q9LHE5 TO401_ARATH Mitochondrial import receptor subunit TOM40-1 OS=Arabidopsis thaliana GN=TOM40-1 PE=1 SV=3	5	0,306	0,133433283	309,83	0,352
Q9FIZ7 OPLA_ARATH 5-oxoprolinase OS=Arabidopsis thaliana GN=OXP1 PE=1 SV=1	3	-0,447	0,133933033	310,99	0,353
Q9ZW17 RER1C_ARATH Protein RER1C OS=Arabidopsis thaliana GN=RER1C PE=2 SV=1	1	-0,605	0,134932534	313,31	0,354
Q9FIF9 RAA2D_ARATH Ras-related protein RABA2d OS=Arabidopsis thaliana GN=RABA2D PE=2 SV=1	2	0,505	0,134432784	312,15	0,354
O22607 MSI4_ARATH WD-40 repeat-containing protein MSI4 OS=Arabidopsis thaliana GN=MSI4 PE=1 SV=3	3	0,42	0,134432784	312,15	0,354
O23016 KCAB_ARATH Probable voltage-gated potassium channel subunit beta OS=Arabidopsis thaliana GN=KAB1 PE=1 SV=1	7	0,28	0,134432784	312,15	0,354
Q9FKI4 NAA10_ARATH N-terminal acetyltransferase A complex catalytic subunit NAA10 OS=Arabidopsis thaliana GN=NAA10 PE=1 SV=1	1	-0,541	0,135932034	315,63	0,355
Q9ZUT9 RS51_ARATH 40S ribosomal protein S5-1 OS=Arabidopsis thaliana GN=RPS5A PE=1 SV=1	2	0,506	0,135432284	314,47	0,355
P10896 RCA_ARATH Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RCA PE=1 SV=2	4	-0,481	0,135932034	315,63	0,355
Q3E902 RS212_ARATH 40S ribosomal protein S21-2 OS=Arabidopsis thaliana GN=RPS21C PE=1 SV=2	2	0,472	0,135932034	315,63	0,355
Q9F180 PP425_ARATH reversed Pentatricopeptide repeat-containing protein At5g48910 OS=Arabidopsis thaliana GN=PCMP-H38 PE=2 SV=1	1	-0,694	0,135932034	315,63	0,356
A8MQD8 A8MQD8_ARATH ER membrane protein complex subunit-like protein OS=Arabidopsis thaliana GN=At5g10780 PE=4 SV=1	1	0,629	0,136431784	316,79	0,356
O24456 GBLPA_ARATH Receptor for activated C kinase 1A OS=Arabidopsis thaliana GN=RACK1A PE=1 SV=2	1	0,482	0,136931534	317,96	0,356
Q9C525 BGL21_ARATH Beta-glucosidase 21 OS=Arabidopsis thaliana GN=BGLU21 PE=1 SV=1	1	-0,438	0,135932034	315,63	0,356
O23629 H2B6_ARATH Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	1	-0,41	0,136931534	317,96	0,356
B9DGT7 TBA2_ARATH Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	8	0,262	0,136931534	317,96	0,356
Q96300 14337_ARATH 14-3-3-like protein GF14 nu OS=Arabidopsis thaliana GN=GRF7 PE=1 SV=1	2	-0,514	0,137431284	319,12	0,357
F4JMJ1 HSP7R_ARATH Heat shock 70 kDa protein 17 OS=Arabidopsis thaliana GN=HSP70-17 PE=2 SV=1	4	0,333	0,137931034	320,28	0,357
Q1G3L1 TIM21_ARATH Probable mitochondrial import inner membrane translocase subunit TIM21 OS=Arabidopsis thaliana GN=TIM21 PE=1 SV=1	1	0,907	0,138930535	322,6	0,358
Q9SZY1 NACA4_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 4 OS=Arabidopsis thaliana GN=At4g10480 PE=1 SV=1	2	0,657	0,138430785	321,44	0,358
P0CZ23 ACOX3_ARATH Acyl-coenzyme A oxidase 3, peroxisomal OS=Arabidopsis thaliana GN=ACX3 PE=1 SV=1	9	-0,293	0,138930535	322,6	0,358
P92994 TCMO_ARATH Trans-cinnamate 4-monooxygenase OS=Arabidopsis thaliana GN=CYP73A5 PE=2 SV=1	15	-0,23	0,138430785	321,44	0,358
Q0WL80 UGGG_ARATH UDP-glucose:glycoprotein glucosyltransferase OS=Arabidopsis thaliana GN=UGGT PE=1 SV=1	2	-0,442	0,138930535	322,6	0,359
Q9SRH5 VDAC1_ARATH Mitochondrial outer membrane protein porin 1 OS=Arabidopsis thaliana GN=VDAC1 PE=1 SV=3	10	-0,239	0,139430285	323,76	0,359
O65719 HSP7C_ARATH Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	5	0,282	0,140429785	326,08	0,36
P47998 CYSK1_ARATH Cysteine synthase 1 OS=Arabidopsis thaliana GN=OASA1 PE=1 SV=2	13	-0,228	0,139930035	324,92	0,36
Q94JX5 WLIM1_ARATH LIM domain-containing protein WLIM1 OS=Arabidopsis thaliana GN=WLIM1 PE=1 SV=1	1	-0,636	0,140429785	326,08	0,361
F4JLM5 SYIC_ARATH Isoleucine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At4g10320 PE=2 SV=1	5	-0,378	0,140929535	327,24	0,361
P42825 DNAJ2_ARATH Chaperone protein dnaJ 2 OS=Arabidopsis thaliana GN=ATJ2 PE=1 SV=2	1	-0,601	0,141429285	328,4	0,362
A0A19LSV1 A0A19LSV1_ARATH reversed Kinesin-like protein 1 OS=Arabidopsis thaliana GN=KP1 PE=3 SV=1	1	-0,476	0,141929035	329,56	0,363
Q94AT1 P2C76_ARATH Probable protein phosphatase 2C 76 OS=Arabidopsis thaliana GN=At5g53140 PE=2 SV=1	2	0,45	0,141929035	329,56	0,363
Q9ASV5 Q9ASV5_ARATH AT4g39690/T19P19_80 OS=Arabidopsis thaliana GN=At4g39690 PE=2 SV=1	5	-0,327	0,142928536	331,88	0,364
Q9FKT3 UBC30_ARATH Ubiquitin-conjugating enzyme E2 30 OS=Arabidopsis thaliana GN=UBC30 PE=1 SV=1	1	-0,838	0,143428286	333,04	0,365
Q9SKC1 U74C1_ARATH UDP-glycosyltransferase 74C1 OS=Arabidopsis thaliana GN=UGT74C1 PE=2 SV=1	1	0,569	0,142928536	331,88	0,365
Q94BN2 SPSY_ARATH Spermine synthase OS=Arabidopsis thaliana GN=SPMS PE=1 SV=1	1	0,864	0,143928036	334,2	0,366
Q9LTF2 RS103_ARATH 40S ribosomal protein S10-3 OS=Arabidopsis thaliana GN=RPS10C PE=2 SV=2	6	0,311	0,144427786	335,36	0,366
Q9LFW1 RGP2_ARATH UDP-arabinopyranose mutase 2 OS=Arabidopsis thaliana GN=RGP2 PE=1 SV=1	5	0,296	0,143928036	334,2	0,366
O04200 PXN_ARATH Peroxisomal nicotinamide adenine dinucleotide carrier OS=Arabidopsis thaliana GN=PXN PE=1 SV=1	1	-0,62	0,144927536	336,52	0,367
Q94BQ2 PRS8B_ARATH 26S proteasome regulatory subunit 8 homolog B OS=Arabidopsis thaliana GN=RPT6B PE=1 SV=1	1	0,47	0,145427286	337,68	0,367

P51818 HS903_ARATH Heat shock protein 90-3 OS=Arabidopsis thaliana GN=HSP90-3 PE=1 SV=2	17	0,223	0,144427786	335,36	0,367
Q9M0B2 Q9M0B2_ARATH AT4G30480 protein OS=Arabidopsis thaliana GN=TPR1 PE=1 SV=1	1	0,857	0,145927036	338,84	0,368
Q43291 RL211_ARATH 60S ribosomal protein L21-1 OS=Arabidopsis thaliana GN=RPL21A PE=2 SV=2	1	0,509	0,146426787	340	0,368
Q9FE18 Q9FE18_ARATH Peptidyl-prolyl cis-trans isomerase OS=Arabidopsis thaliana GN=At1g26550 PE=2 SV=1	2	0,444	0,145927036	338,84	0,368
Q9SF15 PUB24_ARATH reversed E3 ubiquitin-protein ligase PUB24 OS=Arabidopsis thaliana GN=PUB24 PE=1 SV=1	1	-0,436	0,145927036	338,84	0,368
Q9FJH6 AB1F_ARATH ABC transporter F family member 1 OS=Arabidopsis thaliana GN=ABCF1 PE=2 SV=1	4	-0,349	0,147426287	342,32	0,368
P16181 RS111_ARATH 40S ribosomal protein S11-1 OS=Arabidopsis thaliana GN=RPS11A PE=2 SV=1	3	0,3	0,145427286	337,68	0,368
Q9T074 PCKA_ARATH Phosphoenolpyruvate carboxykinase (ATP) OS=Arabidopsis thaliana GN=PCKA PE=1 SV=1	9	0,278	0,146926537	341,16	0,368
Q9C9C5 RL63_ARATH 60S ribosomal protein L6-3 OS=Arabidopsis thaliana GN=RPL6C PE=2 SV=1	4	0,273	0,146426787	340	0,368
Q06327 LOX1_ARATH Linoleate 9S-lipoxygenase 1 OS=Arabidopsis thaliana GN=LOX1 PE=1 SV=1	19	-0,218	0,146426787	340	0,368
P56820 EIF3D_ARATH Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=TIF3D1 PE=1 SV=1	1	-0,539	0,147426287	342,32	0,369
Q9LZ98 AB201_ARATH ABC transporter I family member 20 OS=Arabidopsis thaliana GN=ABC120 PE=2 SV=1	3	-0,478	0,147426287	342,32	0,369
P93032 IDH2_ARATH Isocitrate dehydrogenase [NAD] regulatory subunit 2, mitochondrial OS=Arabidopsis thaliana GN=IDH2 PE=1 SV=2	3	-0,417	0,148425787	344,64	0,37
Q9LQ04 RMLCD_ARATH Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana GN=NRS/t	8	0,263	0,148425787	344,64	0,37
P51418 R18A2_ARATH 60S ribosomal protein L18a-2 OS=Arabidopsis thaliana GN=RPL18AB PE=1 SV=2	8	0,257	0,148925537	345,81	0,37
O24616 PSA7B_ARATH Proteasome subunit alpha type-7-B OS=Arabidopsis thaliana GN=PAD2 PE=1 SV=2	1	0,588	0,149425287	346,97	0,371
Q9SA14 LEU31_ARATH 3-isopropylmalate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=IMDH1 PE=2 SV=2	1	0,521	0,148925537	345,81	0,371
P51407 RLA21_ARATH 60S acidic ribosomal protein P2-1 OS=Arabidopsis thaliana GN=RPP2A PE=3 SV=2	2	0,371	0,148425787	344,64	0,371
Q9S726 RPI3_ARATH Probable ribose-5-phosphate isomerase 3, chloroplastic OS=Arabidopsis thaliana GN=RPI3 PE=1 SV=1	3	-0,456	0,150424788	349,29	0,372
Q9FNP8 RS193_ARATH 40S ribosomal protein S19-3 OS=Arabidopsis thaliana GN=RPS19C PE=2 SV=1	4	0,29	0,149925037	348,13	0,372
Q9LMI0 TPS7_ARATH Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7 OS=Arabidopsis thaliana GN=TPS7 PE=1 SV=1	1	0,624	0,151424288	351,61	0,373
Q9ZW84 LEUD1_ARATH 3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1	1	0,609	0,150424788	349,29	0,373
Q9LYT7 LEUD2_ARATH 3-isopropylmalate dehydratase small subunit 2 OS=Arabidopsis thaliana GN=IPMI1 PE=1 SV=1	2	0,411	0,150924538	350,45	0,373
O81062 SIP_ARATH Signal peptide peptidase OS=Arabidopsis thaliana GN=SPP PE=2 SV=1	3	0,4	0,150924538	350,45	0,373
Q9S7T8 SPZX_ARATH Serpin-ZX OS=Arabidopsis thaliana GN=At1g47710 PE=1 SV=1	6	-0,3	0,151424288	351,61	0,374
Q9SZX3 ASSY_ARATH Argininosuccinate synthase, chloroplastic OS=Arabidopsis thaliana GN=At4g24830 PE=1 SV=3	7	-0,279	0,151924038	352,77	0,374
P17562 METHK2_ARATH S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1	2	0,303	0,153423288	356,25	0,377
O24633 PSB2B_ARATH Proteasome subunit beta type-2-B OS=Arabidopsis thaliana GN=PBD2 PE=1 SV=1	3	0,34	0,153923038	357,41	0,378
Q9SFH9 HEM21_ARATH Delta-aminolevulinic acid dehydratase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMB1 PE=2 SV=1	1	-0,829	0,154922539	359,73	0,38
O04658 NOP5A_ARATH Probable nucleolar protein 5-1 OS=Arabidopsis thaliana GN=NOP5-1 PE=1 SV=2	2	-0,421	0,155422289	360,89	0,381
O64490 O64490_ARATH Eukaryotic translation initiation factor 2 gamma subunit OS=Arabidopsis thaliana GN=EIF2 GAMMA PE=2 SV=1	4	0,308	0,155422289	360,89	0,381
F4HRY1 F4HRY1_ARATH 3-oxo-5-alpha-steroid 4-dehydrogenase (DUF1295) OS=Arabidopsis thaliana GN=At1g73650 PE=4 SV=1	1	-0,747	0,156421789	363,21	0,382
O80929 RL361_ARATH 60S ribosomal protein L36-1 OS=Arabidopsis thaliana GN=RPL36A PE=3 SV=1	1	-0,87	0,157921039	366,69	0,383
P92963 RAB1C_ARATH Ras-related protein RAB1c OS=Arabidopsis thaliana GN=RAB1C PE=1 SV=1	1	0,857	0,156921539	364,37	0,383
F4IYB7 F4IYB7_ARATH Late embryogenesis abundant protein (LEA) family protein OS=Arabidopsis thaliana GN=At3g62580 PE=4 SV=1	1	-0,589	0,15842079	367,85	0,383
Q8L4S3 Q8L4S3_ARATH At5g09390/T5E8_190 OS=Arabidopsis thaliana GN=At5g09390 PE=1 SV=1	1	0,54	0,157921039	366,69	0,383
A0A1P8B098 A0A1P8B098_ARATH Translin family protein OS=Arabidopsis thaliana GN=At2g37020 PE=4 SV=1	2	-0,511	0,156421789	363,21	0,383
O24496 GLO2C_ARATH Hydroxyacylglutathione hydrolase cytoplasmic OS=Arabidopsis thaliana GN=GLX2-2 PE=1 SV=2	1	0,888	0,157921039	366,69	0,384
F4I3J0 F4I3J0_ARATH Obg-like ATPase 1 OS=Arabidopsis thaliana GN=At1g56050 PE=3 SV=1	1	0,887	0,157421289	365,53	0,384
Q9FIE8 UXS3_ARATH UDP-glucuronic acid decarboxylase 3 OS=Arabidopsis thaliana GN=UXS3 PE=1 SV=1	2	0,474	0,15842079	367,85	0,384
Q9LP53 Q9LP53_ARATH Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g29250 PE=1 SV=1	2	-0,444	0,157921039	366,69	0,384
F4IE14 F4IE14_ARATH Ubiquinone biosynthesis COQ9-like protein OS=Arabidopsis thaliana GN=At1g19140 PE=4 SV=1	4	-0,36	0,157921039	366,69	0,384
F4KAS6 F4KAS6_ARATH GroES-like zinc-binding alcohol dehydrogenase family protein OS=Arabidopsis thaliana GN=MBK5.9 PE=4 SV=1	2	-0,43	0,15942029	370,17	0,385
Q9MAH0 CAPP1_ARATH Phosphoenolpyruvate carboxylase 1 OS=Arabidopsis thaliana GN=PPC1 PE=1 SV=1	8	0,278	0,157921039	366,69	0,385
O49304 O49304_ARATH At1g23130/T26J12_10 OS=Arabidopsis thaliana GN=At1g23130 PE=2 SV=1	1	-0,886	0,15992004	371,33	0,386
Q9SKZ0 Q9SKZ0_ARATH At2g32090/F22D22.16 OS=Arabidopsis thaliana GN=At2g32090 PE=2 SV=2	1	-0,617	0,15992004	371,33	0,386
Q9LYA5 Q9LYA5_ARATH Thioredoxin superfamily protein OS=Arabidopsis thaliana GN=At5g14240 PE=2 SV=1	1	0,623	0,162418791	377,14	0,391
Q940V3 U91A1_ARATH UDP-glycosyltransferase 91A1 OS=Arabidopsis thaliana GN=UGT91A1 PE=2 SV=1	1	-0,624	0,162918541	378,3	0,392
Q9LK88 NQR_ARATH NADPH:quinone oxidoreductase OS=Arabidopsis thaliana GN=NQR PE=1 SV=1	5	-0,325	0,162918541	378,3	0,392
O49339 PTI12_ARATH PTI1-like tyrosine-protein kinase 2 OS=Arabidopsis thaliana GN=PTI12 PE=1 SV=1	2	-0,616	0,164835165	382,75	0,393
Q9LZX1 LOR15_ARATH Protein LURP-one-related 15 OS=Arabidopsis thaliana GN=At5g01750 PE=1 SV=1	1	-0,528	0,16983017	394,35	0,393

P49200 RS201_ARATH 40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2	1	0,477	0,168915542	392,22	0,393
Q9SV68 QORH_ARATH Chloroplast envelope quinone oxidoreductase homolog OS=Arabidopsis thaliana GN=CEQORH PE=1 SV=1	3	-0,355	0,168831169	392,03	0,393
P04778 CB1C_ARATH Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1	3	-0,319	0,163918041	380,62	0,393
Q9SKC5 U74D1_ARATH UDP-glycosyltransferase 74D1 OS=Arabidopsis thaliana GN=UGT74D1 PE=1 SV=1	1	0,835	0,164835165	382,75	0,394
Q9CA83 MAOP4_ARATH NADP-dependent malic enzyme 4, chloroplastic OS=Arabidopsis thaliana GN=NADP-ME4 PE=1 SV=1	1	0,832	0,168831169	392,03	0,394
P29516 TBB8_ARATH Tubulin beta-8 chain OS=Arabidopsis thaliana GN=TUBB8 PE=2 SV=2	1	-0,821	0,163918041	380,62	0,394
F4J4K6 F4J4K6_ARATH Tubulin binding cofactor C domain-containing protein OS=Arabidopsis thaliana GN=At3g57890 PE=4 SV=1	1	-0,636	0,16983017	394,35	0,394
F4JGB4 F4JGB4_ARATH Microsomal signal peptidase 25 kDa subunit (SPC25) OS=Arabidopsis thaliana GN=At4g04200 PE=4 SV=1	1	-0,597	0,168831169	392,03	0,394
Q6ID29 Q6ID29_ARATH At4g13860 OS=Arabidopsis thaliana GN=At4g13860 PE=2 SV=1	1	-0,583	0,167832168	389,71	0,394
Q9XF19 AB21I_ARATH ABC transporter I family member 21 OS=Arabidopsis thaliana GN=ABCI21 PE=2 SV=1	2	-0,459	0,16983017	394,35	0,394
P42799 GSA1_ARATH Glutamate-1-semialdehyde 2,1-aminomutase 1, chloroplastic OS=Arabidopsis thaliana GN=GSA1 PE=1 SV=1	3	-0,457	0,16983017	394,35	0,394
O23406 U75D1_ARATH UDP-glycosyltransferase 75D1 OS=Arabidopsis thaliana GN=UGT75D1 PE=2 SV=2	2	0,451	0,164417791	381,78	0,394
P59230 R10A2_ARATH 60S ribosomal protein L10a-2 OS=Arabidopsis thaliana GN=RPL10AB PE=1 SV=1	3	0,39	0,170829171	396,67	0,394
F4I1G1 F4I1G1_ARATH RNA polymerase II degradation factor-like protein (DUF1296) OS=Arabidopsis thaliana GN=At1g29350 PE=4 SV=1	4	-0,381	0,164417791	381,78	0,394
P29514 TBB6_ARATH Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1	1	0,362	0,170829171	396,67	0,394
Q9FFS8 RS102_ARATH 40S ribosomal protein S10-2 OS=Arabidopsis thaliana GN=RPS10B PE=2 SV=1	5	0,31	0,172827173	401,3	0,394
Q9LUG8 Q9LUG8_ARATH ATP3g23600/MDB19_9 OS=Arabidopsis thaliana GN=At3g23600 PE=2 SV=1	4	-0,302	0,168831169	392,03	0,394
O81148 PSA4A_ARATH Proteasome subunit alpha type-4-A OS=Arabidopsis thaliana GN=PAC1 PE=1 SV=1	6	-0,299	0,164835165	382,75	0,394
O04630 SYTM1_ARATH Threonine--tRNA ligase, mitochondrial 1 OS=Arabidopsis thaliana GN=THRRS PE=1 SV=3	7	-0,274	0,167832168	389,71	0,394
B9DHHQ TBA5_ARATH Tubulin alpha-5 chain OS=Arabidopsis thaliana GN=TUBA5 PE=1 SV=2	6	-0,271	0,167916042	389,9	0,394
Q9SGW6 Q9SGW6_ARATH At1g64490 OS=Arabidopsis thaliana GN=At1g64490 PE=2 SV=1	1	0,851	0,170829171	396,67	0,395
Q680H3 PP170_ARATH Pentatricopeptide repeat-containing protein At2g25580 OS=Arabidopsis thaliana GN=PCMP-H75 PE=2 SV=2	1	-0,829	0,168831169	392,03	0,395
Q94AW8 DNAJ3_ARATH Chaperone protein dnaJ 3 OS=Arabidopsis thaliana GN=ATJ3 PE=1 SV=2	1	0,612	0,171828172	398,99	0,395
Q9LYB4 GPX5_ARATH Probable glutathione peroxidase 5 OS=Arabidopsis thaliana GN=GPX5 PE=1 SV=1	1	-0,607	0,173826174	403,62	0,395
O23629 H2B6_ARATH Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	1	-0,582	0,168831169	392,03	0,395
Q6ICX4 PTBP3_ARATH Polypyrimidine tract-binding protein homolog 3 OS=Arabidopsis thaliana GN=At1g43190 PE=2 SV=1	1	0,578	0,167416292	388,74	0,395
Q94EH8 THO4C_ARATH THO complex subunit 4C OS=Arabidopsis thaliana GN=ALY3 PE=1 SV=1	1	-0,56	0,172827173	401,3	0,395
Q42533 BCCP1_ARATH Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=BCCP1 PE=1 SV=2	1	-0,54	0,171828172	398,99	0,395
Q9SJM0 CALSA_ARATH Callose synthase 10 OS=Arabidopsis thaliana GN=CALS10 PE=2 SV=5	2	0,447	0,172827173	401,3	0,395
Q41188 CSP2_ARATH Cold shock protein 2 OS=Arabidopsis thaliana GN=CSP2 PE=1 SV=1	2	-0,422	0,167832168	389,71	0,395
Q8VZU2 SY132_ARATH Syntaxin-132 OS=Arabidopsis thaliana GN=SYP132 PE=1 SV=1	2	-0,414	0,167832168	389,71	0,395
Q9FLB7 Q9FLB7_ARATH At5g05370 OS=Arabidopsis thaliana GN=At5g05370 PE=2 SV=1	1	0,406	0,170829171	396,67	0,395
Q9FFU1 CAF2M_ARATH CRS2-associated factor 2, mitochondrial OS=Arabidopsis thaliana GN=At5g54890 PE=2 SV=1	1	0,399	0,16983017	394,35	0,395
Q9C909 RBG5_ARATH Glycine-rich RNA-binding protein 5, mitochondrial OS=Arabidopsis thaliana GN=RBG5 PE=1 SV=1	2	0,394	0,173826174	403,62	0,395
Q93ZY3 STT3A_ARATH Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Arabidopsis thaliana GN=STT3A PE=2 SV=1	2	0,359	0,171828172	398,99	0,395
Q94K48 Q94K48_ARATH ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g62530 PE=2 SV=1	5	-0,287	0,172827173	401,3	0,395
Q9FJ95 DHSO_ARATH Sorbitol dehydrogenase OS=Arabidopsis thaliana GN=SDH PE=1 SV=1	7	-0,28	0,166833167	387,39	0,395
Q9SK87 ADHL2_ARATH Alcohol dehydrogenase-like 2 OS=Arabidopsis thaliana GN=At1g22440 PE=2 SV=1	5	-0,266	0,166833167	387,39	0,395
O64530 STR1_ARATH Thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial OS=Arabidopsis thaliana GN=STR1 PE=1 SV=1	7	-0,264	0,165834166	385,07	0,395
O81030 GGL05_ARATH L-gulonolactone oxidase 5 OS=Arabidopsis thaliana GN=GULLO5 PE=1 SV=1	1	-0,86	0,166833167	387,39	0,396
F4J8X6 F4J8X6_ARATH Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain-containing protein OS=Arabidopsis thaliana GN=NTF2 PE=1 SV=1	1	-0,847	0,167832168	389,71	0,396
Q39024 MPK4_ARATH Mitogen-activated protein kinase 4 OS=Arabidopsis thaliana GN=MPK4 PE=1 SV=2	1	0,642	0,168831169	392,03	0,396
Q8LE47 PPR87_ARATH Pentatricopeptide repeat-containing protein At1g61870, mitochondrial OS=Arabidopsis thaliana GN=PPR336 PE=2 SV=2	1	0,608	0,167416292	388,74	0,396
Q9SFV3 Q9SFV3_ARATH At3g07230 OS=Arabidopsis thaliana GN=T1B9.10 PE=2 SV=1	1	0,583	0,166833167	387,39	0,396
Q9FT50 FB202_ARATH Putative F-box protein At3g52320 OS=Arabidopsis thaliana GN=At3g52320 PE=4 SV=1	1	-0,537	0,167832168	389,71	0,396
P49688 RS23_ARATH 40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2	1	0,426	0,174912544	406,15	0,396
Q9SKL6 Q9SKL6_ARATH At2g15220/F15A23.4 OS=Arabidopsis thaliana GN=At2g15220 PE=2 SV=1	3	-0,415	0,174825175	405,94	0,396
Q43870 APS2_ARATH ATP sulfurylase 2 OS=Arabidopsis thaliana GN=APS2 PE=1 SV=1	2	-0,402	0,173826174	403,62	0,396
Q9FXD4 Q9FXD4_ARATH Signal recognition particle subunit SRP72 OS=Arabidopsis thaliana GN=At1g67680 PE=1 SV=1	4	-0,394	0,172827173	401,3	0,396
Q93272 Q93272_ARATH AT5g16970/F2K13_120 OS=Arabidopsis thaliana GN=At5g17000 PE=2 SV=1	4	-0,354	0,172827173	401,3	0,396
P29515 TBB7_ARATH Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	3	-0,351	0,173826174	403,62	0,396

Q9M7T0 PRX2F_ARATH Peroxiredoxin-2F, mitochondrial OS=Arabidopsis thaliana GN=PRXIIF PE=1 SV=2	6	-0,256	0,171828172	398,99	0,396
O04499 PMG1_ARATH 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=PGM1 PE=2 SV=3	11	0,223	0,166416792	386,42	0,396
Q8RWP0 Q8RWP0_ARATH NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At3g20790 PE=2 SV=1	1	0,868	0,172827173	401,3	0,397
Q9LFU9 GNA1_ARATH Glucosamine 6-phosphate N-acetyltransferase OS=Arabidopsis thaliana GN=GNA1 PE=1 SV=1	1	-0,579	0,166833167	387,39	0,397
Q9SKU1 CLC1_ARATH Clathrin light chain 1 OS=Arabidopsis thaliana GN=At2g20760 PE=2 SV=1	1	-0,568	0,166833167	387,39	0,397
F41710 ALAT1_ARATH Alanine aminotransferase 1, mitochondrial OS=Arabidopsis thaliana GN=ALAAT1 PE=1 SV=1	1	-0,438	0,175824176	408,26	0,397
Q9M5P2 SCAM3_ARATH Secretory carrier-associated membrane protein 3 OS=Arabidopsis thaliana GN=SCAMP3 PE=1 SV=1	3	-0,345	0,174825175	405,94	0,397
O64806 ACA7_ARATH Putative calcium-transporting ATPase 7, plasma membrane-type OS=Arabidopsis thaliana GN=ACA7 PE=3 SV=2	1	-0,544	0,175824176	408,26	0,398
Q9LJ98 PFD2_ARATH Probable prefoldin subunit 2 OS=Arabidopsis thaliana GN=At3g22480 PE=2 SV=1	2	0,471	0,175824176	408,26	0,398
P59169 H33_ARATH Histone H3.3 OS=Arabidopsis thaliana GN=HTR4 PE=1 SV=2	1	-0,465	0,176411794	409,63	0,398
Q8LAD2 SUC2_ARATH Succinate--CoA ligase [ADP-forming] subunit alpha-2, mitochondrial OS=Arabidopsis thaliana GN=At5g23250 PE=1 SV=2	1	-0,388	0,176823177	410,58	0,398
Q8W4L3 Q8W4L3_ARATH BR-signaling kinase 3 OS=Arabidopsis thaliana GN=BR-signaling kinase 3 PE=2 SV=1	4	-0,358	0,176823177	410,58	0,399
Q9SUN5 Q9SUN5_ARATH Small nuclear ribonucleoprotein-associated protein OS=Arabidopsis thaliana GN=smb PE=2 SV=1	3	-0,378	0,177822178	412,9	0,4
Q9ZV19 DJ1E_ARATH DJ-1 protein homolog E OS=Arabidopsis thaliana GN=DJ1E PE=1 SV=1	4	0,296	0,177822178	412,9	0,4
B9DHK3 B9DHK3_ARATH AT5G14540 protein OS=Arabidopsis thaliana GN=At5g14540 PE=1 SV=1	1	0,797	0,17982018	417,54	0,401
Q8RXN3 PPT1_ARATH Phosphoenolpyruvate/phosphate translocator 1, chloroplastic OS=Arabidopsis thaliana GN=PPT1 PE=1 SV=1	1	-0,485	0,178821179	415,22	0,401
Q9FKM2 VDAC4_ARATH Mitochondrial outer membrane protein porin 4 OS=Arabidopsis thaliana GN=VDAC4 PE=1 SV=1	2	-0,395	0,17982018	417,54	0,401
Q9SIM4 RL141_ARATH 60S ribosomal protein L14-1 OS=Arabidopsis thaliana GN=RPL14A PE=2 SV=1	2	0,386	0,178821179	415,22	0,401
P92966 SRS41_ARATH Serine/arginine-rich splicing factor RS41 OS=Arabidopsis thaliana GN=RS41 PE=1 SV=2	1	-0,85	0,17982018	417,54	0,402
P55852 SUMO1_ARATH Small ubiquitin-related modifier 1 OS=Arabidopsis thaliana GN=SUMO1 PE=1 SV=2	1	-0,843	0,17982018	417,54	0,402
Q9SIE3 Q9SIE3_ARATH At2g22230/T26C19.11 OS=Arabidopsis thaliana GN=At2g22230 PE=2 SV=2	2	-0,596	0,180819181	419,86	0,402
Q9SUR4 Q9SUR4_ARATH Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain-containing protein OS=Arabidopsis thaliana GN=At4g	1	-0,521	0,179410295	416,59	0,402
Q680P8 RS29_ARATH 40S ribosomal protein S29 OS=Arabidopsis thaliana GN=RPS29A PE=3 SV=2	2	0,359	0,178821179	415,22	0,402
O80476 MES2_ARATH Methylesterase 2 OS=Arabidopsis thaliana GN=MES2 PE=1 SV=1	1	-0,849	0,180819181	419,86	0,403
O48844 PSD1A_ARATH 26S proteasome non-ATPase regulatory subunit 1 homolog A OS=Arabidopsis thaliana GN=RPN2A PE=1 SV=1	3	-0,328	0,180819181	419,86	0,403
P29515 TBB7_ARATH Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	2	-0,449	0,181818182	422,18	0,404
P25819 CATA2_ARATH Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3	6	-0,24	0,182817183	424,5	0,405
Q9LZ82 BTR1_ARATH Protein BTR1 OS=Arabidopsis thaliana GN=BTR1 PE=1 SV=1	9	0,238	0,182817183	424,5	0,405
Q9LR44 U75B1_ARATH UDP-glycosyltransferase 75B1 OS=Arabidopsis thaliana GN=UGT75B1 PE=1 SV=1	1	0,854	0,184815185	429,14	0,406
Q9LV66 Y5848_ARATH Uncharacterized protein At5g48480 OS=Arabidopsis thaliana GN=At5g48480 PE=1 SV=1	4	-0,328	0,183816184	426,82	0,406
O04331 PHB3_ARATH Prohibitin-3, mitochondrial OS=Arabidopsis thaliana GN=PHB3 PE=1 SV=1	5	-0,24	0,184815185	429,14	0,406
P31167 ADT1_ARATH ADP,ATP carrier protein 1, mitochondrial OS=Arabidopsis thaliana GN=AAC1 PE=1 SV=2	6	0,204	0,182817183	424,5	0,406
Q6NL24 ECH1P_ARATH Probable enoyl-CoA hydratase 1, peroxisomal OS=Arabidopsis thaliana GN=ECHIA PE=1 SV=1	1	-0,807	0,185814186	431,46	0,407
Q9LXJ2 Q9LXJ2_ARATH Ubiquinol--cytochrome-c reductase-like protein OS=Arabidopsis thaliana GN=F3C22_130 PE=2 SV=1	3	0,359	0,183816184	426,82	0,407
Q9SL42 PIN1_ARATH Peptidyl-prolyl cis-trans isomerase Pin1 OS=Arabidopsis thaliana GN=PIN1 PE=1 SV=1	4	0,299	0,184815185	429,14	0,407
Q9SLA8 FABI_ARATH Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic OS=Arabidopsis thaliana GN=MOD1 PE=1 SV=1	10	-0,239	0,184815185	429,14	0,407
Q9LEU8 ARLY_ARATH Argininosuccinate lyase, chloroplastic OS=Arabidopsis thaliana GN=At5g10920 PE=2 SV=1	1	0,577	0,184815185	429,14	0,408
Q94AU7 GCA3_ARATH Gamma carbonic anhydrase 3, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA3 PE=1 SV=1	1	-0,424	0,184815185	429,14	0,408
Q9FE65 RL342_ARATH 60S ribosomal protein L34-2 OS=Arabidopsis thaliana GN=RPL34B PE=3 SV=1	1	-0,421	0,185814186	431,46	0,408
Q9FHG2 RL322_ARATH 60S ribosomal protein L32-2 OS=Arabidopsis thaliana GN=RPL32B PE=2 SV=1	2	0,361	0,184815185	429,14	0,408
Q9M7Z1 ODB2_ARATH Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Arabidopsi	1	0,791	0,186813187	433,78	0,409
P92941 CLCA_ARATH Chloride channel protein CLC-a OS=Arabidopsis thaliana GN=CLC-A PE=1 SV=2	2	-0,383	0,186813187	433,78	0,409
O64527 Y1926_ARATH UPF0678 fatty acid-binding protein-like protein At1g79260 OS=Arabidopsis thaliana GN=At1g79260 PE=1 SV=1	2	0,487	0,187812188	436,1	0,41
O22862 PER26_ARATH Probable peroxidase 26 OS=Arabidopsis thaliana GN=PER26 PE=2 SV=2	1	-0,808	0,188811189	438,42	0,411
Q2HIK4 Q2HIK4_ARATH At1g29990 OS=Arabidopsis thaliana GN=PFD6 PE=2 SV=1	2	0,459	0,187812188	436,1	0,411
Q0WW26 COPG_ARATH Coatomer subunit gamma OS=Arabidopsis thaliana GN=At4g34450 PE=1 SV=2	17	0,216	0,188811189	438,42	0,411
Q9SU56 GLDH_ARATH L-galactono-1,4-lactone dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=GLDH PE=1 SV=1	1	-0,807	0,188811189	438,42	0,412
Q8GRX1 BGL34_ARATH Myrosinase 4 OS=Arabidopsis thaliana GN=TGG4 PE=1 SV=1	3	-0,356	0,188811189	438,42	0,412
Q8LF20 CAP2_ARATH Putative clathrin assembly protein At2g25430 OS=Arabidopsis thaliana GN=At2g25430 PE=1 SV=2	1	0,577	0,190809191	443,06	0,414
Q94KE3 Q94KE3_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=At3g52990 PE=2 SV=1	3	-0,338	0,190809191	443,06	0,414
Q93WJ8 MDAR2_ARATH Monodehydroascorbate reductase 2 OS=Arabidopsis thaliana GN=MDAR2 PE=1 SV=1	1	-0,498	0,190809191	443,06	0,415

P35510 PAL1_ARATH Phenylalanine ammonia-lyase 1 OS=Arabidopsis thaliana GN=PAL1 PE=1 SV=3	3	-0,34	0,191808192	445,38	0,415
P49572 TRPC_ARATH Indole-3-glycerol phosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=IGPS PE=1 SV=2	4	-0,34	0,191808192	445,38	0,415
Q9LIK0 PKP1_ARATH Plastidial pyruvate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=PKP1 PE=1 SV=1	11	-0,232	0,191808192	445,38	0,415
Q9FGK0 NDUB8_ARATH NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Arabidopsis thaliana GN=At5g47570 PE=2 SV=1	1	0,482	0,191808192	445,38	0,416
Q8L828 COB23_ARATH Coatomer subunit beta'-3 OS=Arabidopsis thaliana GN=At3g15980 PE=2 SV=1	5	-0,316	0,192807193	447,7	0,416
Q8LPK7 Q8LPK7_ARATH Paramyosin OS=Arabidopsis thaliana GN=At1g24560 PE=2 SV=1	1	-0,808	0,193806194	450,02	0,417
O23157 O23157_ARATH AT4g37300/C7A10_60 OS=Arabidopsis thaliana GN=C7A10.60 PE=1 SV=1	1	0,539	0,193806194	450,02	0,418
Q8S528 AL2B7_ARATH Aldehyde dehydrogenase family 2 member B7, mitochondrial OS=Arabidopsis thaliana GN=ALDH2B7 PE=1 SV=2	1	-0,429	0,194805195	452,34	0,418
Q9SSB7 Q9SSB7_ARATH At1g80240 OS=Arabidopsis thaliana GN=DGR1 PE=2 SV=1	5	-0,277	0,193806194	450,02	0,418
P52032 GPX1_ARATH Phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic OS=Arabidopsis thaliana GN=GPX1 PE=2 SV=2	1	-0,558	0,195804196	454,66	0,419
Q9STY6 RS202_ARATH 40S ribosomal protein S20-2 OS=Arabidopsis thaliana GN=RPS20B PE=2 SV=1	1	0,392	0,194805195	452,34	0,419
Q9SUS3 APBLB_ARATH Beta-adaptin-like protein B OS=Arabidopsis thaliana GN=BETAB-AD PE=1 SV=1	4	-0,343	0,194805195	452,34	0,419
Q9LIK9 APS1_ARATH ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=1 SV=1	1	0,542	0,195804196	454,66	0,42
O65201 ACOX2_ARATH Acyl-coenzyme A oxidase 2, peroxisomal OS=Arabidopsis thaliana GN=ACX2 PE=1 SV=2	2	0,45	0,197802198	459,3	0,42
Q9FMG4 SC35_ARATH Serine/arginine-rich splicing factor SC35 OS=Arabidopsis thaliana GN=SC35 PE=1 SV=1	2	-0,399	0,195804196	454,66	0,42
P93832 LEU32_ARATH 3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1	3	0,3	0,196803197	456,98	0,42
Q8L9J9 CAES_ARATH Probable carbohydrate esterase At4g34215 OS=Arabidopsis thaliana GN=At4g34215 PE=1 SV=2	1	-0,796	0,196803197	456,98	0,421
Q9C768 U76B1_ARATH UDP-glycosyltransferase 76B1 OS=Arabidopsis thaliana GN=UGT76B1 PE=2 SV=1	3	0,36	0,197802198	459,3	0,421
P93313 NU4M_ARATH NADH-ubiquinone oxidoreductase chain 4 OS=Arabidopsis thaliana GN=ND4 PE=2 SV=2	1	-0,358	0,198801199	461,62	0,421
O04153 CALR3_ARATH Calreticulin-3 OS=Arabidopsis thaliana GN=CRT3 PE=1 SV=2	3	0,343	0,197802198	459,3	0,421
Q94CE4-2 BCA4_ARATH Isoform 2 of Beta carbonic anhydrase 4 OS=Arabidopsis thaliana GN=BCA4	8	-0,255	0,197802198	459,3	0,421
Q9SYG7 AL7B4_ARATH Aldehyde dehydrogenase family 7 member B4 OS=Arabidopsis thaliana GN=ALDH7B4 PE=2 SV=3	8	-0,245	0,196803197	456,98	0,421
Q9SRX4 PME7_ARATH Probable pectinesterase/pectinesterase inhibitor 7 OS=Arabidopsis thaliana GN=PME7 PE=2 SV=1	1	0,572	0,197802198	459,3	0,422
Q9SZF8 Q9SZF8_ARATH AT4g37660/F19F18_150 OS=Arabidopsis thaliana GN=At4g37660 PE=2 SV=1	1	-0,541	0,198801199	461,62	0,422
P48482 PP12_ARATH Serine/threonine-protein phosphatase PP1 isozyme 2 OS=Arabidopsis thaliana GN=TOPP2 PE=1 SV=1	3	-0,476	0,197802198	459,3	0,422
Q9C8G9 AB1C_ARATH ABC transporter C family member 1 OS=Arabidopsis thaliana GN=ABCC1 PE=1 SV=1	5	0,363	0,198801199	461,62	0,422
Q1PF74 Q1PF74_ARATH reversed Nuclease OS=Arabidopsis thaliana GN=At2g13770 PE=2 SV=1	1	0,79	0,1998002	463,94	0,423
Q9LJE4 CPNB2_ARATH Chaperonin 60 subunit beta 2, chloroplastic OS=Arabidopsis thaliana GN=CPN60B2 PE=1 SV=1	3	-0,333	0,200799201	466,26	0,424
Q7X659 VP35A_ARATH Vacuolar protein sorting-associated protein 35A OS=Arabidopsis thaliana GN=VPS35A PE=1 SV=1	1	-0,814	0,200799201	466,26	0,425
Q9FI53 FUM2_ARATH reversed Fumarate hydratase 2, chloroplastic OS=Arabidopsis thaliana GN=FUM2 PE=2 SV=1	1	0,744	0,201798202	468,58	0,426
P50883 RL121_ARATH 60S ribosomal protein L12-1 OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=2	1	0,567	0,201798202	468,58	0,426
P60039 RL73_ARATH 60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	4	0,281	0,202797203	470,9	0,426
Q9C5D7 CAMT3_ARATH Probable caffeoyl-CoA O-methyltransferase At4g26220 OS=Arabidopsis thaliana GN=At4g26220 PE=2 SV=1	1	0,569	0,202797203	470,9	0,427
P28188 RAD2A_ARATH Ras-related protein RABD2a OS=Arabidopsis thaliana GN=RABD2A PE=1 SV=3	1	-0,549	0,202797203	470,9	0,427
O22909 O22909_ARATH reversed At2g47350 OS=Arabidopsis thaliana GN=At2g47350 PE=2 SV=1	1	0,548	0,203796204	473,21	0,427
Q9C7W1 Q9C7W1_ARATH Filaggrin-like protein OS=Arabidopsis thaliana GN=At1g64370 PE=1 SV=1	1	0,535	0,203796204	473,21	0,427
Q9M8L4 GLPK_ARATH Glycerol kinase OS=Arabidopsis thaliana GN=GLPK PE=1 SV=1	9	-0,209	0,202797203	470,9	0,427
O24653 GDI2_ARATH Guanosine nucleotide diphosphate dissociation inhibitor 2 OS=Arabidopsis thaliana GN=GDI2 PE=2 SV=1	4	0,278	0,204795205	475,53	0,428
Q940B0 RL183_ARATH 60S ribosomal protein L18-3 OS=Arabidopsis thaliana GN=RPL18C PE=2 SV=1	9	0,209	0,203796204	473,21	0,428
O49339 PTI12_ARATH PTI1-like tyrosine-protein kinase 2 OS=Arabidopsis thaliana GN=PTI12 PE=1 SV=1	1	-0,489	0,204795205	475,53	0,429
F4JAU3 P4H2_ARATH Prolyl 4-hydroxylase 2 OS=Arabidopsis thaliana GN=P4H2 PE=1 SV=1	4	0,307	0,205794206	477,85	0,43
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	1	0,529	0,206793207	480,17	0,431
Q9SR52 UREA_ARATH Urease OS=Arabidopsis thaliana GN=URE PE=3 SV=1	1	0,455	0,206793207	480,17	0,431
Q9SSR2 Q9SSR2_ARATH Signal peptidase I OS=Arabidopsis thaliana GN=At1g52600 PE=2 SV=1	2	0,45	0,206793207	480,17	0,431
O22218 ACA4_ARATH reversed Calcium-transporting ATPase 4, plasma membrane-type OS=Arabidopsis thaliana GN=ACA4 PE=1 SV=1	1	0,552	0,206793207	480,17	0,432
B0F9L4 GOGC6_ARATH Golgin candidate 6 OS=Arabidopsis thaliana GN=GC6 PE=1 SV=2	1	-0,53	0,207792208	482,49	0,432
Q9SJQ0 Q9SJQ0_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=At2g36580 PE=1 SV=2	3	0,334	0,207792208	482,49	0,432
Q0WQF7 ODP21_ARATH Dihydrolypoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex, mitochondrial OS=Arabidopsi	4	-0,272	0,207792208	482,49	0,432
F4J5M9 CLC3_ARATH Clathrin light chain 3 OS=Arabidopsis thaliana GN=At3g51890 PE=1 SV=1	1	0,387	0,208791209	484,81	0,433
Q9SUT2 PER39_ARATH Peroxidase 39 OS=Arabidopsis thaliana GN=PER39 PE=1 SV=1	7	0,222	0,208791209	484,81	0,433
Q9M339 RS32_ARATH 40S ribosomal protein S3-2 OS=Arabidopsis thaliana GN=RPS3B PE=1 SV=1	13	0,197	0,20979021	487,13	0,434

Q9SCK3 Q9SCK3_ARATH At3g49560 OS=Arabidopsis thaliana GN=T9C5.150 PE=2 SV=1	1	-0,543	0,210789211	489,45	0,435
Q9SIH4 CASP1_ARATH Casparian strip membrane protein 1 OS=Arabidopsis thaliana GN=CASP1 PE=1 SV=1	2	-0,446	0,210789211	489,45	0,435
O04848 H2AXA_ARATH Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1	2	-0,396	0,211788212	491,77	0,435
Q9STW6 HSP7F_ARATH Heat shock 70 kDa protein 6, chloroplastic OS=Arabidopsis thaliana GN=HSP70-6 PE=1 SV=1	3	-0,353	0,209790211	487,13	0,435
O23708 PSA2A_ARATH Proteasome subunit alpha type-2-A OS=Arabidopsis thaliana GN=PAB1 PE=1 SV=1	7	-0,239	0,210789211	489,45	0,435
Q9LH98 Q9LH98_ARATH reversed Transmembrane protein, putative (DUF1216) OS=Arabidopsis thaliana GN=At3g28770 PE=4 SV=1	1	-0,439	0,212787213	494,09	0,436
Q9FF90 RL133_ARATH 60S ribosomal protein L13-3 OS=Arabidopsis thaliana GN=RPL13D PE=1 SV=1	3	-0,306	0,211788212	491,77	0,436
Q9LM02 SMT1_ARATH Cycloartenol-C-24-methyltransferase OS=Arabidopsis thaliana GN=SMT1 PE=1 SV=1	5	-0,277	0,211788212	491,77	0,436
P49637 R27A3_ARATH 60S ribosomal protein L27a-3 OS=Arabidopsis thaliana GN=RPL27AC PE=2 SV=2	8	0,229	0,211788212	491,77	0,436
O65398 GLX1_ARATH Lactoylglutathione lyase GLX1 OS=Arabidopsis thaliana GN=GLX1 PE=1 SV=1	12	-0,202	0,210789211	489,45	0,436
Q9M651 RAGP2_ARATH RAN GTPase-activating protein 2 OS=Arabidopsis thaliana GN=RANGAP2 PE=1 SV=2	1	0,53	0,212787213	494,09	0,437
Q0WNNQ5 Q0WNNQ5_ARATH LONGIFOLIA protein OS=Arabidopsis thaliana GN=TRM4 PE=2 SV=1	1	-0,489	0,214785215	498,73	0,438
P28185 RAA1A_ARATH Ras-related protein RABA1a OS=Arabidopsis thaliana GN=RABA1A PE=1 SV=1	2	-0,471	0,213786214	496,41	0,438
Q9M012 EXPB3_ARATH Expansin-B3 OS=Arabidopsis thaliana GN=EXPB3 PE=2 SV=2	1	0,527	0,214785215	498,73	0,439
Q9C942 CSE_ARATH Caffeoyleshikimate esterase OS=Arabidopsis thaliana GN=CSE PE=1 SV=1	3	-0,317	0,214785215	498,73	0,439
Q9SGA6 RS191_ARATH 40S ribosomal protein S19-1 OS=Arabidopsis thaliana GN=RPS19A PE=2 SV=1	5	0,267	0,214785215	498,73	0,439
Q56YW9 TBB2_ARATH Tubulin beta-2 chain OS=Arabidopsis thaliana GN=TUBB2 PE=2 SV=2	5	0,235	0,215784216	501,05	0,439
Q9SIU2 NCBP1_ARATH Nuclear cap-binding protein subunit 1 OS=Arabidopsis thaliana GN=ABH1 PE=1 SV=2	1	-0,552	0,216783217	503,37	0,44
Q42545 FTSZ1_ARATH Cell division protein FtsZ homolog 1, chloroplastic OS=Arabidopsis thaliana GN=FTSZ1 PE=1 SV=2	1	-0,537	0,217782218	505,69	0,44
Q9SE33 RAR1_ARATH Cysteine and histidine-rich domain-containing protein RAR1 OS=Arabidopsis thaliana GN=RAR1 PE=1 SV=1	1	-0,525	0,215784216	501,05	0,44
Q9FMH8 RD21B_ARATH Probable cysteine protease RD21B OS=Arabidopsis thaliana GN=RD21B PE=1 SV=1	1	-0,386	0,217782218	505,69	0,44
P48348 14338_ARATH 14-3-3-like protein GF14 kappa OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=2	4	-0,265	0,215784216	501,05	0,44
O22173 PABP4_ARATH Polyadenylate-binding protein 4 OS=Arabidopsis thaliana GN=PAB4 PE=1 SV=1	9	0,221	0,214785215	498,73	0,44
F4HWD5 F4HWD5_ARATH DNAJ heat shock N-terminal domain-containing protein OS=Arabidopsis thaliana GN=At1g21080 PE=4 SV=1	1	-0,708	0,216783217	503,37	0,441
Q6NLG7 RFA3B_ARATH Replication protein A 14 kDa subunit B OS=Arabidopsis thaliana GN=RPA3B PE=1 SV=1	1	0,557	0,217782218	505,69	0,441
Q94A28 ACO2M_ARATH Aconitate hydratase 2, mitochondrial OS=Arabidopsis thaliana GN=ACO2 PE=1 SV=3	17	-0,189	0,217782218	505,69	0,441
Q9ZRE2 RABD1_ARATH Ras-related protein RABD1 OS=Arabidopsis thaliana GN=RABD1 PE=1 SV=1	1	-0,551	0,21978022	510,33	0,442
Q9SA96 AROD1_ARATH Arogenate dehydratase/prephenate dehydratase 1, chloroplastic OS=Arabidopsis thaliana GN=ADT1 PE=1 SV=1	1	-0,524	0,217782218	505,69	0,442
Q8VZG8 MIK2_ARATH MDIS1-interacting receptor like kinase 2 OS=Arabidopsis thaliana GN=MIK2 PE=1 SV=3	1	-0,511	0,218781219	508,01	0,442
Q8VYN6 PFKA5_ARATH ATP-dependent 6-phosphofructokinase 5, chloroplastic OS=Arabidopsis thaliana GN=PFK5 PE=1 SV=1	1	0,466	0,21978022	510,33	0,442
Q9FJD4 IMB1_ARATH Ipectin subunit beta-1 OS=Arabidopsis thaliana GN=KPNB1 PE=1 SV=1	7	-0,238	0,217782218	505,69	0,442
Q940J8 PAE7_ARATH Pectin acetyltransferase 7 OS=Arabidopsis thaliana GN=PAE7 PE=2 SV=1	2	-0,324	0,220779221	512,65	0,443
P41376 IF4A1_ARATH Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	2	0,315	0,21978022	510,33	0,443
O23264 SEBP1_ARATH Selenium-binding protein 1 OS=Arabidopsis thaliana GN=SBP1 PE=1 SV=1	5	-0,278	0,21978022	510,33	0,443
Q9SPK5 FTHS_ARATH Formate--tetrahydrofolate ligase OS=Arabidopsis thaliana GN=THFS PE=2 SV=1	6	0,273	0,21978022	510,33	0,443
Q9LFH5 RL122_ARATH 60S ribosomal protein L12-2 OS=Arabidopsis thaliana GN=RPL12B PE=1 SV=1	1	-0,508	0,221778222	514,97	0,444
Q9SMN1 GCAL2_ARATH Gamma carbonic anhydrase-like 2, mitochondrial OS=Arabidopsis thaliana GN=GAMMACAL2 PE=1 SV=1	1	0,431	0,221778222	514,97	0,445
Q949P2 COPDA_ARATH Probable cytosolic oligopeptidase A OS=Arabidopsis thaliana GN=CYOP PE=1 SV=1	4	-0,265	0,221778222	514,97	0,445
Q9SN35 RAA1D_ARATH Ras-related protein RABA1d OS=Arabidopsis thaliana GN=RABA1D PE=2 SV=1	1	0,538	0,222777223	517,29	0,446
Q93ZH0 LYM1_ARATH LysM domain-containing GPI-anchored protein 1 OS=Arabidopsis thaliana GN=LYM1 PE=1 SV=1	1	-0,473	0,224775225	521,93	0,446
P26568 H11_ARATH Histone H1.1 OS=Arabidopsis thaliana GN=At1g06760 PE=1 SV=1	1	-0,446	0,223776224	519,61	0,446
Q9ZQ87 Q9ZQ87_ARATH Expressed protein OS=Arabidopsis thaliana GN=At2g03510 PE=2 SV=2	3	-0,369	0,223776224	519,61	0,446
F4I9J7 Y14_ARATH RNA-binding protein Y14 OS=Arabidopsis thaliana GN=Y14 PE=1 SV=1	2	-0,323	0,224775225	521,93	0,446
Q94BQ2 PRS8B_ARATH 26S proteasome regulatory subunit 8 homolog B OS=Arabidopsis thaliana GN=RPT6B PE=1 SV=1	4	0,286	0,223776224	519,61	0,446
Q9SMX3 VDAC3_ARATH Mitochondrial outer membrane protein porin 3 OS=Arabidopsis thaliana GN=VDAC3 PE=1 SV=3	10	-0,194	0,222777223	517,29	0,446
Q9XI42 Q9XI42_ARATH F9L1.21 protein OS=Arabidopsis thaliana GN=At1g15270 PE=2 SV=1	1	-0,47	0,224775225	521,93	0,447
Q9LYG2 Q9LYG2_ARATH Classical AGP protein OS=Arabidopsis thaliana GN=At5g11680 PE=2 SV=1	2	0,382	0,223776224	519,61	0,447
Q8LC83 RS242_ARATH 40S ribosomal protein S24-2 OS=Arabidopsis thaliana GN=RPS24B PE=2 SV=2	2	0,309	0,225774226	524,25	0,447
P43296 RD19A_ARATH Cysteine protease RD19A OS=Arabidopsis thaliana GN=RD19A PE=1 SV=1	4	-0,308	0,223776224	519,61	0,447
P53492 ACT7_ARATH Actin-7 OS=Arabidopsis thaliana GN=ACT7 PE=1 SV=1	6	-0,226	0,224775225	521,93	0,447
Q9SW96 SYNC1_ARATH Asparagine--tRNA ligase, cytoplasmic 1 OS=Arabidopsis thaliana GN=SYNC1 PE=1 SV=1	5	-0,224	0,225774226	524,25	0,447

Q9XFD1 NCBP2_ARATH Nuclear cap-binding protein subunit 2 OS=Arabidopsis thaliana GN=CBP20 PE=1 SV=1	1	-0,553	0,226773227	526,57	0,448
Q93ZA5 TBL46_ARATH Putative truncated protein trichome birefringence-like 46 OS=Arabidopsis thaliana GN=TBL46 PE=5 SV=1	1	-0,544	0,225774226	524,25	0,448
P41916 RAN1_ARATH GTP-binding nuclear protein Ran-1 OS=Arabidopsis thaliana GN=RAN1 PE=1 SV=1	7	0,221	0,227772228	528,89	0,449
P42742 PSB1_ARATH Proteasome subunit beta type-1 OS=Arabidopsis thaliana GN=PBF1 PE=1 SV=2	7	-0,215	0,226773227	526,57	0,449
Q42601 CARB_ARATH Carbamoyl-phosphate synthase large chain, chloroplastic OS=Arabidopsis thaliana GN=CARB PE=1 SV=1	15	-0,202	0,227772228	528,89	0,449
Q93ZT6 IF4G1_ARATH Eukaryotic translation initiation factor isoform 4G-1 OS=Arabidopsis thaliana GN=EIF(ISO)4G1 PE=1 SV=1	10	0,21	0,227772228	528,89	0,45
Q6NQMO Q6NQMO_ARATH At3g01800 OS=Arabidopsis thaliana GN=At3g01800 PE=2 SV=1	1	-0,734	0,22977023	533,53	0,451
Q9LHP1 RL74_ARATH 60S ribosomal protein L7-4 OS=Arabidopsis thaliana GN=RPL7D PE=2 SV=1	2	-0,383	0,228771229	531,21	0,451
P55228 GLGS_ARATH Glucose-1-phosphate adenyltransferase small subunit, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=2 SV=2	2	0,371	0,22977023	533,53	0,451
Q8H0U4 TNPO1_ARATH Transportin-1 OS=Arabidopsis thaliana GN=TRN1 PE=1 SV=1	5	-0,281	0,230769231	535,85	0,451
Q93YR3 F10AL_ARATH FAM10 family protein At4g22670 OS=Arabidopsis thaliana GN=At4g22670 PE=1 SV=1	5	0,276	0,230769231	535,85	0,451
Q7G193 ALDO1_ARATH Indole-3-acetaldehyde oxidase OS=Arabidopsis thaliana GN=AAO1 PE=1 SV=2	7	-0,221	0,22977023	533,53	0,451
Q42521 DCE1_ARATH Glutamate decarboxylase 1 OS=Arabidopsis thaliana GN=GAD1 PE=1 SV=2	9	-0,201	0,230769231	535,85	0,451
Q96520 PER12_ARATH Peroxidase 12 OS=Arabidopsis thaliana GN=PER12 PE=1 SV=1	2	0,489	0,231768232	538,17	0,452
Q94A40 COPA1_ARATH Coatomer subunit alpha-1 OS=Arabidopsis thaliana GN=At1g62020 PE=2 SV=2	2	-0,429	0,230769231	535,85	0,452
Q9LIK9 APS1_ARATH ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=1 SV=1	4	0,284	0,232767233	540,49	0,452
O81644 VIL12_ARATH Villin-2 OS=Arabidopsis thaliana GN=VLN2 PE=1 SV=2	5	-0,271	0,22977023	533,53	0,452
Q9STL4 CEP2_ARATH KDEL-tailed cysteine endopeptidase CEP2 OS=Arabidopsis thaliana GN=CEP2 PE=1 SV=1	5	0,262	0,230769231	535,85	0,452
Q9SKK4 GSL_ARATH Probable 2-oxoacid dependent dioxygenase OS=Arabidopsis thaliana GN=GSL-OH PE=2 SV=1	7	-0,237	0,22977023	533,53	0,452
O82179 GCSH2_ARATH Glycine cleavage system H protein 2, mitochondrial OS=Arabidopsis thaliana GN=GDH2 PE=2 SV=1	5	0,226	0,232767233	540,49	0,452
Q944K2 OST48_ARATH Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Arabidopsis thaliana GN=OST48 PE=2 SV=1	11	0,201	0,231768232	538,17	0,452
Q9LFM3 Q9LFM3_ARATH Acyl-CoA N-acyltransferases (NAT) superfamily protein OS=Arabidopsis thaliana GN=At5g11340 PE=2 SV=1	2	-0,449	0,233766234	542,81	0,453
P29511 TBA6_ARATH Tubulin alpha-6 chain OS=Arabidopsis thaliana GN=TUBA6 PE=1 SV=1	1	0,402	0,233766234	542,81	0,453
Q9LTR9 NMT1_ARATH Glycylpeptide N-tetradecanoyltransferase 1 OS=Arabidopsis thaliana GN=NMT1 PE=1 SV=2	3	0,367	0,232767233	540,49	0,453
P20649 PMA1_ARATH ATPase 1, plasma membrane-type OS=Arabidopsis thaliana GN=AHA1 PE=1 SV=3	3	-0,312	0,232767233	540,49	0,453
Q9LZG7 GSTUR_ARATH Glutathione S-transferase U27 OS=Arabidopsis thaliana GN=GSTU27 PE=2 SV=1	2	-0,305	0,232767233	540,49	0,453
Q8LCE1 GLN12_ARATH Glutamine synthetase cytosolic isozyme 1-2 OS=Arabidopsis thaliana GN=GLN1-2 PE=1 SV=2	3	0,25	0,233766234	542,81	0,453
Q9SJD4 LACS8_ARATH Long chain acyl-CoA synthetase 8 OS=Arabidopsis thaliana GN=LACS8 PE=1 SV=1	1	-0,76	0,234765235	545,12	0,454
Q42093 AB2C_ARATH ABC transporter C family member 2 OS=Arabidopsis thaliana GN=ABCC2 PE=1 SV=2	1	-0,478	0,234765235	545,12	0,454
P59223 RS131_ARATH 40S ribosomal protein S13-1 OS=Arabidopsis thaliana GN=RPS13A PE=2 SV=1	1	0,42	0,234765235	545,12	0,454
F4IIM1 CSI1_ARATH Protein CELLULOSE SYNTHASE INTERACTIVE 1 OS=Arabidopsis thaliana GN=CSI1 PE=1 SV=1	1	-0,697	0,235764236	547,44	0,455
Q8L3X8 SRC30_ARATH Serine/arginine-rich SC35-like splicing factor SCL30 OS=Arabidopsis thaliana GN=SCL30 PE=1 SV=1	1	-0,464	0,235764236	547,44	0,455
Q9ZSK4 ADF3_ARATH Actin-depolymerizing factor 3 OS=Arabidopsis thaliana GN=ADF3 PE=1 SV=1	4	-0,267	0,236763237	549,76	0,455
Q9LF46 HACL_ARATH 2-hydroxyacyl-CoA lyase OS=Arabidopsis thaliana GN=HACL PE=1 SV=1	10	-0,222	0,236763237	549,76	0,455
Q94AH9 MD36A_ARATH Mediator of RNA polymerase II transcription subunit 36a OS=Arabidopsis thaliana GN=MED36A PE=1 SV=2	3	-0,317	0,236763237	549,76	0,456
O49299 PGMC1_ARATH Probable phosphoglucosyltransferase, cytoplasmic 1 OS=Arabidopsis thaliana GN=At1g23190 PE=2 SV=2	7	-0,222	0,236763237	549,76	0,456
Q8VZ50 CML14_ARATH Probable calcium-binding protein CML14 OS=Arabidopsis thaliana GN=CML14 PE=2 SV=1	3	0,313	0,237762238	552,08	0,457
O23515 RL151_ARATH 60S ribosomal protein L15-1 OS=Arabidopsis thaliana GN=RPL15A PE=2 SV=1	3	0,324	0,238761239	554,4	0,458
O04151 CALR1_ARATH Calreticulin-1 OS=Arabidopsis thaliana GN=CRT1 PE=1 SV=1	6	0,249	0,238761239	554,4	0,458
Q9SB41 GLPT2_ARATH Putative glycerol-3-phosphate transporter 2 OS=Arabidopsis thaliana GN=At4g25220 PE=2 SV=1	1	0,697	0,23976024	556,72	0,459
Q9SIU4 ALFP1_ARATH Fructose-bisphosphate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=FBA1 PE=1 SV=2	1	-0,482	0,23976024	556,72	0,459
B9DGT7 TBA2_ARATH Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2	7	0,238	0,23976024	556,72	0,459
Q9FJT8 HATB_ARATH Histone acetyltransferase type B catalytic subunit OS=Arabidopsis thaliana GN=HAG2 PE=2 SV=1	1	-0,479	0,242757243	563,68	0,461
Q42529 TRPA2_ARATH Tryptophan synthase alpha chain, chloroplastic OS=Arabidopsis thaliana GN=TSA1 PE=1 SV=1	2	0,444	0,241758242	561,36	0,461
Q9LVQ4 Y5586_ARATH WEB family protein At5g55860 OS=Arabidopsis thaliana GN=At5g55860 PE=1 SV=1	1	0,36	0,241758242	561,36	0,461
O80585 MTHR2_ARATH Methylenetetrahydrofolate reductase 2 OS=Arabidopsis thaliana GN=MTHR2 PE=1 SV=2	3	0,252	0,241758242	561,36	0,461
F413B3 RB47A_ARATH Polyadenylate-binding protein RBP47A OS=Arabidopsis thaliana GN=RBP47A PE=2 SV=1	1	0,492	0,243756244	566	0,462
O80477 MES3_ARATH Methyltransferase 3 OS=Arabidopsis thaliana GN=MES3 PE=2 SV=1	2	-0,373	0,242757243	563,68	0,462
F4IYK3 F4IYK3_ARATH ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g08943 PE=1 SV=2	2	0,356	0,241758242	561,36	0,462
Q9FFD2 RGP5_ARATH Probable UDP-arabinopyranose mutase 5 OS=Arabidopsis thaliana GN=RGP5 PE=1 SV=1	4	0,31	0,242757243	563,68	0,462
Q9S9P1 RS121_ARATH 40S ribosomal protein S12-1 OS=Arabidopsis thaliana GN=RPS12A PE=2 SV=1	3	0,266	0,243756244	566	0,462

O65902 ACAP1_ARATH Cyclase-associated protein 1 OS=Arabidopsis thaliana GN=CAP1 PE=2 SV=1	6	0,217	0,243756244	566	0,462
Q96250 ATPG3_ARATH ATP synthase subunit gamma, mitochondrial OS=Arabidopsis thaliana GN=ATPC PE=1 SV=1	11	-0,195	0,241758242	561,36	0,462
Q9LTV6 DECR2_ARATH Peroxisomal 2,4-dienoyl-CoA reductase OS=Arabidopsis thaliana GN=At3g12800 PE=2 SV=1	4	-0,267	0,243756244	566	0,463
P49691 RL4B_ARATH 60S ribosomal protein L4-2 OS=Arabidopsis thaliana GN=RPL4D PE=1 SV=2	11	0,186	0,244755245	568,32	0,463
Q9SD78 Q9SD78_ARATH Furry OS=Arabidopsis thaliana GN=F13G24.260 PE=2 SV=1	3	-0,287	0,247752248	575,28	0,468
Q1H583 GDL18_ARATH GDSL esterase/lipase 22 OS=Arabidopsis thaliana GN=GLL22 PE=1 SV=1	1	-0,344	0,248751249	577,6	0,47
Q9LXS6 CISY2_ARATH Citrate synthase 2, peroxisomal OS=Arabidopsis thaliana GN=CSY2 PE=2 SV=1	4	-0,274	0,248751249	577,6	0,47
Q9SEU6 TRXM4_ARATH Thioredoxin M4, chloroplastic OS=Arabidopsis thaliana GN=At3g15360 PE=2 SV=2	1	-0,678	0,250749251	582,24	0,471
Q8RXF8 MIRO1_ARATH Mitochondrial Rho GTPase 1 OS=Arabidopsis thaliana GN=MIRO1 PE=1 SV=1	2	-0,52	0,253746254	589,2	0,471
Q9FIG6 DIR1_ARATH Dirigent protein 1 OS=Arabidopsis thaliana GN=DIR1 PE=2 SV=1	1	-0,506	0,250749251	582,24	0,471
P26569 H12_ARATH Histone H1.2 OS=Arabidopsis thaliana GN=At2g30620 PE=1 SV=1	1	-0,48	0,252747253	586,88	0,471
Q9M1D0 BGL16_ARATH Beta-glucosidase 16 OS=Arabidopsis thaliana GN=BGLU16 PE=2 SV=1	1	-0,433	0,252747253	586,88	0,471
Q03250 RBG7_ARATH Glycine-rich RNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1	2	0,279	0,24975025	579,92	0,471
Q9C9C5 RL63_ARATH 60S ribosomal protein L6-3 OS=Arabidopsis thaliana GN=RPL6C PE=2 SV=1	5	0,23	0,24975025	579,92	0,471
Q7DL51 PSB7B_ARATH Proteasome subunit beta type-7-B OS=Arabidopsis thaliana GN=PBB2 PE=1 SV=2	1	0,728	0,255744256	593,84	0,472
Q9LZI4 Q9LZI4_ARATH At3g62810 OS=Arabidopsis thaliana GN=F26K9_240 PE=2 SV=1	1	0,453	0,254745255	591,52	0,472
P60039 RL73_ARATH 60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	1	-0,436	0,254745255	591,52	0,472
Q9C9C9 SOT18_ARATH Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1	3	0,339	0,253746254	589,2	0,472
F4JFN3 H5906_ARATH Heat shock protein 90-6, mitochondrial OS=Arabidopsis thaliana GN=HSP90-6 PE=2 SV=1	2	-0,328	0,252747253	586,88	0,472
Q9FND0 Q9FND0_ARATH Gb AAD20086.1 OS=Arabidopsis thaliana GN=MRH10.6 PE=1 SV=1	2	0,328	0,252747253	586,88	0,472
Q9FFR3 6PGD2_ARATH 6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV=1	6	-0,253	0,250749251	582,24	0,472
Q9FN05 PSL5_ARATH Probable glucan 1,3-alpha-glucosidase OS=Arabidopsis thaliana GN=PSL5 PE=1 SV=1	7	0,226	0,253746254	589,2	0,472
O80774 O80774_ARATH AT2G34250 protein OS=Arabidopsis thaliana GN=At2g34250 PE=2 SV=1	6	0,224	0,253746254	589,2	0,472
Q96255 SERB1_ARATH Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1	6	0,218	0,254745255	591,52	0,472
O50008 METE1_ARATH 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV=1	12	0,186	0,250749251	582,24	0,472
Q9SDS7 VATC_ARATH V-type proton ATPase subunit C OS=Arabidopsis thaliana GN=VHA-C PE=1 SV=1	15	-0,183	0,255744256	593,84	0,472
P93655 LONM1_ARATH Lon protease homolog 1, mitochondrial OS=Arabidopsis thaliana GN=LON1 PE=1 SV=2	1	0,701	0,255744256	593,84	0,473
F4HRT5 CRWN1_ARATH Protein CROWDED NUCLEI 1 OS=Arabidopsis thaliana GN=CRWN1 PE=1 SV=1	1	-0,528	0,252747253	586,88	0,473
Q9GCB9 RT02_ARATH Ribosomal protein S2, mitochondrial OS=Arabidopsis thaliana GN=RPS2 PE=2 SV=1	1	-0,473	0,252747253	586,88	0,473
Q9M1Z2 Q9M1Z2_ARATH LETM1-like protein OS=Arabidopsis thaliana GN=F24G16.90 PE=4 SV=1	1	0,467	0,252747253	586,88	0,473
Q9FJE8 H2A7_ARATH Probable histone H2A.7 OS=Arabidopsis thaliana GN=At5g59870 PE=1 SV=1	1	-0,418	0,255744256	593,84	0,473
F4IPB2 F4IPB2_ARATH reversed Microtubule-associated proteins 70-3 OS=Arabidopsis thaliana GN=MAP70-3 PE=4 SV=1	1	0,388	0,254745255	591,52	0,473
Q04613 MI25_ARATH ATP synthase protein MI25 OS=Arabidopsis thaliana GN=AtMg00640 PE=1 SV=2	4	-0,24	0,251748252	584,56	0,473
Q9SSS7 Q9SSS7_ARATH AT1G52730 protein OS=Arabidopsis thaliana GN=At1g52730 PE=2 SV=1	1	-0,703	0,256743257	596,16	0,474
Q9FN42 CLPP2_ARATH ATP-dependent Clp protease proteolytic subunit 2, mitochondrial OS=Arabidopsis thaliana GN=CLPP2 PE=1 SV=1	2	-0,392	0,252747253	586,88	0,474
Q9FYF8 Q9FYF8_ARATH At1g67350 OS=Arabidopsis thaliana GN=At1g67350 PE=2 SV=1	3	-0,278	0,252747253	586,88	0,474
Q39242 TRXB2_ARATH Thioredoxin reductase 2 OS=Arabidopsis thaliana GN=NTR2 PE=2 SV=2	2	-0,336	0,257742258	598,48	0,475
Q9LJL3 PREP1_ARATH Presequence protease 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=PREP1 PE=1 SV=2	2	0,354	0,258741259	600,8	0,476
Q9SAA2 CLPP6_ARATH ATP-dependent Clp protease proteolytic subunit 6, chloroplastic OS=Arabidopsis thaliana GN=CLPP6 PE=1 SV=1	1	0,414	0,260739261	605,44	0,478
Q9LIL3 Q9LIL3_ARATH Aluminum induced protein with YGL and LRDR motifs OS=Arabidopsis thaliana GN=At3g22850 PE=1 SV=1	2	-0,344	0,25974026	603,12	0,478
Q9LST0 Q9LST0_ARATH AT5g60160/f15i12_20 OS=Arabidopsis thaliana GN=At5g60160 PE=2 SV=1	5	-0,248	0,260739261	605,44	0,478
P51413 RL172_ARATH 60S ribosomal protein L17-2 OS=Arabidopsis thaliana GN=RPL17B PE=2 SV=2	6	0,219	0,25974026	603,12	0,478
Q96292 ACT2_ARATH Actin-2 OS=Arabidopsis thaliana GN=ACT2 PE=1 SV=1	1	0,496	0,261738262	607,76	0,479
Q94AI6 SEC6_ARATH Exocyst complex component SEC6 OS=Arabidopsis thaliana GN=SEC6 PE=1 SV=1	1	-0,444	0,261738262	607,76	0,479
Q9FK35 KAD3_ARATH Adenylate kinase 3 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	4	0,284	0,261738262	607,76	0,479
Q8H1F4 COPZ3_ARATH Coatome subunit zeta-3 OS=Arabidopsis thaliana GN=At4g08520 PE=2 SV=1	4	0,263	0,260739261	605,44	0,479
P19456 PMA2_ARATH ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	7	0,218	0,260739261	605,44	0,479
P43333 RU2A_ARATH U2 small nuclear ribonucleoprotein A' OS=Arabidopsis thaliana GN=At1g09760 PE=2 SV=2	3	0,318	0,263736264	612,4	0,481
O49457 O49457_ARATH DNAJ heat shock family protein OS=Arabidopsis thaliana GN=At4g28480 PE=2 SV=1	1	-0,486	0,263736264	612,4	0,482
Q9SHE7 RUB1_ARATH Ubiquitin-NEDD8-like protein RUB1 OS=Arabidopsis thaliana GN=RUB1 PE=1 SV=3	2	-0,381	0,264735265	614,72	0,482
Q94CE3 BCA5_ARATH Beta carbonic anhydrase 5, chloroplastic OS=Arabidopsis thaliana GN=BCA5 PE=2 SV=1	1	0,447	0,264735265	614,72	0,483

Q9SA73 OLA1_ARATH Olg-like ATPase 1 OS=Arabidopsis thaliana GN=YchF1 PE=1 SV=1	14	0,168	0,264735265	614,72	0,483
Q9LF37 CLPB3_ARATH Chaperone protein ClpB3, chloroplastic OS=Arabidopsis thaliana GN=CLPB3 PE=1 SV=1	2	0,35	0,266733267	619,35	0,484
Q8L5U0 CSN4_ARATH COP9 signalosome complex subunit 4 OS=Arabidopsis thaliana GN=CSN4 PE=1 SV=2	6	-0,239	0,265734266	617,03	0,484
Q8H1G6 PTI11_ARATH PTI1-like tyrosine-protein kinase 1 OS=Arabidopsis thaliana GN=PTI11 PE=1 SV=1	1	0,671	0,267732268	621,67	0,485
Q8GYB8 OPR2_ARATH 12-oxophytodienoate reductase 2 OS=Arabidopsis thaliana GN=OPR2 PE=1 SV=2	1	0,482	0,267732268	621,67	0,485
Q8VZ50 CML14_ARATH Probable calcium-binding protein CML14 OS=Arabidopsis thaliana GN=CML14 PE=2 SV=1	2	-0,395	0,266733267	619,35	0,485
P92963 RAB1C_ARATH Ras-related protein RAB1C OS=Arabidopsis thaliana GN=RAB1C PE=1 SV=1	5	0,277	0,266733267	619,35	0,485
P31167 ADT1_ARATH ADP,ATP carrier protein 1, mitochondrial OS=Arabidopsis thaliana GN=AAC1 PE=1 SV=2	11	0,175	0,267732268	621,67	0,485
Q84WU7 Q84WU7_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At3g51330 PE=2 SV=1	2	-0,404	0,267732268	621,67	0,486
O64903 NDK2_ARATH Nucleoside diphosphate kinase II, chloroplastic OS=Arabidopsis thaliana GN=NDPK2 PE=1 SV=2	2	-0,313	0,26973027	626,31	0,486
Q9LYG3 MAOP2_ARATH NADP-dependent malic enzyme 2 OS=Arabidopsis thaliana GN=NADP-ME2 PE=1 SV=1	17	-0,168	0,268731269	623,99	0,486
Q84MC0 UGPI4_ARATH Uncharacterized GPI-anchored protein At3g06035 OS=Arabidopsis thaliana GN=At3g06035 PE=2 SV=1	1	-0,645	0,26973027	626,31	0,487
Q9FND9 RFSS_ARATH Probable galactinol--sucrose galactosyltransferase 5 OS=Arabidopsis thaliana GN=RFSS PE=1 SV=1	2	0,375	0,270729271	628,63	0,487
Q9FJ62 GPD4_ARATH Glycerophosphodiester phosphodiesterase GDP4 OS=Arabidopsis thaliana GN=GPD4 PE=1 SV=1	7	-0,232	0,26973027	626,31	0,487
Q39227 SMT2_ARATH 24-methylenesterol C-methyltransferase 2 OS=Arabidopsis thaliana GN=SMT2 PE=1 SV=2	5	0,227	0,26973027	626,31	0,487
Q9FMU6 MPCP3_ARATH Mitochondrial phosphate carrier protein 3, mitochondrial OS=Arabidopsis thaliana GN=MPT3 PE=1 SV=1	11	0,18	0,270729271	628,63	0,487
Q9FI78 HST_ARATH Shikimate O-hydroxycinnamoyltransferase OS=Arabidopsis thaliana GN=HST PE=1 SV=1	1	-0,419	0,272727273	633,27	0,488
Q70E96 AL3F1_ARATH reversed Aldehyde dehydrogenase family 3 member F1 OS=Arabidopsis thaliana GN=ALDH3F1 PE=2 SV=2	1	0,366	0,272727273	633,27	0,488
Q8LFQ6 GRXC4_ARATH Glutaredoxin-C4 OS=Arabidopsis thaliana GN=GRXC4 PE=2 SV=2	2	0,324	0,271728272	630,95	0,488
Q9S517 RS241_ARATH 40S ribosomal protein S24-1 OS=Arabidopsis thaliana GN=RPS24A PE=2 SV=1	3	0,266	0,273726274	635,59	0,488
Q9C912 R35A3_ARATH 60S ribosomal protein L35a-3 OS=Arabidopsis thaliana GN=RPL35AC PE=3 SV=1	4	0,206	0,273726274	635,59	0,488
Q94IQ4 RIDA_ARATH Reactive Intermediate Deaminase A, chloroplastic OS=Arabidopsis thaliana GN=RIDA PE=1 SV=1	8	-0,198	0,272727273	633,27	0,488
Q84VW9 CAPP3_ARATH Phosphoenolpyruvate carboxylase 3 OS=Arabidopsis thaliana GN=PPC3 PE=1 SV=2	15	0,178	0,270729271	628,63	0,488
Q9SRT4 Q9SRT4_ARATH O-Glycosyl hydrolases family 17 protein OS=Arabidopsis thaliana GN=F2103.3 PE=2 SV=1	1	0,496	0,274725275	637,91	0,489
Q9FF53 PIP24_ARATH Probable aquaporin PIP2-4 OS=Arabidopsis thaliana GN=PIP2-4 PE=1 SV=1	1	0,445	0,273726274	635,59	0,489
Q9M356 Q9M356_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=F15G16.210 PE=3 SV=1	1	-0,433	0,272727273	633,27	0,489
Q9C5N2 TMN9_ARATH Transmembrane 9 superfamily member 9 OS=Arabidopsis thaliana GN=TMN9 PE=2 SV=1	2	0,378	0,272727273	633,27	0,489
Q42547 CATA3_ARATH Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3	1	-0,367	0,274725275	637,91	0,489
Q9SXC0 Q9SXC0_ARATH NAD(P)-linked oxidoreductase superfamily protein OS=Arabidopsis thaliana GN=At1g59960 PE=1 SV=1	5	0,256	0,272727273	633,27	0,489
Q93VP9 Q93VP9_ARATH SPFH/Band 7/PHB domain-containing membrane-associated protein family OS=Arabidopsis thaliana GN=AtSLP1 PE=1 SV=1	7	0,218	0,273726274	635,59	0,489
Q8H1B3 MD37B_ARATH Probable mediator of RNA polymerase II transcription subunit 37b OS=Arabidopsis thaliana GN=MED37B PE=1 SV=1	7	0,358	0,275724276	640,23	0,49
Q9C969 ISS1_ARATH Aromatic aminotransferase ISS1 OS=Arabidopsis thaliana GN=ISS1 PE=1 SV=1	1	-0,231	0,272727273	633,27	0,49
Q9SA06 Q9SA06_ARATH F28K20.6 protein OS=Arabidopsis thaliana GN=F28K20.6 PE=2 SV=1	1	0,482	0,276723277	642,55	0,491
Q8L719 THO4B_ARATH THO complex subunit 4B OS=Arabidopsis thaliana GN=ALY2 PE=1 SV=1	1	0,409	0,277722278	644,87	0,492
Q940J8 PAE7_ARATH Pectin acetyltransferase 7 OS=Arabidopsis thaliana GN=PAE7 PE=2 SV=1	6	-0,199	0,277722278	644,87	0,492
Q94CE5 GATP_ARATH Gamma-aminobutyrate transaminase POP2, mitochondrial OS=Arabidopsis thaliana GN=POP2 PE=1 SV=1	11	-0,169	0,276723277	642,55	0,492
F4HPK3 F4HPK3_ARATH YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein OS=Arabidopsis thaliana GN=At1g44835 PE=4 SV=1	1	0,429	0,278721279	647,19	0,493
O50008 METE1_ARATH 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV=1	4	0,229	0,277722278	644,87	0,493
Q9XE51 ECA4_ARATH Calcium-transporting ATPase 4, endoplasmic reticulum-type OS=Arabidopsis thaliana GN=ECA4 PE=2 SV=2	6	0,224	0,278721279	647,19	0,493
A8MQE3 A8MQE3_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g25770 PE=4 SV=1	1	-0,684	0,281718282	654,15	0,494
Q8RWV5 Q8RWV5_ARATH Cell differentiation, Rcd1-like protein OS=Arabidopsis thaliana GN=At3g20800 PE=2 SV=1	1	0,664	0,281718282	654,15	0,494
Q9S850 SUOX_ARATH Sulfite oxidase OS=Arabidopsis thaliana GN=SOX PE=1 SV=1	4	-0,244	0,27972028	649,51	0,494
Q9LQQ3 Q9LQQ3_ARATH At1g07750/F24B9_13 OS=Arabidopsis thaliana GN=At1g07750 PE=1 SV=1	4	-0,24	0,282717283	656,47	0,494
O49613 HIP25_ARATH Heavy metal-associated isoprenylated plant protein 25 OS=Arabidopsis thaliana GN=HIP25 PE=2 SV=1	4	-0,229	0,27972028	649,51	0,494
Q9CAV0 RS3A1_ARATH 40S ribosomal protein S3a-1 OS=Arabidopsis thaliana GN=RPS3AA PE=1 SV=3	5	0,222	0,27972028	649,51	0,494
P48421 C83A1_ARATH Cytochrome P450 83A1 OS=Arabidopsis thaliana GN=CYP83A1 PE=1 SV=2	1	0,672	0,281718282	654,15	0,495
Q9T030 Q9T030_ARATH NAD(P)H oxidoreductase, isoflavone reductase-like protein OS=Arabidopsis thaliana GN=At4g39230 PE=2 SV=1	1	-0,652	0,281718282	654,15	0,495
Q9SFC6 GDIR_ARATH Rho GDP-dissociation inhibitor 1 OS=Arabidopsis thaliana GN=GDI1 PE=1 SV=1	1	-0,486	0,282717283	656,47	0,495
Q8VZ13 Y1816_ARATH Uncharacterized protein At1g08160 OS=Arabidopsis thaliana GN=At1g08160 PE=2 SV=1	1	0,464	0,283716284	658,79	0,495
Q9M7T1 Q9M7T1_ARATH Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein OS=Arabidopsis thaliana GN=At3g06	1	0,44	0,280719281	651,83	0,495
Q67XJ2 NFYBA_ARATH Nuclear transcription factor Y subunit B-10 OS=Arabidopsis thaliana GN=NFYB10 PE=1 SV=1	1	0,42	0,282717283	656,47	0,495

Q93VM8 COPT5_ARATH Copper transporter 5 OS=Arabidopsis thaliana GN=COPT5 PE=1 SV=1	1	-0,337	0,284715285	661,11	0,495
Q8LSY6 CAND1_ARATH Cullin-associated NEDD8-dissociated protein 1 OS=Arabidopsis thaliana GN=CAND1 PE=1 SV=1	5	0,264	0,280719281	651,83	0,495
Q9LP45 PSD11_ARATH 26S proteasome non-ATPase regulatory subunit 11 homolog OS=Arabidopsis thaliana GN=RPN6 PE=1 SV=1	4	-0,241	0,283716284	658,79	0,495
Q5E924 G3PP2_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPCP2, chloroplastic OS=Arabidopsis thaliana GN=GAPCP2 PE=2 SV=1	5	0,223	0,282717283	656,47	0,495
Q9ZP06 MDHM1_ARATH Malate dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana GN=At1g53240 PE=1 SV=1	4	0,213	0,283716284	658,79	0,495
F4JD16 F4JD16_ARATH C2 calcium/lipid-binding endonuclease/exonuclease/phosphatase OS=Arabidopsis thaliana GN=At3g60950 PE=4 SV=1	1	-0,425	0,281718282	654,15	0,496
Q94IX9 NACA2_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 2 OS=Arabidopsis thaliana GN=At3g49470 PE=2 SV=2	2	0,349	0,281718282	654,15	0,496
P68209 SUCA1_ARATH Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1	2	-0,293	0,284715285	661,11	0,496
Q9FKC0 R13A4_ARATH 60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	2	0,281	0,283716284	658,79	0,496
Q9S7Y7 XYL1_ARATH Alpha-xylosidase 1 OS=Arabidopsis thaliana GN=XYL1 PE=1 SV=1	9	-0,188	0,284715285	661,11	0,496
Q9SEI3 PS10A_ARATH 26S proteasome regulatory subunit 10B homolog A OS=Arabidopsis thaliana GN=RPT4A PE=1 SV=1	10	-0,186	0,286713287	665,75	0,496
Q9LVC5 Q9LVC5_ARATH Glucose-6-phosphate 1-epimerase OS=Arabidopsis thaliana GN=MJB24.14 PE=1 SV=1	1	0,664	0,286713287	665,75	0,497
Q9LVQ8 P2C80_ARATH Probable protein phosphatase 2C 80 OS=Arabidopsis thaliana GN=At5g66720 PE=2 SV=1	1	-0,477	0,287712288	668,07	0,497
Q8L636 NCL_ARATH Sodium/calcium exchanger NCL OS=Arabidopsis thaliana GN=NCL PE=2 SV=1	2	-0,344	0,286713287	665,75	0,497
Q9LFF33 UGDH3_ARATH UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1	2	0,327	0,285714286	663,43	0,497
Q9SGC1 PGMC2_ARATH Probable phosphoglucomutase, cytoplasmic 2 OS=Arabidopsis thaliana GN=At1g70730 PE=1 SV=1	4	-0,256	0,287712288	668,07	0,497
Q9SE96 GEM11_ARATH GEM-like protein 1 OS=Arabidopsis thaliana GN=FIP1 PE=1 SV=1	1	0,639	0,288711289	670,39	0,498
Q5XEP2 HSOP2_ARATH Hsp70-Hsp90 organizing protein 2 OS=Arabidopsis thaliana GN=HOP2 PE=1 SV=1	1	0,471	0,288711289	670,39	0,498
Q9LK72 LECT5_ARATH Lectin-like protein At3g16530 OS=Arabidopsis thaliana GN=At3g16530 PE=1 SV=1	1	-0,44	0,288711289	670,39	0,498
Q9C500 WPP2_ARATH WPP domain-containing protein 2 OS=Arabidopsis thaliana GN=WPP2 PE=1 SV=1	3	0,286	0,286713287	665,75	0,498
P49688 RS23_ARATH 40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2	5	0,228	0,287712288	668,07	0,498
P24102 PER22_ARATH Peroxidase 22 OS=Arabidopsis thaliana GN=PER22 PE=1 SV=2	3	-0,22	0,286713287	665,75	0,498
Q9M8D3 PUR4_ARATH Probable phosphoribosylformylglycinamide synthase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At1g74260 PE=	3	-0,283	0,28971029	672,71	0,499
Q93Y35 PSMD6_ARATH 26S proteasome non-ATPase regulatory subunit 6 homolog OS=Arabidopsis thaliana GN=RPN7 PE=1 SV=1	7	-0,219	0,28971029	672,71	0,499
Q2HIQ2 Q2HIQ2_ARATH At1g01170 OS=Arabidopsis thaliana GN=At1g01170 PE=2 SV=1	1	-0,412	0,291708292	677,35	0,501
Q8L828 COB23_ARATH Coatomer subunit beta'-3 OS=Arabidopsis thaliana GN=At3g15980 PE=2 SV=1	1	-0,46	0,292707293	679,67	0,502
P42733 RS113_ARATH 40S ribosomal protein S11-3 OS=Arabidopsis thaliana GN=RPS11C PE=2 SV=2	1	-0,372	0,291708292	677,35	0,502
Q9S7E6 SMD3A_ARATH Small nuclear ribonucleoprotein Smd3a OS=Arabidopsis thaliana GN=SMD3A PE=2 SV=1	1	-0,633	0,293706294	681,99	0,503
Q8H0Y1 OP24B_ARATH Outer envelope pore protein 24B, chloroplastic OS=Arabidopsis thaliana GN=OEP24B PE=2 SV=1	1	0,502	0,292707293	679,67	0,503
P93026 VSR1_ARATH Vacuolar-sorting receptor 1 OS=Arabidopsis thaliana GN=VSR1 PE=1 SV=2	1	0,448	0,293706294	681,99	0,503
Q9S762 HIS1A_ARATH ATP phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN1A PE=1 SV=1	1	0,408	0,294705295	684,31	0,503
Q9LT02 PDR2_ARATH Probable manganese-transporting ATPase PDR2 OS=Arabidopsis thaliana GN=PDR2 PE=1 SV=1	2	0,362	0,294705295	684,31	0,503
Q8LCW9 RLA11_ARATH 60S acidic ribosomal protein P1-1 OS=Arabidopsis thaliana GN=RPP1A PE=3 SV=2	2	0,286	0,297702298	691,26	0,503
Q9FWR4 DHAR1_ARATH Glutathione S-transferase DHAR1, mitochondrial OS=Arabidopsis thaliana GN=DHAR1 PE=1 SV=1	9	0,173	0,295704296	686,63	0,503
P92947 MDAR_ARATH Monodehydroascorbate reductase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MDAR5 PE=1 SV=3	17	-0,155	0,293706294	681,99	0,503
O04486 RAA2A_ARATH Ras-related protein RABA2a OS=Arabidopsis thaliana GN=RABA2A PE=2 SV=1	1	-0,637	0,294705295	684,31	0,504
O64760 O64760_ARATH At2g34970 OS=Arabidopsis thaliana GN=At2g34970 PE=1 SV=1	1	-0,633	0,294705295	684,31	0,504
Q1JPP0 Q1JPP0_ARATH Adenylyl cyclase OS=Arabidopsis thaliana GN=At4g15640 PE=2 SV=1	1	-0,626	0,295704296	686,63	0,504
Q8H0S3 Q8H0S3_ARATH At1g05520/T25N20_16 OS=Arabidopsis thaliana GN=At1g05520 PE=1 SV=1	1	-0,474	0,296703297	688,95	0,504
Q39230 SYSC_ARATH Serine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At5g27470 PE=2 SV=1	5	-0,239	0,293706294	681,99	0,504
P60039 RL73_ARATH 60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	3	0,234	0,297702298	691,26	0,504
Q80977 VSR3_ARATH Vacuolar-sorting receptor 3 OS=Arabidopsis thaliana GN=VSR3 PE=2 SV=1	5	-0,213	0,295704296	686,63	0,504
Q9ZST4 GLNB_ARATH Nitrogen regulatory protein P-II homolog OS=Arabidopsis thaliana GN=GLB1 PE=1 SV=1	6	-0,206	0,297702298	691,26	0,504
Q9LQ81 ADF10_ARATH Actin-depolymerizing factor 10 OS=Arabidopsis thaliana GN=ADF10 PE=2 SV=1	1	0,622	0,297702298	691,26	0,505
Q8LDC9 Q8LDC9_ARATH GroES-like family protein OS=Arabidopsis thaliana GN=At1g23100 PE=2 SV=1	3	0,258	0,297702298	691,26	0,505
Q38931 FKB62_ARATH Peptidyl-prolyl cis-trans isomerase FKBP62 OS=Arabidopsis thaliana GN=FKBP62 PE=1 SV=2	7	-0,204	0,297702298	691,26	0,505
Q94BV7 NDB2_ARATH External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial OS=Arabidopsis thaliana GN=NDB2 PE=1 SV=1	8	-0,202	0,296703297	688,95	0,505
Q9ZVC3 Q9ZVC3_ARATH At2g41380 OS=Arabidopsis thaliana GN=At2g41380 PE=2 SV=1	8	0,19	0,298701299	693,58	0,505
Q8L3W1 VRN1_ARATH B3 domain-containing transcription factor VRN1 OS=Arabidopsis thaliana GN=VRN1 PE=1 SV=1	1	-0,433	0,2997003	695,9	0,506
F4JUG3 F4JUG3_ARATH reversed Nucleoporin (DUF3414) OS=Arabidopsis thaliana GN=At4g38760 PE=4 SV=1	1	-0,39	0,297702298	691,26	0,506
Q9LZ23 ACR12_ARATH ACT domain-containing protein ACR12 OS=Arabidopsis thaliana GN=ACR12 PE=2 SV=1	4	-0,208	0,2997003	695,9	0,506

F4K455 F4K455_ARATH Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein OS=Arabidopsis thaliana GN=At5g20160 PE=4 SV=1	2	0,309	0,300699301	698,22	0,507
P93031 GMD2_ARATH GDP-mannose 4,6 dehydratase 2 OS=Arabidopsis thaliana GN=MUR1 PE=1 SV=3	1	0,446	0,301698302	700,54	0,508
O81852 AKH2_ARATH Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH2 PE=1 SV=1	1	-0,61	0,302697303	702,86	0,51
F4K1B2 TMN8_ARATH Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1	1	-0,44	0,303696304	705,18	0,511
Q9CAX6 RS142_ARATH 40S ribosomal protein S14-2 OS=Arabidopsis thaliana GN=RPS14B PE=1 SV=1	1	0,326	0,303696304	705,18	0,511
P55217 CGS1_ARATH Cystathionine gamma-synthase 1, chloroplastic OS=Arabidopsis thaliana GN=CGS1 PE=1 SV=3	2	-0,301	0,304695305	707,5	0,511
O22683 CYN5_ARATH Cynate hydratase OS=Arabidopsis thaliana GN=CYN PE=2 SV=1	1	-0,45	0,304695305	707,5	0,512
Q8L7F7 NUP62_ARATH Nuclear pore complex protein NUP62 OS=Arabidopsis thaliana GN=NUP62 PE=1 SV=1	1	-0,416	0,304695305	707,5	0,512
Q9LHI0 NDUA6_ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Arabidopsis thaliana GN=At3g12260 PE=2 SV=1	4	-0,242	0,305694306	709,82	0,513
Q9LRX8 R13A2_ARATH 60S ribosomal protein L13a-2 OS=Arabidopsis thaliana GN=RPL13AB PE=2 SV=1	2	0,347	0,306693307	712,14	0,514
Q93YW5 P2C58_ARATH Probable protein phosphatase 2C 58 OS=Arabidopsis thaliana GN=At4g28400 PE=2 SV=1	2	-0,291	0,307692308	714,46	0,514
Q7XJ7 FAAH_ARATH Fatty acid amide hydrolase OS=Arabidopsis thaliana GN=FAAH PE=1 SV=1	3	-0,273	0,307692308	714,46	0,514
O81417 O81417_ARATH At4g02270 OS=Arabidopsis thaliana GN=RHS13 PE=2 SV=1	1	0,653	0,308691309	716,78	0,515
Q9SUM3 NCPR2_ARATH NADPH--cytochrome P450 reductase 2 OS=Arabidopsis thaliana GN=ATR2 PE=1 SV=1	1	0,447	0,30969031	719,1	0,515
Q8VY61 Q8VY61_ARATH 50S ribosomal protein L4 OS=Arabidopsis thaliana GN=At2g20060 PE=2 SV=1	1	-0,436	0,308691309	716,78	0,515
Q8RUH0 Q8RUH0_ARATH Putative small nuclear ribonucleoprotein D2 OS=Arabidopsis thaliana GN=At2g47640 PE=4 SV=1	2	-0,302	0,307692308	714,46	0,515
A0A1P8BB34 A0A1P8BB34_ARATH ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At5g36230 PE=4 SV=1	3	0,295	0,308691309	716,78	0,515
Q9ZNT7 PHB2_ARATH Prohibitin-2, mitochondrial OS=Arabidopsis thaliana GN=PHB2 PE=1 SV=1	3	0,261	0,307692308	714,46	0,515
O82264 NPL42_ARATH NPL4-like protein 2 OS=Arabidopsis thaliana GN=At2g47970 PE=1 SV=1	2	-0,37	0,30969031	719,1	0,516
Q96291 BAS1A_ARATH 2-Cys peroxiredoxin BAS1, chloroplastic OS=Arabidopsis thaliana GN=BAS1 PE=1 SV=2	2	-0,288	0,310689311	721,42	0,516
Q96252 ATP4_ARATH ATP synthase subunit delta', mitochondrial OS=Arabidopsis thaliana GN=At5g47030 PE=1 SV=1	3	0,221	0,310689311	721,42	0,516
Q8RWZ7 VHAA1_ARATH V-type proton ATPase subunit a1 OS=Arabidopsis thaliana GN=VHA-a1 PE=2 SV=1	1	-0,648	0,311688312	723,74	0,517
Q949S7 Q949S7_ARATH NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At5g15910 PE=2 SV=1	2	-0,47	0,310689311	721,42	0,517
P54970 ILL2_ARATH IAA-amino acid hydrolase ILR1-like 2 OS=Arabidopsis thaliana GN=ILL2 PE=1 SV=2	1	-0,446	0,311688312	723,74	0,517
Q9SNY3 GMD1_ARATH GDP-mannose 4,6 dehydratase 1 OS=Arabidopsis thaliana GN=GMD1 PE=1 SV=1	1	0,328	0,311688312	723,74	0,517
Q9FGH3 Q9FGH3_ARATH Cinnamoyl-CoA reductase-like protein OS=Arabidopsis thaliana GN=MQJ2.6 PE=2 SV=1	1	-0,396	0,313686314	728,38	0,518
Q9SCX3 EF1B2_ARATH Elongation factor 1-beta 2 OS=Arabidopsis thaliana GN=At5g19510 PE=1 SV=1	6	0,176	0,312687313	726,06	0,518
O80608 FB96_ARATH reversed Putative F-box protein At2g02890 OS=Arabidopsis thaliana GN=At2g02890 PE=4 SV=1	1	0,419	0,313686314	728,38	0,519
P42497 PHYD_ARATH Phytochrome D OS=Arabidopsis thaliana GN=PHYD PE=1 SV=2	1	-0,415	0,313686314	728,38	0,519
Q9LZQ4 Q9LZQ4_ARATH Carbohydrate-binding-like fold OS=Arabidopsis thaliana GN=T12C14_60 PE=4 SV=1	10	0,174	0,314685315	730,7	0,519
A0A1I9LP30 A0A1I9LP30_ARATH Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=	1	0,622	0,314685315	730,7	0,52
O80944 AKRC8_ARATH Aldo-keto reductase family 4 member C8 OS=Arabidopsis thaliana GN=AKR4C8 PE=1 SV=2	2	-0,277	0,316683317	735,34	0,521
Q8VYV7 DHQS_ARATH 3-dehydroquinate synthase, chloroplastic OS=Arabidopsis thaliana GN=DHQS PE=1 SV=1	7	-0,197	0,315684316	733,02	0,521
Q93XX8 NOP10_ARATH H/ACA ribonucleoprotein complex subunit 3-like protein OS=Arabidopsis thaliana GN=At2g20490 PE=3 SV=2	1	-0,621	0,316683317	735,34	0,522
P48491 TPIS_ARATH Triosephosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=CTIMC PE=1 SV=2	1	0,372	0,317682318	737,66	0,522
Q9FPJ4 RAD2B_ARATH Ras-related protein RABD2b OS=Arabidopsis thaliana GN=RABD2B PE=2 SV=1	7	0,228	0,316683317	735,34	0,522
Q9TOK2 C71AK_ARATH Cytochrome P450 71A20 OS=Arabidopsis thaliana GN=CYP71A20 PE=2 SV=2	1	0,62	0,31968032	742,3	0,523
Q8LBU2 GPX8_ARATH Probable glutathione peroxidase 8 OS=Arabidopsis thaliana GN=GPX8 PE=2 SV=1	1	0,428	0,320679321	744,62	0,523
P48006 EF1D1_ARATH Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2	3	-0,242	0,318681319	739,98	0,523
Q9C9K3 PFP2_ARATH Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2 OS=Arabidopsis thaliana GN=PFP-ALPHA2 PE=2 SV=	6	0,205	0,318681319	739,98	0,523
Q9SJ12 ATP7_ARATH Probable ATP synthase 24 kDa subunit, mitochondrial OS=Arabidopsis thaliana GN=At2g21870 PE=1 SV=1	11	-0,175	0,318681319	739,98	0,523
O04983 ACCC_ARATH Biotin carboxylase, chloroplastic OS=Arabidopsis thaliana GN=CAC2 PE=1 SV=1	10	-0,169	0,31968032	742,3	0,523
Q9LJR2 LECT2_ARATH Lectin-like protein LEC OS=Arabidopsis thaliana GN=LEC PE=1 SV=1	1	-0,421	0,320679321	744,62	0,524
P55034 PSMD4_ARATH 26S proteasome non-ATPase regulatory subunit 4 homolog OS=Arabidopsis thaliana GN=RPN10 PE=1 SV=1	2	0,285	0,320679321	744,62	0,524
P29514 TBB6_ARATH Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1	3	0,283	0,31968032	742,3	0,524
P57742 PFD5_ARATH Probable prefoldin subunit 5 OS=Arabidopsis thaliana GN=At5g23290 PE=2 SV=1	3	-0,248	0,318681319	739,98	0,524
Q9X110 Q9X110_ARATH DPP6 N-terminal domain-like protein OS=Arabidopsis thaliana GN=At1g21680 PE=2 SV=1	5	-0,244	0,320679321	744,62	0,524
O80988 GCSP2_ARATH Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana GN=GLDP2 PE=1 SV=1	4	0,237	0,321678322	746,94	0,524
P51413 RL172_ARATH 60S ribosomal protein L17-2 OS=Arabidopsis thaliana GN=RPL17B PE=2 SV=2	1	0,393	0,322677323	749,26	0,525
P68209 SUCA1_ARATH Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1	3	0,262	0,321678322	746,94	0,525
Q8RXU5 R37A2_ARATH 60S ribosomal protein L37a-2 OS=Arabidopsis thaliana GN=RPL37AC PE=3 SV=1	3	0,216	0,322677323	749,26	0,525

Q96254 GDI1_ARATH Guanosine nucleotide diphosphate dissociation inhibitor 1 OS=Arabidopsis thaliana GN=GDI1 PE=1 SV=1	6	0,212	0,322677323	749,26	0,525
Q94CB1 PME25_ARATH Probable pectinesterase/pectinesterase inhibitor 25 OS=Arabidopsis thaliana GN=PME25 PE=2 SV=1	1	-0,41	0,323676324	751,58	0,526
Q9SLE2 Q9SLE2_ARATH Calcium-dependent phosphotriesterase superfamily protein OS=Arabidopsis thaliana GN=At2g16760 PE=2 SV=1	2	-0,406	0,324675325	753,9	0,526
O50008 METE1_ARATH 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV=1	1	0,285	0,323676324	751,58	0,526
Q9S116 PER15_ARATH Peroxidase 15 OS=Arabidopsis thaliana GN=PER15 PE=2 SV=1	1	-0,432	0,325674326	756,22	0,527
PODI76 CIN1_ARATH 1,8-cineole synthase 1, chloroplastic OS=Arabidopsis thaliana GN=TPS27 PE=1 SV=1	2	-0,351	0,324675325	753,9	0,527
Q9SF40 RL4A_ARATH 60S ribosomal protein L4-1 OS=Arabidopsis thaliana GN=RPL4A PE=1 SV=1	4	0,234	0,325674326	756,22	0,527
F4HPB7 F4HPB7_ARATH Uncharacterized protein OS=Arabidopsis thaliana GN=At1g26750 PE=4 SV=1	1	0,395	0,325674326	756,22	0,528
O22957 O22957_ARATH Apoptosis inhibitory protein 5 (API5) OS=Arabidopsis thaliana GN=At2g34040 PE=1 SV=2	3	-0,266	0,326673327	758,54	0,528
Q9FVQ1 NUCL1_ARATH Nucleolin 1 OS=Arabidopsis thaliana GN=NUCL1 PE=1 SV=1	7	-0,191	0,326673327	758,54	0,528
O81126 RSZ22_ARATH Serine/arginine-rich splicing factor RSZ22 OS=Arabidopsis thaliana GN=RSZ22 PE=1 SV=1	1	-0,371	0,327672328	760,86	0,529
Q8L557 EM514_ARATH Protein EMBRYO DEFECTIVE 514 OS=Arabidopsis thaliana GN=EMB514 PE=1 SV=1	1	0,441	0,330669331	767,81	0,53
P28186 RAE1C_ARATH Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	1	0,327	0,330669331	767,81	0,53
Q9ZQQ0 SCP26_ARATH Serine carboxypeptidase-like 26 OS=Arabidopsis thaliana GN=SCPL26 PE=2 SV=1	2	-0,308	0,328671329	763,17	0,53
P48006 EF1D1_ARATH Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2	1	0,293	0,32967033	765,49	0,53
P46422 GSTF2_ARATH Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3	1	0,278	0,328671329	763,17	0,53
Q9SUU5 QCR71_ARATH Cytochrome b-c1 complex subunit 7-1 OS=Arabidopsis thaliana GN=QCR7-1 PE=1 SV=1	3	-0,262	0,32967033	765,49	0,53
Q94CJ5 RER4_ARATH Protein RETICULATA-RELATED 4, chloroplastic OS=Arabidopsis thaliana GN=RER4 PE=2 SV=1	8	-0,191	0,328671329	763,17	0,53
F4JHJ0 F4JHJ0_ARATH HSP20-like chaperones superfamily protein OS=Arabidopsis thaliana GN=At4g02450 PE=1 SV=1	5	0,19	0,32967033	765,49	0,53
Q8L4N1 PHO34_ARATH Universal stress protein PHOS34 OS=Arabidopsis thaliana GN=PHOS34 PE=1 SV=1	1	0,371	0,330669331	767,81	0,531
Q9CAX6 RS142_ARATH 40S ribosomal protein S14-2 OS=Arabidopsis thaliana GN=RPS14B PE=1 SV=1	1	0,301	0,32967033	765,49	0,531
P38666 RL242_ARATH 60S ribosomal protein L24-2 OS=Arabidopsis thaliana GN=RPL24B PE=1 SV=2	6	0,179	0,330669331	767,81	0,531
Q9FJX2 RL262_ARATH 60S ribosomal protein L26-2 OS=Arabidopsis thaliana GN=RPL26B PE=2 SV=1	1	-0,405	0,332667333	772,45	0,532
P50318 PGKH2_ARATH Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=1 SV=3	2	0,35	0,332667333	772,45	0,532
P45724 PAL2_ARATH Phenylalanine ammonia-lyase 2 OS=Arabidopsis thaliana GN=PAL2 PE=1 SV=2	2	-0,27	0,332667333	772,45	0,532
Q38955 Q38955_ARATH Orf03 protein OS=Arabidopsis thaliana GN=orf03 PE=2 SV=1	1	-0,425	0,335664336	779,41	0,533
Q9FHL4 Q9FHL4_ARATH At5g23440 OS=Arabidopsis thaliana GN=FTRA1 PE=2 SV=1	1	0,412	0,337662338	784,05	0,533
X5JB51 SECAB_ARATH Exocyst complex component SEC10b OS=Arabidopsis thaliana GN=SEC10b PE=1 SV=1	1	-0,394	0,340659341	791,01	0,533
Q9LM92 SMD3B_ARATH Small nuclear ribonucleoprotein SmD3b OS=Arabidopsis thaliana GN=SMD3B PE=2 SV=1	1	-0,301	0,335664336	779,41	0,533
Q9FJW4 NDUS4_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Arabidopsis thaliana GN=FRO1 PE=1 SV=1	3	0,219	0,335664336	779,41	0,533
P29402 CALX1_ARATH Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1	4	0,2	0,333666334	774,77	0,533
Q8GUM2 HSP71_ARATH Heat shock 70 kDa protein 9, mitochondrial OS=Arabidopsis thaliana GN=HSP70-9 PE=1 SV=1	14	0,154	0,332667333	772,45	0,533
Q9FGF0 PGML1_ARATH Phosphoglycerate mutase-like protein 1 OS=Arabidopsis thaliana GN=At5g64460 PE=2 SV=1	1	0,58	0,334665335	777,09	0,534
Q84MD7 Q84MD7_ARATH At1g72880 OS=Arabidopsis thaliana GN=At1g72880 PE=2 SV=1	1	-0,436	0,33966034	788,69	0,534
Q9ZUV1 HIP1_ARATH Heavy metal-associated isoprenylated plant protein 1 OS=Arabidopsis thaliana GN=HIPPO1 PE=2 SV=1	1	0,399	0,337662338	784,05	0,534
O23081 CRK41_ARATH Cysteine-rich receptor-like protein kinase 41 OS=Arabidopsis thaliana GN=CRK41 PE=3 SV=2	1	-0,385	0,33966034	788,69	0,534
O82762 O82762_ARATH F17H15.1/F17H15.1 OS=Arabidopsis thaliana GN=At2g25970 PE=1 SV=1	2	-0,33	0,337662338	784,05	0,534
Q94JT5 Q94JT5_ARATH AT4g35220/F23E12_220 OS=Arabidopsis thaliana GN=At4g35220 PE=2 SV=1	2	-0,296	0,340659341	791,01	0,534
Q9LDN9 PER37_ARATH Peroxidase 37 OS=Arabidopsis thaliana GN=PER37 PE=2 SV=1	1	0,29	0,341658342	793,33	0,534
Q9LYF0 Q9LYF0_ARATH At5g11810 OS=Arabidopsis thaliana GN=T22P22_200 PE=2 SV=1	2	-0,286	0,337662338	784,05	0,534
Q39129 STR16_ARATH Thiosulfate sulfurtransferase 16, chloroplastic OS=Arabidopsis thaliana GN=STR16 PE=1 SV=2	2	-0,286	0,340659341	791,01	0,534
P42643 14331_ARATH 14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	-0,266	0,338661339	786,37	0,534
P49692 RL7A1_ARATH 60S ribosomal protein L7a-1 OS=Arabidopsis thaliana GN=RPL7AA PE=2 SV=2	2	-0,253	0,335664336	779,41	0,534
Q42564 APX3_ARATH L-ascorbate peroxidase 3 OS=Arabidopsis thaliana GN=APX3 PE=1 SV=1	4	-0,229	0,336663337	781,73	0,534
O48528 OP163_ARATH Outer envelope pore protein 16-3, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OEP163 PE=1 SV=1	3	-0,221	0,335664336	779,41	0,534
Q9FG81 Q9FG81_ARATH Aluminum induced protein with YGL and LRDR motifs OS=Arabidopsis thaliana GN=MQD19.19 PE=1 SV=1	4	0,215	0,33966034	788,69	0,534
Q96292 ACT2_ARATH Actin-2 OS=Arabidopsis thaliana GN=ACT2 PE=1 SV=1	8	0,166	0,340659341	791,01	0,534
Q94JY3 Q94JY3_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=MDB19.5 PE=2 SV=1	1	-0,544	0,341658342	793,33	0,535
Q38845 2AAA_ARATH Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Arabidopsis thaliana GN=PP2AA1 PE=1 S	1	-0,431	0,335664336	779,41	0,535
O82782 HIS3_ARATH 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic OS=Arabid	1	0,402	0,33966034	788,69	0,535
Q39097 ERF1X_ARATH Eukaryotic peptide chain release factor subunit 1-1 OS=Arabidopsis thaliana GN=ERF1-1 PE=1 SV=2	1	0,391	0,342657343	795,65	0,535

Q6DBI3 Q6DBI3_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g18630 PE=2 SV=1	2	-0,371	0,335664336	779,41	0,535
Q38950 2AAB_ARATH Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Arabidopsis thaliana GN=PP2AA2 PE=1 SV	2	-0,356	0,340659341	791,01	0,535
O49513 RAA1E_ARATH Ras-related protein RABA1e OS=Arabidopsis thaliana GN=RABA1E PE=2 SV=1	2	0,316	0,342657343	795,65	0,535
Q9S1T7 VHAA2_ARATH V-type proton ATPase subunit a2 OS=Arabidopsis thaliana GN=VHA-a2 PE=1 SV=1	2	0,313	0,335664336	779,41	0,535
P48349 14336_ARATH 14-3-3-like protein GF14 lambda OS=Arabidopsis thaliana GN=GRF6 PE=1 SV=1	2	-0,271	0,337662338	784,05	0,535
P47192 VA722_ARATH Vesicle-associated membrane protein 722 OS=Arabidopsis thaliana GN=VAMP722 PE=2 SV=2	4	-0,257	0,337662338	784,05	0,535
Q9ZU66 Q9ZU66_ARATH Putative spliceosome-associated protein OS=Arabidopsis thaliana GN=emb2444 PE=2 SV=1	2	-0,251	0,33966034	788,69	0,535
F4JZY1 CIP1_ARATH COP1-interactive protein 1 OS=Arabidopsis thaliana GN=CIP1 PE=1 SV=1	3	-0,248	0,33966034	788,69	0,535
F4I7X1 F4I7X1_ARATH SKU5-similar 6 OS=Arabidopsis thaliana GN=SKS6 PE=4 SV=1	4	0,236	0,342657343	795,65	0,535
Q42262 RS3A2_ARATH 40S ribosomal protein S3a-2 OS=Arabidopsis thaliana GN=RPS3AB PE=2 SV=3	5	0,169	0,338661339	786,37	0,535
Q9T091 VP26B_ARATH Vacuolar protein sorting-associated protein 26B OS=Arabidopsis thaliana GN=VPS26B PE=2 SV=2	1	-0,394	0,343656344	797,97	0,536
Q9LK23 G6PD5_ARATH Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform 1 OS=Arabidopsis thaliana GN=ACG9 PE=2 SV=1	2	-0,342	0,344655345	800,29	0,537
O65782 C83B1_ARATH Cytochrome P450 83B1 OS=Arabidopsis thaliana GN=CYP83B1 PE=1 SV=1	4	-0,234	0,345654346	802,61	0,538
Q9XGZ3 Q9XGZ3_ARATH Early nodulin-like protein OS=Arabidopsis thaliana GN=At5g25940 PE=2 SV=1	1	-0,538	0,346653347	804,93	0,539
Q9ZQ26 Q9ZQ26_ARATH AT2G24420 protein OS=Arabidopsis thaliana GN=At2g24420 PE=2 SV=2	1	-0,401	0,346653347	804,93	0,539
Q39172 AER_ARATH NADPH-dependent oxidoreductase 2-alkenal reductase OS=Arabidopsis thaliana GN=AER PE=1 SV=1	1	-0,391	0,347652348	807,25	0,539
O22832 STAD7_ARATH Stearoyl-[acyl-carrier-protein] 9-desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1	2	-0,344	0,347652348	807,25	0,539
Q8GYA6 PS13B_ARATH 26S proteasome non-ATPase regulatory subunit 13 homolog B OS=Arabidopsis thaliana GN=RPN9B PE=1 SV=1	2	0,307	0,348651349	809,57	0,539
Q9ZV45 Q9ZV45_ARATH Putative small nuclear ribonucleoprotein E OS=Arabidopsis thaliana GN=MSF3.12 PE=2 SV=1	3	-0,285	0,347652348	807,25	0,539
Q9SEI2 PS6AA_ARATH 26S proteasome regulatory subunit 6A homolog A OS=Arabidopsis thaliana GN=RPT5A PE=1 SV=1	7	-0,199	0,346653347	804,93	0,539
Q9SH59 RTNLC_ARATH Reticulon-like protein B3 OS=Arabidopsis thaliana GN=RTNLB3 PE=2 SV=1	1	0,564	0,347652348	807,25	0,54
Q8LG79 Q8LG79_ARATH AWP1-19-like family protein OS=Arabidopsis thaliana GN=At5g18970 PE=2 SV=1	1	-0,37	0,348651349	809,57	0,54
Q9LZW6 Q9LZW6_ARATH AT5g01800/T20L15_70 OS=Arabidopsis thaliana GN=At5g01800 PE=2 SV=1	2	-0,31	0,34965035	811,89	0,54
O81235 SODM1_ARATH Superoxide dismutase [Mn] 1, mitochondrial OS=Arabidopsis thaliana GN=MSD1 PE=1 SV=2	3	0,198	0,347652348	807,25	0,54
P24102 PER22_ARATH Peroxidase 22 OS=Arabidopsis thaliana GN=PER22 PE=1 SV=2	2	-0,294	0,34965035	811,89	0,541
Q8L940 PDX13_ARATH Pyridoxal 5'-phosphate synthase subunit PDX1.3 OS=Arabidopsis thaliana GN=PDX13 PE=1 SV=2	3	0,25	0,350649351	814,21	0,541
Q9SR59 MDAR3_ARATH Monodehydroascorbate reductase 3 OS=Arabidopsis thaliana GN=MDAR3 PE=2 SV=1	4	-0,223	0,350649351	814,21	0,541
A0A1P8B128 A0A1P8B128_ARATH SKU5 similar 16 OS=Arabidopsis thaliana GN=sks16 PE=4 SV=1	1	0,544	0,352647353	818,85	0,542
Q9SAA9 CP511_ARATH Sterol 14-demethylase OS=Arabidopsis thaliana GN=CYP51G1 PE=1 SV=1	1	0,373	0,351648352	816,53	0,542
Q9LY48 DIOX3_ARATH Probable 2-oxoglutarate-dependent dioxygenase JRG21 OS=Arabidopsis thaliana GN=JRG21 PE=2 SV=1	1	0,354	0,351648352	816,53	0,542
Q9SFX3 OST1A_ARATH Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1A OS=Arabidopsis thaliana GN=OST1A PE=2 SV=1	1	-0,392	0,353646354	821,17	0,543
P49200 RS201_ARATH 40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2	1	0,282	0,352647353	818,85	0,543
F4K2Y3 F4K2Y3_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=MAB16.20 PE=1 SV=1	3	-0,247	0,352647353	818,85	0,543
Q9ZQ36 Q9ZQ36_ARATH reversed TPRXL OS=Arabidopsis thaliana GN=At2g24310 PE=4 SV=1	1	-0,41	0,354645355	823,49	0,544
F4HUG9 F4HUG9_ARATH Ribonuclease T2 family protein OS=Arabidopsis thaliana GN=At1g14210 PE=3 SV=1	1	-0,351	0,355644356	825,81	0,544
Q8HOT4 UPL2_ARATH E3 ubiquitin-protein ligase UPL2 OS=Arabidopsis thaliana GN=UPL2 PE=1 SV=3	2	0,32	0,354645355	823,49	0,544
Q7PC86 AB35G_ARATH ABC transporter G family member 35 OS=Arabidopsis thaliana GN=ABCG35 PE=2 SV=1	3	-0,249	0,355644356	825,81	0,544
O80840 PMM_ARATH Phosphomannomutase OS=Arabidopsis thaliana GN=PMM PE=1 SV=1	4	0,205	0,355644356	825,81	0,544
P31265 TCTP1_ARATH Translationally-controlled tumor protein 1 OS=Arabidopsis thaliana GN=TCTP1 PE=1 SV=2	6	0,2	0,354645355	823,49	0,544
Q9SSB5 PRS7A_ARATH 26S proteasome regulatory subunit 7 homolog A OS=Arabidopsis thaliana GN=RPT1A PE=1 SV=1	11	-0,149	0,356643357	828,13	0,544
Q9SMQ6 RAA4B_ARATH Ras-related protein RABA4b OS=Arabidopsis thaliana GN=RABA4B PE=1 SV=1	1	-0,379	0,355644356	825,81	0,545
P19456 PMA2_ARATH ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	1	-0,315	0,357642358	830,45	0,545
Q8VYN9 PHO32_ARATH Universal stress protein PHOS32 OS=Arabidopsis thaliana GN=PHOS32 PE=1 SV=1	2	-0,295	0,358641359	832,77	0,545
Q84TI2 Q84TI2_ARATH Phosphoribosylaminoimidazole carboxylase like protein OS=Arabidopsis thaliana GN=At2g37690 PE=2 SV=1	4	-0,227	0,356643357	828,13	0,545
Q9SQI8 ODP24_ARATH Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic OS=Arabidopsis th	7	-0,185	0,354645355	823,49	0,545
O22315 SR34_ARATH Serine/arginine-rich-splicing factor SR34 OS=Arabidopsis thaliana GN=SR34 PE=1 SV=1	1	-0,397	0,357642358	830,45	0,546
F4J9W8 F4J9W8_ARATH Transducin family protein / WD-40 repeat family protein OS=Arabidopsis thaliana GN=At3g18860 PE=4 SV=1	1	-0,374	0,358641359	832,77	0,546
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	1	-0,326	0,358641359	832,77	0,546
O80998 JAL20_ARATH Jacalin-related lectin 20 OS=Arabidopsis thaliana GN=JAL20 PE=2 SV=1	3	0,235	0,358641359	832,77	0,546
Q8RXM5 Q8RXM5_ARATH Tryptophan RNA-binding attenuator protein-like protein OS=Arabidopsis thaliana GN=MLQ5.28 PE=2 SV=1	1	-0,555	0,360639361	837,4	0,547
O80480 IMPA4_ARATH Importin subunit alpha-4 OS=Arabidopsis thaliana GN=IMPA4 PE=1 SV=1	1	-0,554	0,360639361	837,4	0,547

Q8L953 RS273_ARATH 40S ribosomal protein S27-3 OS=Arabidopsis thaliana GN=RPS27D PE=2 SV=2	2	0,285	0,361638362	839,72	0,547
Q9C514 RS71_ARATH 40S ribosomal protein S7-1 OS=Arabidopsis thaliana GN=RPS7A PE=2 SV=1	4	-0,229	0,360639361	837,4	0,547
P25701 ACP2_ARATH Acyl carrier protein 2, chloroplastic OS=Arabidopsis thaliana GN=ACP2 PE=1 SV=2	1	0,413	0,360639361	837,4	0,548
Q9LEV6 Q9LEV6_ARATH At5g10830 OS=Arabidopsis thaliana GN=At5g10830 PE=2 SV=1	2	0,3	0,360639361	837,4	0,548
O22785 PR19B_ARATH Pre-mRNA-processing factor 19 homolog 2 OS=Arabidopsis thaliana GN=PRP19B PE=1 SV=3	1	-0,286	0,362637363	842,04	0,548
Q8LC68 NRP2_ARATH NAP1-related protein 2 OS=Arabidopsis thaliana GN=NRP2 PE=1 SV=2	2	0,274	0,362637363	842,04	0,548
Q9LX88 R15A4_ARATH 40S ribosomal protein S15a-4 OS=Arabidopsis thaliana GN=RPS15AD PE=2 SV=3	2	0,252	0,361638362	839,72	0,548
Q39251 ADF2_ARATH Actin-depolymerizing factor 2 OS=Arabidopsis thaliana GN=ADF2 PE=1 SV=1	2	-0,313	0,363636364	844,36	0,549
Q9LV21 TCPD_ARATH T-complex protein 1 subunit delta OS=Arabidopsis thaliana GN=CCT4 PE=1 SV=1	16	0,14	0,362637363	842,04	0,549
O04922 GPX2_ARATH Probable glutathione peroxidase 2 OS=Arabidopsis thaliana GN=GPX2 PE=1 SV=1	7	-0,159	0,364635365	846,68	0,55
Q9M263 GL24_ARATH Germin-like protein subfamily 2 member 4 OS=Arabidopsis thaliana GN=GLP10 PE=2 SV=1	1	-0,392	0,366633367	851,32	0,551
Q9CB01 RABF1_ARATH Ras-related protein RABF1 OS=Arabidopsis thaliana GN=RABF1 PE=1 SV=1	2	-0,256	0,365634366	849	0,551
Q8GYA6 PS13B_ARATH 26S proteasome non-ATPase regulatory subunit 13 homolog B OS=Arabidopsis thaliana GN=RPN9B PE=1 SV=1	3	0,231	0,365634366	849	0,551
Q39242 TRXB2_ARATH Thioredoxin reductase 2 OS=Arabidopsis thaliana GN=NTR2 PE=2 SV=2	6	0,178	0,366633367	851,32	0,551
P93028 UBE11_ARATH Ubiquitin-activating enzyme E1 1 OS=Arabidopsis thaliana GN=UBA1 PE=1 SV=1	10	0,16	0,365634366	849	0,551
F4IRR2 SAD2_ARATH Importin beta-like SAD2 OS=Arabidopsis thaliana GN=SAD2 PE=1 SV=1	1	-0,367	0,367632368	853,64	0,552
P38605 CAS1_ARATH Cycloartenol synthase OS=Arabidopsis thaliana GN=CAS1 PE=1 SV=2	1	0,345	0,366633367	851,32	0,552
Q05212 DR102_ARATH DNA damage-repair/toleration protein DRT102 OS=Arabidopsis thaliana GN=DRT102 PE=1 SV=2	2	-0,331	0,367632368	853,64	0,552
Q9FL29 Q9FL29_ARATH reversed MADS-box family protein OS=Arabidopsis thaliana GN=MPL12.11 PE=2 SV=1	1	-0,535	0,368631369	855,96	0,553
F4IA48 F4IA48_ARATH N-lysine methyltransferase OS=Arabidopsis thaliana GN=At1g78150 PE=1 SV=1	1	0,39	0,368631369	855,96	0,553
Q9FG04 Q9FG04_ARATH Calcium load-activated calcium channel OS=Arabidopsis thaliana GN=At5g06660 PE=1 SV=1	1	0,363	0,370629371	860,6	0,555
Q9FDZ9 RL212_ARATH 60S ribosomal protein L21-2 OS=Arabidopsis thaliana GN=RPL21E PE=2 SV=1	1	0,362	0,370629371	860,6	0,555
Q38946 DHE2_ARATH Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1	2	-0,231	0,370629371	860,6	0,555
P45725 PAL3_ARATH Phenylalanine ammonia-lyase 3 OS=Arabidopsis thaliana GN=PAL3 PE=1 SV=3	1	0,54	0,372627373	865,24	0,556
Q941B2 Q941B2_ARATH At1g09870/F21M12_26 OS=Arabidopsis thaliana GN=At1g09870 PE=2 SV=1	2	0,331	0,372627373	865,24	0,556
Q9MAM3 KCS1_ARATH reversed 3-ketoacyl-CoA synthase 1 OS=Arabidopsis thaliana GN=KCS1 PE=1 SV=1	1	-0,283	0,371628372	862,92	0,556
Q9FWR5 GCA1_ARATH Gamma carboxic anhydride 1, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA1 PE=1 SV=1	2	0,254	0,373626374	867,56	0,556
O23627 SYGM1_ARATH Glycine--tRNA ligase, mitochondrial 1 OS=Arabidopsis thaliana GN=At1g29880 PE=1 SV=1	15	-0,152	0,372627373	865,24	0,556
O23617 TP55_ARATH Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabidopsis thaliana GN=TP55 PE=1 SV=2	1	-0,548	0,373626374	867,56	0,557
Q8VZF3 CGEP_ARATH Probable glutamyl endopeptidase, chloroplastic OS=Arabidopsis thaliana GN=GEP PE=2 SV=2	5	-0,214	0,372627373	865,24	0,557
Q93VA8 Q93VA8_ARATH Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g76010 PE=2 SV=1	5	-0,192	0,374625375	869,88	0,558
Q8H126 Q8H126_ARATH Selenoprotein O OS=Arabidopsis thaliana GN=At5g13030 PE=1 SV=1	1	-0,334	0,375624376	872,2	0,559
Q9C6D2 MTK_ARATH Methylthioribose kinase OS=Arabidopsis thaliana GN=MTK PE=1 SV=1	1	0,382	0,376623377	874,52	0,56
Q9SMW7 BTF3_ARATH Basic transcription factor 3 OS=Arabidopsis thaliana GN=BTF3 PE=1 SV=1	2	-0,329	0,376623377	874,52	0,56
Q42586 UMPS_ARATH Uridine 5'-monophosphate synthase OS=Arabidopsis thaliana GN=PYRE-F PE=2 SV=2	7	-0,176	0,377622378	876,84	0,56
Q9FG81 Q9FG81_ARATH Aluminum induced protein with YGL and LRDR motifs OS=Arabidopsis thaliana GN=MQD19.19 PE=1 SV=1	1	-0,361	0,378621379	879,16	0,561
F4JM19 MYO14_ARATH reversed Myosin-14 OS=Arabidopsis thaliana GN=XI-H PE=3 SV=1	1	0,293	0,378621379	879,16	0,561
Q9LJI5 VA0D1_ARATH V-type proton ATPase subunit d1 OS=Arabidopsis thaliana GN=VHA-d1 PE=2 SV=1	7	-0,19	0,378621379	879,16	0,561
O23255 SAHH1_ARATH Adenosylhomocysteinase 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1	15	0,135	0,380619381	883,8	0,561
Q84WV1 TCPG_ARATH T-complex protein 1 subunit gamma OS=Arabidopsis thaliana GN=CCT3 PE=1 SV=1	16	0,133	0,377622378	876,84	0,561
F4K0E8 ISPG_ARATH 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic OS=Arabidopsis thaliana GN=ISPG PE=1 SV=1	1	-0,545	0,37962038	881,48	0,562
Q8LG98 OTUBL_ARATH Ubiquitin thioesterase otubain-like OS=Arabidopsis thaliana GN=At1g28120 PE=2 SV=2	1	-0,356	0,380619381	883,8	0,562
Q9LV35 AIP12_ARATH Actin-interacting protein 1-2 OS=Arabidopsis thaliana GN=AIP1-2 PE=2 SV=1	5	0,2	0,380619381	883,8	0,562
Q8H0X6-2 CYT6_ARATH Isoform 2 of Cysteine proteinase inhibitor 6 OS=Arabidopsis thaliana GN=CYS6	5	-0,172	0,381618382	886,12	0,562
Q96522 PER45_ARATH Peroxidase 45 OS=Arabidopsis thaliana GN=PER45 PE=1 SV=1	14	0,134	0,382617383	888,44	0,562
Q38798 CALX2_ARATH Calnexin homolog 2 OS=Arabidopsis thaliana GN=At5g07340 PE=2 SV=2	1	-0,566	0,380619381	883,8	0,563
Q9M330 PSMF1_ARATH Probable proteasome inhibitor OS=Arabidopsis thaliana GN=At3g53970 PE=1 SV=1	1	-0,505	0,380619381	883,8	0,563
Q9SIV9 PPA10_ARATH Purple acid phosphatase 10 OS=Arabidopsis thaliana GN=PAP10 PE=2 SV=1	1	-0,393	0,386613387	897,72	0,563
B7ZWR6 OEP61_ARATH Outer envelope protein 61 OS=Arabidopsis thaliana GN=OEP61 PE=1 SV=1	1	0,352	0,385614386	895,4	0,563
F4I8M8 F4I8M8_ARATH Phosphoglycerate/bisphosphoglycerate mutase OS=Arabidopsis thaliana GN=PGM PE=3 SV=1	1	0,347	0,382617383	888,44	0,563
O23523 RGGA_ARATH RGG repeats nuclear RNA binding protein A OS=Arabidopsis thaliana GN=RGGA PE=1 SV=1	1	0,329	0,384615385	893,08	0,563

Q0WQ75 VPS51_ARATH Vacuolar protein sorting-associated protein 51 homolog OS=Arabidopsis thaliana GN=VPS51 PE=1 SV=1	2	-0,311	0,387612388	900,04	0,563
Q9LNC5 CLO_ARATH 110 kDa U5 small nuclear ribonucleoprotein component CLO OS=Arabidopsis thaliana GN=CLO PE=1 SV=1	2	0,266	0,382617383	888,44	0,563
Q9LY75 CYP63_ARATH Peptidyl-prolyl cis-trans isomerase CYP63 OS=Arabidopsis thaliana GN=CYP63 PE=1 SV=1	1	0,251	0,381618382	886,12	0,563
Q9FLX7 NDUA5_ARATH Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial OS=Arabidopsis thaliana GN=At5g52:	5	-0,18	0,382617383	888,44	0,563
P42036 RS143_ARATH 40S ribosomal protein S14-3 OS=Arabidopsis thaliana GN=RPS14C PE=2 SV=2	7	0,17	0,385614386	895,4	0,563
O24653 GDI2_ARATH Guanosine nucleotide diphosphate dissociation inhibitor 2 OS=Arabidopsis thaliana GN=GDI2 PE=2 SV=1	9	0,154	0,383616384	890,76	0,563
Q94CI7 EDL17_ARATH Sugar transporter ERD6-like 17 OS=Arabidopsis thaliana GN=SGP1 PE=2 SV=2	1	-0,531	0,386613387	897,72	0,564
F4HXV6 NU155_ARATH Nuclear pore complex protein NUP155 OS=Arabidopsis thaliana GN=NUP155 PE=1 SV=1	1	0,5	0,388611389	902,36	0,564
Q94AM9 CID4_ARATH Polyadenylate-binding protein-interacting protein 4 OS=Arabidopsis thaliana GN=CID4 PE=2 SV=1	1	0,493	0,388611389	902,36	0,564
O23710 PSB7A_ARATH Proteasome subunit beta type-7-A OS=Arabidopsis thaliana GN=PBB1 PE=1 SV=2	1	-0,387	0,384615385	893,08	0,564
O04308 MPPA2_ARATH Probable mitochondrial-processing peptidase subunit alpha-2, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MPPA2	1	-0,378	0,385614386	895,4	0,564
Q9LVG6 Q9LVG6_ARATH reversed Protein kinase family protein OS=Arabidopsis thaliana GN=MGO3.6 PE=2 SV=1	1	0,378	0,38961039	904,68	0,564
Q8VXZ5 XG113_ARATH Arabinosyltransferase XEG113 OS=Arabidopsis thaliana GN=XEG113 PE=2 SV=1	1	0,328	0,387612388	900,04	0,564
P83755 PSBA_ARATH Photosystem II protein D1 OS=Arabidopsis thaliana GN=psbA PE=1 SV=2	1	-0,313	0,385614386	895,4	0,564
Q9C5E8 SDH7A_ARATH Succinate dehydrogenase subunit 7A, mitochondrial OS=Arabidopsis thaliana GN=SDH7A PE=1 SV=1	1	0,308	0,387612388	900,04	0,564
Q56ZN6 AVP2_ARATH Pyrophosphate-energized membrane proton pump 2 OS=Arabidopsis thaliana GN=AVPL1 PE=1 SV=2	2	-0,281	0,384615385	893,08	0,564
Q9FJY1 Q9FJY1_ARATH CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein OS=Arabidopsis thaliana	3	-0,247	0,390609391	907	0,564
Q9FE65 RL342_ARATH 60S ribosomal protein L34-2 OS=Arabidopsis thaliana GN=RPL34B PE=3 SV=1	1	0,247	0,391608392	909,31	0,564
O65896 CDA1_ARATH Cytidine deaminase 1 OS=Arabidopsis thaliana GN=CDA1 PE=1 SV=1	4	0,217	0,386613387	897,72	0,564
Q9M8X9 RS162_ARATH 40S ribosomal protein S16-2 OS=Arabidopsis thaliana GN=RPS16B PE=1 SV=1	2	0,215	0,387612388	900,04	0,564
O65719 HSP7C_ARATH Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	9	0,143	0,386613387	897,72	0,564
Q8L7Z3 DRE2_ARATH Anamorsin homolog OS=Arabidopsis thaliana GN=At5g18400 PE=1 SV=1	1	-0,522	0,391608392	909,31	0,565
Q9FYA6 BCAT5_ARATH Branched-chain-amino-acid aminotransferase 5, chloroplastic OS=Arabidopsis thaliana GN=BCAT5 PE=1 SV=1	1	0,502	0,384615385	893,08	0,565
O23095 RLA12_ARATH 60S acidic ribosomal protein P1-2 OS=Arabidopsis thaliana GN=RPP1B PE=1 SV=2	1	0,391	0,38961039	904,68	0,565
P53799 FDF11_ARATH Squalene synthase 1 OS=Arabidopsis thaliana GN=SQS1 PE=1 SV=1	1	0,368	0,38961039	904,68	0,565
Q9LSC2 Y3589_ARATH PTI1-like tyrosine-protein kinase At3g15890 OS=Arabidopsis thaliana GN=At3g15890 PE=2 SV=1	1	-0,362	0,391608392	909,31	0,565
O80574 DAPB1_ARATH 4-hydroxy-tetrahydronicotinamide reductase 1, chloroplastic OS=Arabidopsis thaliana GN=DAPB1 PE=1 SV=2	1	-0,358	0,390609391	907	0,565
Q94JQ3 GLYP3_ARATH Serine hydroxymethyltransferase 3, chloroplastic OS=Arabidopsis thaliana GN=SHM3 PE=1 SV=2	2	-0,357	0,390609391	907	0,565
Q1PDF5 Q1PDF5_ARATH P-loop containing nucleoside triphosphate hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g66970 PE=2 SV=1	1	-0,355	0,385614386	895,4	0,565
Q9S120 EF1D2_ARATH Elongation factor 1-delta 2 OS=Arabidopsis thaliana GN=At2g18110 PE=1 SV=1	2	0,337	0,390609391	907	0,565
P93832 LEU32_ARATH 3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1	2	0,299	0,393606394	913,95	0,565
Q9LX13 Q9LX13_ARATH (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-like protein OS=Arabidopsis thaliana GN=At5g10160 PE=2 SV=1	1	-0,276	0,393606394	913,95	0,565
Q7XA74 GDL21_ARATH Inactive GDSL esterase/lipase-like protein 25 OS=Arabidopsis thaliana GN=MVP1 PE=1 SV=1	2	-0,241	0,391608392	909,31	0,565
P32961 NRL1_ARATH Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2	3	-0,219	0,394605395	916,27	0,565
Q9ZPY7 XPO2_ARATH Exportin-2 OS=Arabidopsis thaliana GN=CAS PE=2 SV=1	8	0,186	0,393606394	913,95	0,565
Q9LK25 PHB4_ARATH Prohibitin-4, mitochondrial OS=Arabidopsis thaliana GN=PHB4 PE=1 SV=1	1	-0,391	0,393606394	913,95	0,566
Q94B78 GCSP1_ARATH Glycine dehydrogenase (decarboxylating) 1, mitochondrial OS=Arabidopsis thaliana GN=GLDP1 PE=1 SV=2	1	0,338	0,392607393	911,63	0,566
Q38935 FK151_ARATH Peptidyl-prolyl cis-trans isomerase FKBP15-1 OS=Arabidopsis thaliana GN=FKBP15-1 PE=2 SV=2	1	-0,28	0,395604396	918,59	0,566
Q9SSD2 PRP8A_ARATH Pre-mRNA-processing-splicing factor 8A OS=Arabidopsis thaliana GN=PRP8A PE=1 SV=1	3	-0,238	0,393606394	913,95	0,566
O22769 NDUV2_ARATH NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Arabidopsis thaliana GN=At4g02580 PE=1 SV=3	3	0,232	0,394605395	916,27	0,566
Q08112 RS151_ARATH 40S ribosomal protein S15-1 OS=Arabidopsis thaliana GN=RPS15A PE=2 SV=1	3	0,203	0,396603397	920,91	0,566
P35510 PAL1_ARATH Phenylalanine ammonia-lyase 1 OS=Arabidopsis thaliana GN=PAL1 PE=1 SV=3	9	-0,186	0,393606394	913,95	0,566
Q9C9C4 ENO1_ARATH Enolase 1, chloroplastic OS=Arabidopsis thaliana GN=ENO1 PE=1 SV=1	12	0,154	0,395604396	918,59	0,566
Q9LY31 Q9LY31_ARATH AT3G60340 protein OS=Arabidopsis thaliana GN=F27H5_130 PE=2 SV=1	1	-0,498	0,3996004	927,87	0,567
Q8L866 Q8L866_ARATH Amine oxidase OS=Arabidopsis thaliana GN=MHK10.21 PE=2 SV=1	1	0,364	0,400599401	930,19	0,567
Q38868 CDPK9_ARATH Calcium-dependent protein kinase 9 OS=Arabidopsis thaliana GN=CPK9 PE=1 SV=1	1	0,359	0,396603397	920,91	0,567
Q8LGE7 NDA8B_ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B OS=Arabidopsis thaliana GN=At5g18800 PE=1 SV=1	1	-0,356	0,398601399	925,55	0,567
Q9ZU91 E133_ARATH Glucan endo-1,3-beta-glucosidase 3 OS=Arabidopsis thaliana GN=At2g01630 PE=1 SV=2	1	0,355	0,397602398	923,23	0,567
Q8H0X5 Q8H0X5_ARATH Low-density receptor-like protein OS=Arabidopsis thaliana GN=MTG13.11 PE=2 SV=1	1	0,346	0,398601399	925,55	0,567
F417Y2 VP53B_ARATH reversed Vacuolar protein sorting-associated protein 53 B OS=Arabidopsis thaliana GN=At1g50970 PE=2 SV=1	1	-0,333	0,396603397	920,91	0,567
P34789 RS282_ARATH 40S ribosomal protein S28-2 OS=Arabidopsis thaliana GN=RPS28C PE=3 SV=1	2	0,248	0,398601399	925,55	0,567

Q9LYR2 UCR12_ARATH Cytochrome b-c1 complex subunit Rieske-2, mitochondrial OS=Arabidopsis thaliana GN=UCR1-2 PE=1 SV=1	4	-0,191	0,397602398	923,23	0,567
Q94BT9 ATOX1_ARATH Copper transport protein ATX1 OS=Arabidopsis thaliana GN=ATX1 PE=1 SV=2	3	0,187	0,401598402	932,51	0,567
P29197 CH60A_ARATH Chaperonin CPN60, mitochondrial OS=Arabidopsis thaliana GN=CPN60 PE=1 SV=2	12	-0,128	0,393606394	913,95	0,567
Q8VZK9 CSLE1_ARATH Cellulose synthase-like protein E1 OS=Arabidopsis thaliana GN=CSLE1 PE=2 SV=1	1	-0,508	0,3996004	927,87	0,568
O22467 MSI1_ARATH Histone-binding protein MSI1 OS=Arabidopsis thaliana GN=MSI1 PE=1 SV=1	1	-0,375	0,404595405	939,47	0,568
Q9ASS6 PNSL5_ARATH Photosynthetic NDH subunit of lumenal location 5, chloroplastic OS=Arabidopsis thaliana GN=PNSL5 PE=1 SV=1	1	-0,367	0,402597403	934,83	0,568
P22954 MD37D_ARATH Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37D PE=1 SV=2	1	-0,361	0,400599401	930,19	0,568
O22912 CX5C1_ARATH Probable cytochrome c oxidase subunit 5C-1 OS=Arabidopsis thaliana GN=At2g47380 PE=1 SV=1	1	-0,301	0,400599401	930,19	0,568
Q9LXZ4 Q9LXZ4_ARATH GroES-like zinc-binding alcohol dehydrogenase family protein OS=Arabidopsis thaliana GN=T5P19_110 PE=2 SV=1	2	0,288	0,398601399	925,55	0,568
F4JUM1 F4JUM1_ARATH Sec23/Sec24 protein transport family protein OS=Arabidopsis thaliana GN=At4g14160 PE=1 SV=1	2	-0,285	0,400599401	930,19	0,568
Q948K6 RABG1_ARATH Ras-related protein RABG1 OS=Arabidopsis thaliana GN=RABG1 PE=2 SV=1	1	0,253	0,398601399	925,55	0,568
Q94B60 CLPP4_ARATH ATP-dependent Clp protease proteolytic subunit 4, chloroplastic OS=Arabidopsis thaliana GN=CLPP4 PE=1 SV=1	3	-0,252	0,401598402	932,51	0,568
Q93XW5 NSP5_ARATH Nitrile-specifier protein 5 OS=Arabidopsis thaliana GN=NSP5 PE=2 SV=1	4	0,214	0,401598402	932,51	0,568
Q9SX77 SDH5_ARATH Succinate dehydrogenase subunit 5, mitochondrial OS=Arabidopsis thaliana GN=SDH5 PE=1 SV=1	3	0,203	0,404595405	939,47	0,568
P34795 G6PI_ARATH Glucose-6-phosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=PGIC PE=1 SV=1	6	-0,174	0,401598402	932,51	0,568
Q9SK66 NDUA9_ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Arabidopsis thaliana GN=At2g20360 PE=1	7	-0,172	0,403596404	937,15	0,568
Q8GUN2 HINT1_ARATH Adenyllysulfatase HINT1 OS=Arabidopsis thaliana GN=HINT1 PE=1 SV=1	6	0,168	0,3996004	927,87	0,568
P50883 RL121_ARATH 60S ribosomal protein L12-1 OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=2	4	0,159	0,404595405	939,47	0,568
Q9LJH9 Q9LJH9_ARATH Exocyst subunit exo70 family protein D3 OS=Arabidopsis thaliana GN=EXO70D3 PE=4 SV=1	1	0,495	0,404595405	939,47	0,569
Q9SSP5 THRC2_ARATH Threonine synthase 2, chloroplastic OS=Arabidopsis thaliana GN=TS2 PE=1 SV=1	1	-0,49	0,404595405	939,47	0,569
Q9FEF9 Q9FEF9_ARATH At2g20820 OS=Arabidopsis thaliana GN=At2g20820 PE=2 SV=1	1	-0,364	0,403596404	937,15	0,569
Q9C8P0 ODP25_ARATH Dihydropyridyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic OS=Arabidopsis th	2	-0,215	0,403596404	937,15	0,569
O80626 RL352_ARATH 60S ribosomal protein L35-2 OS=Arabidopsis thaliana GN=RPL35B PE=2 SV=1	3	0,2	0,404595405	939,47	0,569
O65719 HSP7C_ARATH Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	8	-0,141	0,403596404	937,15	0,569
O23569 O23569_ARATH L-lactate dehydrogenase OS=Arabidopsis thaliana GN=dl4665w PE=2 SV=1	1	0,345	0,406593407	944,11	0,57
Q9LD90 CBF5_ARATH H/ACA ribonucleoprotein complex subunit 4 OS=Arabidopsis thaliana GN=CBF5 PE=1 SV=1	4	0,197	0,406593407	944,11	0,57
Q93VQ0 VCL1_ARATH Protein VACUOLELESS1 OS=Arabidopsis thaliana GN=VCL1 PE=1 SV=1	1	0,334	0,407592408	946,43	0,571
Q9XI98 RAG3E_ARATH Ras-related protein RABG3e OS=Arabidopsis thaliana GN=RABG3E PE=2 SV=1	1	-0,305	0,408591409	948,75	0,572
F4JJC1 F4JJC1_ARATH HAT transposon superfamily OS=Arabidopsis thaliana GN=At4g15020 PE=1 SV=1	1	-0,5	0,413586414	960,35	0,573
Q9FZD1 PPR58_ARATH Pentatricopeptide repeat-containing protein At1g26460, mitochondrial OS=Arabidopsis thaliana GN=At1g26460 PE=1 SV=1	1	-0,457	0,414585415	962,67	0,573
O23676 MGN_ARATH Protein mago nashi homolog OS=Arabidopsis thaliana GN=MAGO PE=1 SV=1	1	-0,34	0,411588412	955,71	0,573
P93045 BSH_ARATH Chromatin structure-remodeling complex protein BSH OS=Arabidopsis thaliana GN=BSH PE=1 SV=2	1	0,272	0,40959041	951,07	0,573
F4IYK3 F4IYK3_ARATH ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g08943 PE=1 SV=2	2	0,258	0,410589411	953,39	0,573
Q9SZ11 GPDL3_ARATH Glycerophosphodiester phosphodiesterase GDPDL3 OS=Arabidopsis thaliana GN=GDPDL3 PE=1 SV=3	8	0,164	0,40959041	951,07	0,573
P49691 RL4B_ARATH 60S ribosomal protein L4-2 OS=Arabidopsis thaliana GN=RPL4D PE=1 SV=2	5	-0,159	0,411588412	955,71	0,573
Q9FJX3 VDAC2_ARATH Mitochondrial outer membrane protein porin 2 OS=Arabidopsis thaliana GN=VDAC2 PE=1 SV=1	10	-0,143	0,413586414	960,35	0,573
P48491 TPIS_ARATH Triosephosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=CTIMC PE=1 SV=2	12	0,132	0,412587413	958,03	0,573
F4KBW6 NU205_ARATH Nuclear pore complex protein NUP205 OS=Arabidopsis thaliana GN=NUP205 PE=1 SV=1	1	0,488	0,413586414	960,35	0,574
Q9LJW6 RL343_ARATH 60S ribosomal protein L34-3 OS=Arabidopsis thaliana GN=RPL34C PE=2 SV=1	1	0,325	0,414585415	962,67	0,574
Q39091 Q39091_ARATH Dr4 protein OS=Arabidopsis thaliana GN=Dr4 PE=2 SV=1	2	-0,301	0,411588412	955,71	0,574
Q9LS01 AOC3_ARATH Allene oxide cyclase 3, chloroplastic OS=Arabidopsis thaliana GN=AOC3 PE=2 SV=1	2	0,291	0,411588412	955,71	0,574
Q9ZUY6 AXS1_ARATH UDP-D-xylose synthase 1 OS=Arabidopsis thaliana GN=AXS1 PE=1 SV=1	1	0,279	0,414585415	962,67	0,574
Q8LG77 IDH6_ARATH Isocitrate dehydrogenase [NAD] catalytic subunit 6, mitochondrial OS=Arabidopsis thaliana GN=IDH6 PE=1 SV=2	4	-0,21	0,412587413	958,03	0,574
P60039 RL73_ARATH 60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1	2	0,202	0,410589411	953,39	0,574
P31166-2 APT1_ARATH Isoform 2 of Adenine phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=APT1	5	-0,175	0,411588412	955,71	0,574
Q9SIF2 HS905_ARATH Heat shock protein 90-5, chloroplastic OS=Arabidopsis thaliana GN=HSP90-5 PE=1 SV=1	6	0,163	0,412587413	958,03	0,574
Q9C9D0 SOT16_ARATH Cytosolic sulfotransferase 16 OS=Arabidopsis thaliana GN=SOT16 PE=1 SV=1	6	0,156	0,413586414	960,35	0,574
Q29Q34 Q29Q34_ARATH At5g19440 OS=Arabidopsis thaliana GN=At5g19440 PE=2 SV=1	9	-0,143	0,413586414	960,35	0,574
Q9SBA5 ITPK1_ARATH Inositol-tetrakisphosphate 1-kinase 1 OS=Arabidopsis thaliana GN=ITPK1 PE=1 SV=1	2	-0,293	0,416583417	967,31	0,576
O81816 MO2_ARATH Monooxygenase 2 OS=Arabidopsis thaliana GN=MO2 PE=2 SV=1	3	-0,205	0,417582418	969,63	0,577
Q9T080 U79B2_ARATH UDP-glycosyltransferase 79B2 OS=Arabidopsis thaliana GN=UGT79B2 PE=2 SV=1	1	0,459	0,41958042	974,27	0,578

P30186 PSA7A_ARATH Proteasome subunit alpha type-7-A OS=Arabidopsis thaliana GN=PAD1 PE=1 SV=1	1	-0,341	0,418581419	971,95	0,578
Q9S2X9 RL92_ARATH 60S ribosomal protein L9-2 OS=Arabidopsis thaliana GN=RPL9D PE=2 SV=1	1	0,333	0,420579421	976,59	0,578
P25856 G3PA1_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3	5	-0,184	0,420579421	976,59	0,578
Q9C5C4 ARGE_ARATH Acetylornithine deacetylase OS=Arabidopsis thaliana GN=At4g17830 PE=2 SV=1	5	-0,179	0,418581419	971,95	0,578
P57720 AROC_ARATH Chorismate synthase, chloroplastic OS=Arabidopsis thaliana GN=EMB1144 PE=2 SV=2	8	-0,15	0,41958042	974,27	0,578
Q9LXC9 IPYR6_ARATH Soluble inorganic pyrophosphatase 6, chloroplastic OS=Arabidopsis thaliana GN=PPA6 PE=1 SV=1	6	0,148	0,41958042	974,27	0,578
Q94EJ6 PMTE_ARATH Probable methyltransferase PMT14 OS=Arabidopsis thaliana GN=At4g18030 PE=2 SV=1	1	0,494	0,421578422	978,91	0,579
Q9LP15 CID11_ARATH Polyadenylate-binding protein-interacting protein 11 OS=Arabidopsis thaliana GN=CID11 PE=2 SV=1	1	0,36	0,422577423	981,22	0,579
Q9SUW2 APT3_ARATH Adenine phosphoribosyltransferase 3 OS=Arabidopsis thaliana GN=APT3 PE=1 SV=1	1	-0,36	0,424575425	985,86	0,579
O04658 NOP5A_ARATH Probable nucleolar protein 5-1 OS=Arabidopsis thaliana GN=NOP5-1 PE=1 SV=2	1	0,337	0,422577423	981,22	0,579
Q94BR4 PR19A_ARATH Pre-mRNA-processing factor 19 homolog 1 OS=Arabidopsis thaliana GN=PRP19A PE=1 SV=1	1	-0,329	0,425574426	988,18	0,579
Q9SV20 COPB2_ARATH Coatomer subunit beta-2 OS=Arabidopsis thaliana GN=At4g31490 PE=2 SV=2	2	-0,299	0,425574426	988,18	0,579
Q06588 ACCO4_ARATH 1-aminocyclopropane-1-carboxylate oxidase 4 OS=Arabidopsis thaliana GN=ACO4 PE=1 SV=2	2	0,287	0,420579421	976,59	0,579
Q96321 IMPA1_ARATH Importin subunit alpha-1 OS=Arabidopsis thaliana GN=IMPA1 PE=1 SV=2	2	-0,263	0,421578422	978,91	0,579
Q9SN96 Q9SN96_ARATH AT3g46430/F18L15_150 OS=Arabidopsis thaliana GN=F18L15.150 PE=2 SV=1	2	0,225	0,422577423	981,22	0,579
Q9SKC9 NDUB7_ARATH NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Arabidopsis thaliana GN=At2g02050 PE=3 SV=1	6	-0,158	0,424575425	985,86	0,579
Q8RWV0 TKTC1_ARATH Transketolase-1, chloroplastic OS=Arabidopsis thaliana GN=TKL-1 PE=1 SV=1	13	-0,143	0,41958042	974,27	0,579
Q9SMT7 4CLLA_ARATH Oxalate--CoA ligase OS=Arabidopsis thaliana GN=AAE3 PE=1 SV=1	10	-0,136	0,426573427	990,5	0,579
F4JPD8 F4JPD8_ARATH Nucleoside diphosphate kinase OS=Arabidopsis thaliana GN=At4g23895 PE=3 SV=1	1	0,495	0,424575425	985,86	0,58
Q9SEU7 TRXM3_ARATH Thioredoxin M3, chloroplastic OS=Arabidopsis thaliana GN=GAT1 PE=2 SV=2	1	-0,489	0,423576424	983,54	0,58
Q94C57 U73B2_ARATH UDP-glucosyl transferase 73B2 OS=Arabidopsis thaliana GN=UGT73B2 PE=1 SV=1	1	-0,345	0,427572428	992,82	0,58
Q4V3B0 Q4V3B0_ARATH reversed At4g11990 OS=Arabidopsis thaliana GN=At4g11990 PE=2 SV=1	1	0,331	0,425574426	988,18	0,58
Q9FG34 PER54_ARATH Peroxidase 54 OS=Arabidopsis thaliana GN=PER54 PE=2 SV=1	1	-0,33	0,426573427	990,5	0,58
A0A1P8BEI2 A0A1P8BEI2_ARATH reversed GRF zinc finger / Zinc knuckle protein OS=Arabidopsis thaliana GN=MAC12.12 PE=4 SV=1	1	0,298	0,424575425	985,86	0,58
P52577 IFRH_ARATH Isoflavone reductase homolog P3 OS=Arabidopsis thaliana GN=At1g75280 PE=2 SV=1	3	-0,199	0,422577423	981,22	0,58
Q9M5K2 DLDH2_ARATH Dihydrolipoyl dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=LPD2 PE=1 SV=1	3	0,185	0,425574426	988,18	0,58
Q9SJV2 Q9SJV2_ARATH NAD(P)-linked oxidoreductase superfamily protein OS=Arabidopsis thaliana GN=At2g21250 PE=2 SV=1	7	-0,153	0,424575425	985,86	0,58
P17094 RL31_ARATH 60S ribosomal protein L3-1 OS=Arabidopsis thaliana GN=ARP1 PE=1 SV=5	17	0,11	0,426573427	990,5	0,58
P59226 H32_ARATH Histone H3.2 OS=Arabidopsis thaliana GN=HTR2 PE=1 SV=2	1	-0,458	0,424575425	985,86	0,581
Q8VZ19 RL302_ARATH 60S ribosomal protein L30-2 OS=Arabidopsis thaliana GN=RPL30B PE=3 SV=1	1	0,361	0,428571429	995,14	0,581
Q9LNJ3 APF2_ARATH Aspartyl protease family protein 2 OS=Arabidopsis thaliana GN=APF2 PE=2 SV=1	1	-0,308	0,428571429	995,14	0,581
Q38936 FK152_ARATH Peptidyl-prolyl cis-trans isomerase FKBP15-2 OS=Arabidopsis thaliana GN=FKBP15-2 PE=2 SV=2	3	0,18	0,42957043	997,46	0,581
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	9	0,136	0,42957043	997,46	0,581
Q9FMR9 RIN1_ARATH RuvB-like protein 1 OS=Arabidopsis thaliana GN=RIN1 PE=1 SV=1	2	-0,347	0,42957043	997,46	0,582
O22785 PR19B_ARATH Pre-mRNA-processing factor 19 homolog 2 OS=Arabidopsis thaliana GN=PRP19B PE=1 SV=3	1	0,337	0,430569431	999,78	0,582
Q01474 SAR1B_ARATH GTP-binding protein SAR1B OS=Arabidopsis thaliana GN=SAR1B PE=1 SV=1	4	-0,186	0,430569431	999,78	0,582
B9DG73 B9DG73_ARATH AT3G11930 protein OS=Arabidopsis thaliana GN=At3g11930 PE=1 SV=1	4	0,18	0,42957043	997,46	0,582
O65788 C71B2_ARATH Cytochrome P450 71B2 OS=Arabidopsis thaliana GN=CYP71B2 PE=2 SV=2	1	-0,507	0,431568432	1002,1	0,583
Q84WW2 6PGL5_ARATH Probable 6-phosphogluconolactonase 5, chloroplastic OS=Arabidopsis thaliana GN=EMB2024 PE=2 SV=1	1	-0,26	0,433566434	1006,74	0,584
Q5QIT3 2AB2B_ARATH Serine/threonine protein phosphatase 2A regulatory subunit B''beta OS=Arabidopsis thaliana GN=B''BETA PE=1 SV=1	2	-0,25	0,433566434	1006,74	0,584
O82514 KAD4_ARATH Adenylate kinase 4 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=2	2	0,226	0,432567433	1004,42	0,584
Q9FNN5 NDUV1_ARATH NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Arabidopsis thaliana GN=At5g08530 PE=1 SV=1	7	-0,165	0,433566434	1006,74	0,584
Q39255 SKP1A_ARATH SKP1-like protein 1A OS=Arabidopsis thaliana GN=SKP1A PE=1 SV=1	1	0,46	0,434565435	1009,06	0,585
Q8VZP3 Q8VZP3_ARATH Uncharacterized protein At2g35810 OS=Arabidopsis thaliana GN=At2g35810 PE=2 SV=1	1	0,454	0,436563437	1013,7	0,585
Q9M339 RS32_ARATH 40S ribosomal protein S3-2 OS=Arabidopsis thaliana GN=RPS3B PE=1 SV=1	1	-0,305	0,433566434	1006,74	0,585
Q9LVC9 RLA32_ARATH 60S acidic ribosomal protein P3-2 OS=Arabidopsis thaliana GN=RPP3B PE=2 SV=1	2	0,196	0,436563437	1013,7	0,585
Q9ZQH3 Q9ZQH3_ARATH At2g27460 OS=Arabidopsis thaliana GN=At2g27460 PE=2 SV=1	1	-0,474	0,435564436	1011,38	0,586
O80860 FTSH2_ARATH ATP-dependent zinc metalloprotease FTSH 2, chloroplastic OS=Arabidopsis thaliana GN=FTSH2 PE=1 SV=1	1	0,312	0,436563437	1013,7	0,586
Q9C6K5 LSM3B_ARATH Sm-like protein LSM3B OS=Arabidopsis thaliana GN=LSM3B PE=1 SV=1	2	0,252	0,437562438	1016,02	0,586
Q9SMU7 SRP09_ARATH Signal recognition particle 9 kDa protein OS=Arabidopsis thaliana GN=SRP9 PE=3 SV=1	2	0,236	0,437562438	1016,02	0,586
P29976 AROF_ARATH Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2	1	0,224	0,436563437	1013,7	0,586

Q8LD27 PSB6_ARATH Proteasome subunit beta type-6 OS=Arabidopsis thaliana GN=PBA1 PE=1 SV=2	5	0,171	0,436563437	1013,7	0,586
Q9ZUA0 OST1B_ARATH Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1B OS=Arabidopsis thaliana GN=OST1B PE=1 SV=1	2	-0,285	0,436563437	1013,7	0,587
Q24JN5 P4H5_ARATH Prolyl 4-hydroxylase 5 OS=Arabidopsis thaliana GN=P4H5 PE=2 SV=1	2	0,237	0,438561439	1018,34	0,587
Q9LFW1 RGP2_ARATH UDP-arabinopyranose mutase 2 OS=Arabidopsis thaliana GN=RGP2 PE=1 SV=1	9	0,124	0,441558442	1025,3	0,59
Q9C525 BGL21_ARATH Beta-glucosidase 21 OS=Arabidopsis thaliana GN=BGLU21 PE=1 SV=1	4	-0,174	0,442557443	1027,62	0,591
Q9C681 H2A1_ARATH Probable histone H2A.1 OS=Arabidopsis thaliana GN=At1g51060 PE=1 SV=1	2	-0,293	0,443556444	1029,94	0,592
COLGN2 Y3148_ARATH Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840 OS=Arabidopsis thaliana GN=LRR-RLK PE=1 SV=1	1	0,285	0,444555445	1032,26	0,593
Q9ZQI8 NLT12_ARATH Non-specific lipid-transfer protein-like protein At2g13820 OS=Arabidopsis thaliana GN=At2g13820 PE=1 SV=1	2	-0,22	0,444555445	1032,26	0,593
Q9FMD7 Y5659_ARATH Probable inactive receptor kinase At5g16590 OS=Arabidopsis thaliana GN=At5g16590 PE=1 SV=1	1	0,288	0,445554446	1034,58	0,594
Q9C826 ABA2_ARATH Xanthoxin dehydrogenase OS=Arabidopsis thaliana GN=ABA2 PE=1 SV=1	2	0,238	0,446553447	1036,9	0,595
Q9FMN4 TCLOT_ARATH Thioredoxin-like protein Clot OS=Arabidopsis thaliana GN=At5g42850 PE=2 SV=1	1	-0,327	0,447552448	1039,22	0,596
P92549 ATPAM_ARATH ATP synthase subunit alpha, mitochondrial OS=Arabidopsis thaliana GN=ATPA PE=1 SV=2	19	-0,115	0,447552448	1039,22	0,596
Q9SGR6 Q9SGR6_ARATH AT1G76160 protein OS=Arabidopsis thaliana GN=sk5 PE=2 SV=1	2	0,209	0,44955045	1043,86	0,597
Q9S158 Q9S158_ARATH 60S ribosomal export protein NMD3 OS=Arabidopsis thaliana GN=NMD3 PE=2 SV=1	1	0,313	0,451548452	1048,5	0,598
Q9LTX9 HSP7G_ARATH Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana GN=HSP70-7 PE=2 SV=1	3	0,202	0,450549451	1046,18	0,598
Q39043 MD37F_ARATH Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	2	0,198	0,44955045	1043,86	0,598
O64688 ODPB3_ARATH Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic OS=Arabidopsis thaliana GN=E1-BETA-2 PE=2 SV=1	2	0,198	0,450549451	1046,18	0,598
A8MSC5 A8MSC5_ARATH AT2G47470 protein OS=Arabidopsis thaliana GN=UNE5 PE=2 SV=1	8	0,137	0,44955045	1043,86	0,598
Q8S2T0 GRIP_ARATH Protein GRIP OS=Arabidopsis thaliana GN=GRIP PE=1 SV=2	1	-0,453	0,457542458	1062,41	0,599
P32068 TRPE_ARATH Anthranilate synthase alpha subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ASA1 PE=1 SV=1	1	-0,342	0,455544456	1057,77	0,599
Q9LTH8 ACH11_ARATH 1-aminocyclopropane-1-carboxylate oxidase homolog 11 OS=Arabidopsis thaliana GN=At5g59530 PE=2 SV=1	1	-0,333	0,453546454	1053,13	0,599
P19456 PMA2_ARATH ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	1	0,31	0,453546454	1053,13	0,599
Q9LF41 UBE4_ARATH Probable ubiquitin conjugation factor E4 OS=Arabidopsis thaliana GN=PUB1 PE=2 SV=1	1	0,302	0,452547453	1050,82	0,599
Q8L7H8 MPC2_ARATH Mitochondrial pyruvate carrier 2 OS=Arabidopsis thaliana GN=MPC2 PE=3 SV=1	1	-0,293	0,452547453	1050,82	0,599
Q9SZU1 C81F4_ARATH Cytochrome P450 81F4 OS=Arabidopsis thaliana GN=CYP81F4 PE=1 SV=1	2	0,264	0,451548452	1048,5	0,599
Q94AD1 D1861_ARATH Putative DNA-binding protein At1g48610 OS=Arabidopsis thaliana GN=At1g48610 PE=1 SV=1	2	0,234	0,452547453	1050,82	0,599
O48661 SPD2_ARATH Spermidine synthase 2 OS=Arabidopsis thaliana GN=SPDSYN2 PE=1 SV=2	4	-0,174	0,453546454	1053,13	0,599
Q9FKS5 CYC1B_ARATH Cytochrome c1 2, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC12 PE=1 SV=1	3	0,163	0,455544456	1057,77	0,599
Q8L743 G6PD3_ARATH Glucose-6-phosphate 1-dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=At1g24280 PE=1 SV=2	9	0,137	0,457542458	1062,41	0,599
P29513 TBB5_ARATH Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1	1	-0,475	0,455544456	1057,77	0,6
Q8VZC7 DRL36_ARATH Probable disease resistance protein At5g45510 OS=Arabidopsis thaliana GN=At5g45510 PE=1 SV=2	1	-0,457	0,456543457	1060,09	0,6
Q9M1T1 SETH3_ARATH reversed Probable arabinose 5-phosphate isomerase OS=Arabidopsis thaliana GN=SETH3 PE=2 SV=1	1	-0,447	0,456543457	1060,09	0,6
O80998 JAL20_ARATH Jacalin-related lectin 20 OS=Arabidopsis thaliana GN=JAL20 PE=2 SV=1	1	0,334	0,455544456	1057,77	0,6
Q9LVM0 Y5830_ARATH Probable inactive receptor kinase At5g58300 OS=Arabidopsis thaliana GN=At5g58300 PE=2 SV=1	1	-0,33	0,455544456	1057,77	0,6
O48737 TRXM1_ARATH Thioredoxin M1, chloroplastic OS=Arabidopsis thaliana GN=At1g03680 PE=2 SV=1	1	-0,302	0,457542458	1062,41	0,6
Q96291 BAS1A_ARATH 2-Cys peroxiredoxin BAS1, chloroplastic OS=Arabidopsis thaliana GN=BAS1 PE=1 SV=2	3	-0,201	0,457542458	1062,41	0,6
Q9ZUF6 SBT18_ARATH Subtilisin-like protease SBT1.8 OS=Arabidopsis thaliana GN=SBT1.8 PE=1 SV=1	4	0,191	0,454545455	1055,45	0,6
Q9FIB6 PS12A_ARATH 26S proteasome non-ATPase regulatory subunit 12 homolog A OS=Arabidopsis thaliana GN=RPN5A PE=1 SV=1	10	-0,123	0,457542458	1062,41	0,6
Q9C5A9 ATPBO_ARATH ATP synthase subunit beta-3, mitochondrial OS=Arabidopsis thaliana GN=At5g08680 PE=1 SV=1	25	-0,102	0,453546454	1053,13	0,6
Q9FM19 HIR1_ARATH Hypersensitive-induced response protein 1 OS=Arabidopsis thaliana GN=HIR1 PE=1 SV=1	1	-0,456	0,460539461	1069,37	0,601
Q9S785 GPDH2_ARATH Glycerol-3-phosphate dehydrogenase [NAD(+)] At3g07690, cytosolic OS=Arabidopsis thaliana GN=At3g07690 PE=3 SV=2	1	-0,287	0,45954046	1067,05	0,601
Q9FMT1 LEU33_ARATH 3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMDH3 PE=1 SV=1	2	-0,213	0,457542458	1062,41	0,601
Q9M0A7 GGP1_ARATH Gamma-glutamyl peptidase 1 OS=Arabidopsis thaliana GN=GGP1 PE=1 SV=1	4	0,178	0,455544456	1057,77	0,601
Q9ZUP3 NAP1B_ARATH Nucleosome assembly protein 1;2 OS=Arabidopsis thaliana GN=NAP1;2 PE=1 SV=1	6	-0,165	0,45954046	1067,05	0,601
Q8L4B2 NFYC9_ARATH Nuclear transcription factor Y subunit C-9 OS=Arabidopsis thaliana GN=NFYC9 PE=1 SV=1	2	0,249	0,460539461	1069,37	0,602
Q9LXM8 RLA24_ARATH 60S acidic ribosomal protein P2-4 OS=Arabidopsis thaliana GN=RPP2D PE=3 SV=1	1	-0,448	0,463536464	1076,33	0,603
Q8S8K6 SCP28_ARATH Serine carboxypeptidase-like 28 OS=Arabidopsis thaliana GN=SCPL28 PE=2 SV=2	1	0,332	0,462537463	1074,01	0,603
Q94K18 TPC1_ARATH Two pore calcium channel protein 1 OS=Arabidopsis thaliana GN=TPC1 PE=1 SV=1	1	-0,28	0,464535465	1078,65	0,603
Q38871 CDPK5_ARATH Calcium-dependent protein kinase 5 OS=Arabidopsis thaliana GN=CPK5 PE=2 SV=1	1	0,274	0,464535465	1078,65	0,603
Q8W4A0 Q8W4A0_ARATH Eukaryotic translation initiation factor 3 subunit M OS=Arabidopsis thaliana GN=F14P3.15 PE=1 SV=1	2	0,242	0,462537463	1074,01	0,603
P22953 MD37E_ARATH Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	4	0,184	0,463536464	1076,33	0,603

O80852 GSTF9_ARATH Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1	1	0,18	0,463536464	1076,33	0,603
Q39085 DIM_ARATH Delta(24)-sterol reductase OS=Arabidopsis thaliana GN=DIM PE=1 SV=2	12	0,123	0,462537463	1074,01	0,603
Q8S8T4 UXS4_ARATH UDP-glucuronic acid decarboxylase 4 OS=Arabidopsis thaliana GN=UXS4 PE=2 SV=1	1	-0,455	0,463536464	1076,33	0,604
Q9LHN8 F6H1_ARATH Feruloyl CoA ortho-hydroxylase 1 OS=Arabidopsis thaliana GN=F6'H1 PE=1 SV=1	1	0,432	0,468531469	1087,93	0,604
O82768 HIS2_ARATH Histidine biosynthesis bifunctional protein hisE, chloroplastic OS=Arabidopsis thaliana GN=HISN2 PE=1 SV=1	1	-0,31	0,465534466	1080,97	0,604
COLGG3 Y5182_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g51820 OS=Arabidopsis thaliana GN=At1g51820 PE=2 SV=1	1	-0,306	0,466533467	1083,29	0,604
Q944P7 AMPL2_ARATH Leucine aminopeptidase 2, chloroplastic OS=Arabidopsis thaliana GN=LAP2 PE=2 SV=2	3	-0,279	0,462537463	1074,01	0,604
Q8RXN1 Q8RXN1_ARATH Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=TPR3 PE=2 SV=1	1	0,263	0,467532468	1085,61	0,604
O48661 SPD2_ARATH Spermidine synthase 2 OS=Arabidopsis thaliana GN=SPDSYN2 PE=1 SV=2	2	-0,201	0,467532468	1085,61	0,604
Q9C522 ACLB1_ARATH ATP-citrate synthase beta chain protein 1 OS=Arabidopsis thaliana GN=ACLB-1 PE=2 SV=1	4	-0,17	0,466533467	1083,29	0,604
Q9SQT8 DHQSD_ARATH Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=EMB3004 PE=	9	-0,141	0,464535465	1078,65	0,604
Q9XI01 PDI11_ARATH Protein disulfide isomerase-like 1-1 OS=Arabidopsis thaliana GN=PDIL1-1 PE=1 SV=1	16	0,118	0,466533467	1083,29	0,604
Q39189 RH7_ARATH DEAD-box ATP-dependent RNA helicase 7 OS=Arabidopsis thaliana GN=RH7 PE=1 SV=2	1	-0,445	0,468531469	1087,93	0,605
Q9S2E4 VP322_ARATH Vacuolar protein sorting-associated protein 32 homolog 2 OS=Arabidopsis thaliana GN=VPS32.2 PE=1 SV=1	1	0,299	0,46953047	1090,25	0,605
Q43873 PER73_ARATH Peroxidase 73 OS=Arabidopsis thaliana GN=PER73 PE=1 SV=1	1	0,236	0,466533467	1083,29	0,605
Q9MA55-2 ACBP4_ARATH Isoform 2 of Acyl-CoA-binding domain-containing protein 4 OS=Arabidopsis thaliana GN=ACBP4	5	0,158	0,46953047	1090,25	0,605
O82399 MDHX1_ARATH Malate dehydrogenase 1, peroxisomal OS=Arabidopsis thaliana GN=PMDH1 PE=1 SV=1	6	-0,154	0,466533467	1083,29	0,605
Q96511 PER69_ARATH Peroxidase 69 OS=Arabidopsis thaliana GN=PER69 PE=1 SV=1	8	-0,135	0,468531469	1087,93	0,605
Q39054 CNX1_ARATH Molybdopterin biosynthesis protein CNX1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=2	1	0,291	0,470529471	1092,57	0,606
Q9S834 CLPP5_ARATH ATP-dependent Clp protease proteolytic subunit 5, chloroplastic OS=Arabidopsis thaliana GN=CLPP5 PE=1 SV=1	1	0,284	0,470529471	1092,57	0,606
Q9SD80 TOM5_ARATH Mitochondrial import receptor subunit TOM5 homolog OS=Arabidopsis thaliana GN=TOM5 PE=1 SV=3	2	0,237	0,471528472	1094,89	0,606
Q9SAK9 Q9SAK9_ARATH At1g79390 OS=Arabidopsis thaliana GN=T8K14.19 PE=2 SV=1	1	-0,303	0,474525475	1101,85	0,607
Q9MAU6 PDI22_ARATH Protein disulfide-isomerase like 2-2 OS=Arabidopsis thaliana GN=PDIL2-2 PE=2 SV=2	2	-0,233	0,471528472	1094,89	0,607
O65449 O65449_ARATH At4g22010 OS=Arabidopsis thaliana GN=sks4 PE=1 SV=1	4	-0,181	0,472527473	1097,21	0,607
Q38900 CP19A_ARATH Peptidyl-prolyl cis-trans isomerase CYP19-1 OS=Arabidopsis thaliana GN=CYP19-1 PE=1 SV=1	6	0,136	0,472527473	1097,21	0,607
Q8LG70 6PGL2_ARATH Probable 6-phosphogluconolactonase 2 OS=Arabidopsis thaliana GN=At3g49360 PE=2 SV=2	1	0,315	0,476523477	1106,49	0,608
Q9C9R6 PUM7_ARATH Putative pumilio homolog 7, chloroplastic OS=Arabidopsis thaliana GN=APUM7 PE=3 SV=2	1	-0,28	0,475524476	1104,17	0,608
P42793 RM05_ARATH 60S ribosomal protein L5, mitochondrial OS=Arabidopsis thaliana GN=RPL5 PE=2 SV=1	1	0,269	0,47952048	1113,45	0,608
O65272 KEA2_ARATH K(+) efflux antiporter 2, chloroplastic OS=Arabidopsis thaliana GN=KEA2 PE=1 SV=2	2	-0,254	0,475524476	1104,17	0,608
Q9M8Z5 NSN1_ARATH Guanine nucleotide-binding protein-like NSN1 OS=Arabidopsis thaliana GN=NSN1 PE=1 SV=1	1	-0,224	0,47952048	1113,45	0,608
F4IG73-2 BCHC2_ARATH Isoform 2 of BEACH domain-containing protein C2 OS=Arabidopsis thaliana GN=BCHC2	2	0,209	0,477522478	1108,81	0,608
Q8VYF5 NILP1_ARATH N-carbamoylputrescine amidase OS=Arabidopsis thaliana GN=CPA PE=1 SV=1	3	-0,194	0,474525475	1101,85	0,608
Q84W89 RH37_ARATH DEAD-box ATP-dependent RNA helicase 37 OS=Arabidopsis thaliana GN=RH37 PE=2 SV=2	4	0,179	0,476523477	1106,49	0,608
Q9SF53 RL351_ARATH 60S ribosomal protein L35-1 OS=Arabidopsis thaliana GN=RPL35A PE=2 SV=1	3	0,163	0,476523477	1106,49	0,608
O49203 NDK3_ARATH Nucleoside diphosphate kinase III, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=NDPK3 PE=1 SV=1	4	0,142	0,474525475	1101,85	0,608
Q8LPJ5 ICDHP_ARATH Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At5g14590 PE=1 SV=1	4	0,142	0,474525475	1101,85	0,608
Q05758 ILV5_ARATH Ketol-acid reductoisomerase, chloroplastic OS=Arabidopsis thaliana GN=At3g58610 PE=1 SV=2	11	0,117	0,473526474	1099,53	0,608
Q9XEE2 ANXD2_ARATH Annexin D2 OS=Arabidopsis thaliana GN=ANN2 PE=1 SV=1	11	0,117	0,478521479	1111,13	0,608
Q39161 NIR_ARATH Ferredoxin--nitrite reductase, chloroplastic OS=Arabidopsis thaliana GN=NIR1 PE=1 SV=1	15	0,108	0,477522478	1108,81	0,608
Q9FFF6 DIOX5_ARATH Probable 2-oxoglutarate-dependent dioxygenase At5g05600 OS=Arabidopsis thaliana GN=At5g05600 PE=2 SV=1	1	-0,439	0,47952048	1113,45	0,609
Q9FE78 IF2A_ARATH Eukaryotic translation initiation factor 2 subunit alpha OS=Arabidopsis thaliana GN=EIF2A PE=1 SV=1	1	-0,341	0,478521479	1111,13	0,609
Q9M081 SC24B_ARATH Protein transport protein Sec24-like At4g32640 OS=Arabidopsis thaliana GN=At4g32640 PE=3 SV=3	1	0,291	0,476523477	1106,49	0,609
O04147 CPD_ARATH Cyclic phosphodiesterase OS=Arabidopsis thaliana GN=At4g18930 PE=1 SV=1	2	0,257	0,476523477	1106,49	0,609
P10796 RBS1B_ARATH Ribulose bisphosphate carboxylase small chain 1B, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1B PE=1 SV=1	2	-0,233	0,478521479	1111,13	0,609
Q9SHP0 SERB2_ARATH Phosphoserine aminotransferase 2, chloroplastic OS=Arabidopsis thaliana GN=PSAT2 PE=1 SV=1	2	-0,227	0,47952048	1113,45	0,609
A0A1I9LMR3 A0A1I9LMR3_ARATH reversed Plastidic type i signal peptidase 1 OS=Arabidopsis thaliana GN=PLSP1 PE=4 SV=1	1	0,22	0,483516484	1122,73	0,609
Q9M5K3 DLDH1_ARATH Dihydrolipoyl dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana GN=LPD1 PE=1 SV=2	4	0,195	0,480519481	1115,77	0,609
Q42577 NDUS7_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Arabidopsis thaliana GN=At5g11770 PE=1 SV=1	3	-0,185	0,480519481	1115,77	0,609
Q9C891 DIR20_ARATH Dirigent protein 20 OS=Arabidopsis thaliana GN=DIR20 PE=2 SV=1	2	0,169	0,477522478	1108,81	0,609
Q9S7B5 THRC1_ARATH Threonine synthase 1, chloroplastic OS=Arabidopsis thaliana GN=TS1 PE=1 SV=1	6	-0,14	0,474525475	1101,85	0,609
Q9SRG3 PDI12_ARATH Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1	5	-0,14	0,484515485	1125,04	0,609

O80574 DAPB1_ARATH 4-hydroxy-tetrahydrodipicolinate reductase 1, chloroplastic OS=Arabidopsis thaliana GN=DAPB1 PE=1 SV=2	1	-0,309	0,485514486	1127,36	0,61
Q8RWM6 P24D5_ARATH Transmembrane emp24 domain-containing protein p24delta5 OS=Arabidopsis thaliana GN=At1g21900 PE=1 SV=1	1	0,293	0,483516484	1122,73	0,61
Q9FY71 EXOL4_ARATH Protein EXORDIUM-like 4 OS=Arabidopsis thaliana GN=EXL4 PE=2 SV=1	1	0,286	0,488511489	1134,32	0,61
Q93WL3 CLPT1_ARATH ATP-dependent Clp protease ATP-binding subunit CLPT1, chloroplastic OS=Arabidopsis thaliana GN=CLPT1 PE=1 SV=1	1	-0,276	0,482517483	1120,41	0,61
F4IL68 F4IL68_ARATH reversed SH3 domain-containing protein OS=Arabidopsis thaliana GN=At2g07360 PE=1 SV=1	1	-0,274	0,481518482	1118,09	0,61
Q9LHK4 AB8B_ARATH Putative ABC transporter B family member 8 OS=Arabidopsis thaliana GN=ABCB8 PE=5 SV=1	1	-0,27	0,483516484	1122,73	0,61
O23247 SYRM_ARATH Arginine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=EMB1027 PE=1 SV=1	1	-0,25	0,488511489	1134,32	0,61
Q9SCM3 RS24_ARATH 40S ribosomal protein S2-4 OS=Arabidopsis thaliana GN=RPS2D PE=2 SV=1	2	0,242	0,484515485	1125,04	0,61
Q93V13 RL171_ARATH 60S ribosomal protein L17-1 OS=Arabidopsis thaliana GN=RPL17A PE=2 SV=1	1	0,241	0,483516484	1122,73	0,61
Q9CA90 HPR2_ARATH Glyoxylate/hydroxypyruvate reductase A HPR2 OS=Arabidopsis thaliana GN=HPR2 PE=1 SV=1	2	0,206	0,48951049	1136,64	0,61
O80929 RL361_ARATH 60S ribosomal protein L36-1 OS=Arabidopsis thaliana GN=RPL36A PE=3 SV=1	2	0,191	0,490509491	1138,96	0,61
O23247 SYRM_ARATH Arginine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=EMB1027 PE=1 SV=1	4	-0,174	0,482517483	1120,41	0,61
O04130 SERA2_ARATH D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2	2	0,17	0,484515485	1125,04	0,61
Q9M266 Q9M266_ARATH S-adenosyl-L-methionine-dependent methyltransferases superfamily protein OS=Arabidopsis thaliana GN=F21F14.160 PE=2 S	4	-0,167	0,48951049	1136,64	0,61
Q56WN1 GLN11_ARATH Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2	4	-0,152	0,487512488	1132	0,61
Q94A52 RH2_ARATH Eukaryotic initiation factor 4A-III homolog OS=Arabidopsis thaliana GN=EIF4A3 PE=1 SV=2	6	-0,146	0,486513487	1129,68	0,61
Q9FM97 Q9FM97_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=MCD7.8 PE=2 SV=1	5	-0,136	0,485514486	1127,36	0,61
Q38799 ODPB1_ARATH Pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial OS=Arabidopsis thaliana GN=PDH2 PE=1 SV=2	8	-0,122	0,487512488	1132	0,61
Q9LXG1 RS91_ARATH 40S ribosomal protein S9-1 OS=Arabidopsis thaliana GN=RPS9B PE=1 SV=1	9	0,107	0,488511489	1134,32	0,61
Q05431 APX1_ARATH L-ascorbate peroxidase 1, cytosolic OS=Arabidopsis thaliana GN=APX1 PE=1 SV=2	13	0,101	0,485514486	1127,36	0,61
P92558 NU1M_ARATH NADH-ubiquinone oxidoreductase chain 1 OS=Arabidopsis thaliana GN=ND1 PE=1 SV=4	1	0,435	0,491508492	1141,28	0,611
Q9LVU1 VAP21_ARATH Vesicle-associated protein 2-1 OS=Arabidopsis thaliana GN=PVA21 PE=1 SV=1	1	0,406	0,491508492	1141,28	0,611
Q8LF28 Q8LF28_ARATH Anthranilate N-hydroxycinnamoyl/benzoyltransferase, putative OS=Arabidopsis thaliana GN=At1g28680 PE=2 SV=1	2	0,262	0,483516484	1122,73	0,611
Q9SL48 SLY1_ARATH SEC1 family transport protein SLY1 OS=Arabidopsis thaliana GN=SLY1 PE=1 SV=1	2	0,243	0,488511489	1134,32	0,611
Q6ICZ8 NACA3_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 3 OS=Arabidopsis thaliana GN=At5g13850 PE=1 SV=1	2	-0,205	0,483516484	1122,73	0,611
F4J9K9 F4J9K9_ARATH Neurofilament protein-like protein OS=Arabidopsis thaliana GN=At3g05900 PE=1 SV=1	3	-0,204	0,487512488	1132	0,611
Q93Y31 ARL8B_ARATH ADP-ribosylation factor-like protein 8b OS=Arabidopsis thaliana GN=ARL8B PE=2 SV=1	3	-0,19	0,487512488	1132	0,611
Q9FIJ2 NDUA2_ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Arabidopsis thaliana GN=At5g47890 PE=3 SV=1	2	0,189	0,491508492	1141,28	0,611
Q945Q1 CYT1_ARATH Cysteine proteinase inhibitor 1 OS=Arabidopsis thaliana GN=CYS1 PE=1 SV=2	2	0,187	0,490509491	1138,96	0,611
Q9SAB3 RB45B_ARATH Polyadenylate-binding protein RBP45B OS=Arabidopsis thaliana GN=RBP45B PE=1 SV=1	4	-0,181	0,482517483	1120,41	0,611
Q9FZK4 NTF2A_ARATH Nuclear transport factor 2A OS=Arabidopsis thaliana GN=NTF2A PE=1 SV=1	3	0,175	0,492507493	1143,6	0,611
Q9LPG6 RHM2_ARATH Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RH	4	0,172	0,487512488	1132	0,611
Q42472 DCE2_ARATH Glutamate decarboxylase 2 OS=Arabidopsis thaliana GN=GAD2 PE=1 SV=1	3	-0,151	0,488511489	1134,32	0,611
P59230 R10A2_ARATH 60S ribosomal protein L10a-2 OS=Arabidopsis thaliana GN=RPL10AB PE=1 SV=1	4	0,148	0,486513487	1129,68	0,611
Q9SRZ6 ICDHC_ARATH Cytosolic isocitrate dehydrogenase [NADP] OS=Arabidopsis thaliana GN=CICDH PE=2 SV=1	19	0,098	0,490509491	1138,96	0,611
Q94A24 CML13_ARATH Probable calcium-binding protein CML13 OS=Arabidopsis thaliana GN=CML13 PE=2 SV=1	3	0,161	0,492507493	1143,6	0,612
Q9FMV1 GCAL1_ARATH Gamma carbonic anhydrase-like 1, mitochondrial OS=Arabidopsis thaliana GN=GAMMACAL1 PE=1 SV=1	6	-0,142	0,494505495	1148,24	0,613
P35131 UBC8_ARATH Ubiquitin-conjugating enzyme E2 8 OS=Arabidopsis thaliana GN=UBC8 PE=1 SV=1	1	0,296	0,497502498	1155,2	0,614
Q8H0Y9 Q8H0Y9_ARATH Acyl-CoA N-acyltransferases (NAT) superfamily protein OS=Arabidopsis thaliana GN=At1g21770 PE=2 SV=1	1	-0,283	0,495504496	1150,56	0,614
F4K7W6 F4K7W6_ARATH Retinal-binding protein OS=Arabidopsis thaliana GN=TOPTELOMER.1 PE=1 SV=1	4	-0,231	0,497502498	1155,2	0,614
F4JL11 IMPA2_ARATH Importin subunit alpha-2 OS=Arabidopsis thaliana GN=IMPA2 PE=1 SV=1	2	-0,2	0,495504496	1150,56	0,614
P59232 R27AB_ARATH Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=2 SV=2	7	-0,142	0,496503497	1152,88	0,614
Q93WJ8 MDAR2_ARATH Monodehydroascorbate reductase 2 OS=Arabidopsis thaliana GN=MDAR2 PE=1 SV=1	18	-0,104	0,495504496	1150,56	0,614
Q84LM4 AARE_ARATH Acylamino-acid-releasing enzyme OS=Arabidopsis thaliana GN=AARE PE=1 SV=1	1	0,419	0,497502498	1155,2	0,615
Q9SJH7 CISY3_ARATH Citrate synthase 3, peroxisomal OS=Arabidopsis thaliana GN=CSY3 PE=2 SV=1	1	0,379	0,498501499	1157,52	0,615
Q9FI97 U76C5_ARATH UDP-glycosyltransferase 76C5 OS=Arabidopsis thaliana GN=UGT76C5 PE=2 SV=1	1	-0,361	0,4995005	1159,84	0,615
Q9SUP0 CSPLQ_ARATH CASP-like protein 1B2 OS=Arabidopsis thaliana GN=At4g20390 PE=2 SV=1	1	-0,305	0,498501499	1157,52	0,615
Q9FFS8 RS102_ARATH 40S ribosomal protein S10-2 OS=Arabidopsis thaliana GN=RPS10B PE=2 SV=1	1	0,291	0,4995005	1159,84	0,615
P23686 METK1_ARATH S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2	2	0,2	0,4995005	1159,84	0,615
Q9SGE0 AXS2_ARATH UDP-D-apiiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1	5	-0,144	0,496503497	1152,88	0,615
O04487 EF1G1_ARATH Probable elongation factor 1-gamma 1 OS=Arabidopsis thaliana GN=At1g09640 PE=1 SV=1	5	-0,136	0,497502498	1155,2	0,615

Q9ZVJ6 ANXD4_ARATH Annexin D4 OS=Arabidopsis thaliana GN=ANN4 PE=1 SV=1	1	-0,39	0,501498501	1164,48	0,616
Q9ZVA5 EP1L4_ARATH EP1-like glycoprotein 4 OS=Arabidopsis thaliana GN=At1g78860 PE=3 SV=1	1	0,264	0,5004995	1162,16	0,616
Q9FLW9 PKP2_ARATH Plastidial pyruvate kinase 2 OS=Arabidopsis thaliana GN=PKP2 PE=1 SV=1	4	0,17	0,4995005	1159,84	0,616
Q8LD46 R23A1_ARATH 60S ribosomal protein L23a-1 OS=Arabidopsis thaliana GN=RPL23AA PE=2 SV=2	4	0,142	0,501498501	1164,48	0,616
Q9M060 IF62_ARATH Eukaryotic translation initiation factor 6-2 OS=Arabidopsis thaliana GN=EIF6-2 PE=2 SV=1	2	-0,188	0,503496503	1169,12	0,617
O04331 PHB3_ARATH Prohibitin-3, mitochondrial OS=Arabidopsis thaliana GN=PHB3 PE=1 SV=1	6	-0,145	0,502497502	1166,8	0,617
Q42592 APXS_ARATH L-ascorbate peroxidase 5, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=APXS PE=1 SV=2	6	0,125	0,502497502	1166,8	0,617
F4JY11 F4JY11_ARATH Lung seven transmembrane receptor family protein OS=Arabidopsis thaliana GN=Cand7 PE=4 SV=1	1	0,383	0,503496503	1169,12	0,618
Q9LD43 ACCA_ARATH Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=CAC3 PE=1 SV=1	7	0,127	0,505494505	1173,76	0,618
F4J9A0 F4J9A0_ARATH Nodulin/glutamine synthase-like protein OS=Arabidopsis thaliana GN=NodGS PE=1 SV=1	10	-0,121	0,504495504	1171,44	0,618
Q94F62 BAK1_ARATH BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 OS=Arabidopsis thaliana GN=BAK1 PE=1 SV=2	2	-0,295	0,505494505	1173,76	0,619
O23710 PSB7A_ARATH Proteasome subunit beta type-7-A OS=Arabidopsis thaliana GN=PBB1 PE=1 SV=2	2	-0,238	0,506493506	1176,08	0,619
Q9SMV6 XPO1A_ARATH Protein EXPORTIN 1A OS=Arabidopsis thaliana GN=XPO1 PE=1 SV=1	3	0,195	0,506493506	1176,08	0,619
Q9XFM6 MSBP1_ARATH Membrane steroid-binding protein 1 OS=Arabidopsis thaliana GN=MSBP1 PE=1 SV=2	2	-0,191	0,506493506	1176,08	0,619
Q93VP3 IF5A2_ARATH Eukaryotic translation initiation factor 5A-2 OS=Arabidopsis thaliana GN=ELF5A-2 PE=1 SV=1	2	0,177	0,505494505	1173,76	0,619
Q9TOA0 LACS4_ARATH Long chain acyl-CoA synthetase 4 OS=Arabidopsis thaliana GN=LACS4 PE=2 SV=1	5	-0,152	0,507492507	1178,4	0,619
Q9LK57 PP226_ARATH Pentatricopeptide repeat-containing protein At3g13160, mitochondrial OS=Arabidopsis thaliana GN=At3g13160 PE=1 SV=1	1	0,282	0,509490509	1183,04	0,62
Q9ZWT2 CYB5D_ARATH Cytochrome B5 isoform D OS=Arabidopsis thaliana GN=CYTB5-D PE=1 SV=1	2	0,204	0,509490509	1183,04	0,62
Q9SR13 FLK_ARATH Flowering locus K homology domain OS=Arabidopsis thaliana GN=FLK PE=1 SV=1	2	-0,199	0,513486513	1192,32	0,62
F4IXW2 BIG5_ARATH Brefeldin A-inhibited guanine nucleotide-exchange protein 5 OS=Arabidopsis thaliana GN=BIG5 PE=1 SV=2	5	-0,146	0,507492507	1178,4	0,62
F4K5B9 F4K5B9_ARATH Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=MOJ9.20 PE=3 SV=1	12	-0,102	0,508491508	1180,72	0,62
P54609 CD48A_ARATH Cell division control protein 48 homolog A OS=Arabidopsis thaliana GN=CD48A PE=1 SV=1	27	0,088	0,508491508	1180,72	0,62
F4J6I6 F4J6I6_ARATH Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Arabidopsis thaliana GN=COQ6 PE=3 SV=1	1	0,392	0,511488511	1187,68	0,621
Q8VZV6 Q8VZV6_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g19290 PE=2 SV=1	1	-0,282	0,513486513	1192,32	0,621
P54150 MSRA4_ARATH Peptide methionine sulfoxide reductase A4, chloroplastic OS=Arabidopsis thaliana GN=MSRA4 PE=1 SV=2	1	-0,275	0,514485514	1194,64	0,621
O49203 NDK3_ARATH reversed Nucleoside diphosphate kinase III, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=NDPK3 PE=1 SV=1	1	0,261	0,513486513	1192,32	0,621
O04350 TBCA_ARATH Tubulin-folding cofactor A OS=Arabidopsis thaliana GN=TFCA PE=1 SV=2	2	-0,237	0,513486513	1192,32	0,621
Q9SIP1 UP3_ARATH Stress-response A/B barrel domain-containing protein UP3 OS=Arabidopsis thaliana GN=UP3 PE=1 SV=1	2	-0,187	0,51048951	1185,36	0,621
F4HXZ1 BRO1_ARATH Vacuolar-sorting protein BRO1 OS=Arabidopsis thaliana GN=BRO1 PE=1 SV=1	3	-0,166	0,512487512	1190	0,621
Q84L30 RD23D_ARATH Ubiquitin receptor RAD23d OS=Arabidopsis thaliana GN=RAD23D PE=1 SV=2	2	-0,16	0,511488511	1187,68	0,621
Q9SRI1 SC13A_ARATH Protein transport protein SEC13 homolog A OS=Arabidopsis thaliana GN=SEC13A PE=1 SV=1	4	-0,154	0,509490509	1183,04	0,621
Q9M084 SYDC2_ARATH Aspartate--tRNA ligase 2, cytoplasmic OS=Arabidopsis thaliana GN=IBI1 PE=1 SV=1	8	0,125	0,51048951	1185,36	0,621
Q9SRT9 RGP1_ARATH UDP-arabinopyranose mutase 1 OS=Arabidopsis thaliana GN=RGP1 PE=1 SV=1	7	0,122	0,514485514	1194,64	0,621
F4HQD4 HSP7P_ARATH Heat shock 70 kDa protein 15 OS=Arabidopsis thaliana GN=HSP70-15 PE=1 SV=1	18	0,106	0,515484515	1196,96	0,621
Q9LHK1 NUD16_ARATH Nudix hydrolase 16, mitochondrial OS=Arabidopsis thaliana GN=NUDT16 PE=2 SV=1	1	0,382	0,516483516	1199,27	0,622
Q8LGC6 NACA5_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 5 OS=Arabidopsis thaliana GN=At1g33040 PE=2 SV=2	1	-0,283	0,515484515	1196,96	0,622
Q9MAH3 DJ1B_ARATH Protein DJ-1 homolog B OS=Arabidopsis thaliana GN=DJ1B PE=1 SV=1	2	-0,209	0,512487512	1190	0,622
Q9SIU8 P2C20_ARATH Probable protein phosphatase 2C 20 OS=Arabidopsis thaliana GN=PPC3-1.2 PE=1 SV=3	2	-0,178	0,513486513	1192,32	0,622
P51424 RL391_ARATH 60S ribosomal protein L39-1 OS=Arabidopsis thaliana GN=RPL39A PE=3 SV=2	2	0,176	0,513486513	1192,32	0,622
F4I7X1 F4I7X1_ARATH SKU5-similar 6 OS=Arabidopsis thaliana GN=SKS6 PE=4 SV=1	4	0,152	0,516483516	1199,27	0,622
Q9LVT8 RGGC_ARATH RGG repeats nuclear RNA binding protein C OS=Arabidopsis thaliana GN=RGGC PE=1 SV=1	7	0,118	0,512487512	1190	0,622
Q42290 MPPB_ARATH Probable mitochondrial-processing peptidase subunit beta, mitochondrial OS=Arabidopsis thaliana GN=At3g02090 PE=1 SV=2	17	-0,096	0,513486513	1192,32	0,622
O22792 O22792_ARATH Uncharacterized protein At2g33420 OS=Arabidopsis thaliana GN=At2g33420 PE=4 SV=1	1	-0,271	0,517482517	1201,59	0,623
Q94EH2 TI222_ARATH Mitochondrial import inner membrane translocase subunit TIM22-2 OS=Arabidopsis thaliana GN=TIM22-2 PE=1 SV=1	1	-0,375	0,519480519	1206,23	0,624
P57691 RLA03_ARATH 60S acidic ribosomal protein P0-3 OS=Arabidopsis thaliana GN=RPP0C PE=1 SV=1	1	0,265	0,521478521	1210,87	0,624
Q9FG38 SNX1_ARATH Sorting nexin 1 OS=Arabidopsis thaliana GN=SNX1 PE=1 SV=1	1	0,261	0,518481518	1203,91	0,624
Q93YZ7 ILVH2_ARATH Acetolactate synthase small subunit 2, chloroplastic OS=Arabidopsis thaliana GN=At2g31810 PE=1 SV=1	3	-0,214	0,522477522	1213,19	0,624
P49077 PYRB_ARATH Aspartate carbamoyltransferase, chloroplastic OS=Arabidopsis thaliana GN=PYRB PE=2 SV=2	5	-0,144	0,521478521	1210,87	0,624
Q8LG77 IDH6_ARATH Isocitrate dehydrogenase [NAD] catalytic subunit 6, mitochondrial OS=Arabidopsis thaliana GN=IDH6 PE=1 SV=2	4	-0,142	0,52047952	1208,55	0,624
Q949W8 Q949W8_ARATH Putative xylulose kinase OS=Arabidopsis thaliana GN=XK-2 PE=2 SV=1	4	-0,142	0,521478521	1210,87	0,624
Q9XI93 Q9XI93_ARATH At1g13930/F16A14.27 OS=Arabidopsis thaliana GN=F7A19.2 PE=1 SV=1	4	-0,13	0,52047952	1208,55	0,624

Q9LTT8 VCS_ARATH Enhancer of mRNA-decapping protein 4 OS=Arabidopsis thaliana GN=VCS PE=1 SV=1	7	0,124	0,52047952	1208,55	0,624
Q42599 NDS8A_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial OS=Arabidopsis thaliana GN=At1g79010 PE=1 SV=1	1	-0,278	0,522477522	1213,19	0,625
Q67252 TBCB_ARATH Tubulin-folding cofactor B OS=Arabidopsis thaliana GN=TFCB PE=1 SV=1	1	-0,26	0,524475524	1217,83	0,625
Q95VC2 SY122_ARATH Syntaxin-122 OS=Arabidopsis thaliana GN=SYP122 PE=1 SV=1	2	0,238	0,519480519	1206,23	0,625
Q38896 CSP4_ARATH Cold shock domain-containing protein 4 OS=Arabidopsis thaliana GN=CSP4 PE=1 SV=1	1	-0,223	0,52047952	1208,55	0,625
Q9FGX1 ACLB2_ARATH ATP-citrate synthase beta chain protein 2 OS=Arabidopsis thaliana GN=ACLB-2 PE=1 SV=1	2	0,211	0,52047952	1208,55	0,625
Q9XQC7 Q9XQC7_ARATH GrpE protein homolog OS=Arabidopsis thaliana GN=grpE PE=2 SV=1	2	0,189	0,52047952	1208,55	0,625
Q9SFU0 SC24A_ARATH Protein transport protein Sec24-like At3g07100 OS=Arabidopsis thaliana GN=At3g07100 PE=2 SV=2	4	-0,159	0,523476523	1215,51	0,625
P49206 RS261_ARATH 40S ribosomal protein S26-1 OS=Arabidopsis thaliana GN=RPS26A PE=2 SV=2	1	-0,27	0,524475524	1217,83	0,626
Q9LUD4 R18A3_ARATH 60S ribosomal protein L18a-3 OS=Arabidopsis thaliana GN=RPL18AC PE=2 SV=1	1	0,247	0,524475524	1217,83	0,626
Q9S7Z3 PCS1_ARATH Glutathione gamma-glutamylcysteinyltransferase 1 OS=Arabidopsis thaliana GN=PCS1 PE=1 SV=1	1	-0,243	0,527472527	1224,79	0,626
Q9FMV1 GCAL1_ARATH Gamma carbonic anhydrase-like 1, mitochondrial OS=Arabidopsis thaliana GN=GAMMACAL1 PE=1 SV=1	1	-0,211	0,526473526	1222,47	0,626
Q42560 ACO1_ARATH Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2	1	0,164	0,525474525	1220,15	0,626
Q9S2I2 NAP1A_ARATH Nucleosome assembly protein 1;1 OS=Arabidopsis thaliana GN=NAP1;1 PE=1 SV=1	5	0,145	0,527472527	1224,79	0,626
Q94AU7 GCA3_ARATH Gamma carbonic anhydrase 3, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA3 PE=1 SV=1	5	0,134	0,525474525	1220,15	0,626
F416B2 F416B2_ARATH SIT4 phosphatase-associated family protein OS=Arabidopsis thaliana GN=At1g30470 PE=1 SV=1	1	0,261	0,526473526	1222,47	0,627
O23267 O23267_ARATH AT4g14060/dl3070w OS=Arabidopsis thaliana GN=dl3070w PE=2 SV=1	1	0,246	0,526473526	1222,47	0,627
Q1H595 LSM2_ARATH Sm-like protein LSM2 OS=Arabidopsis thaliana GN=LSM2 PE=1 SV=1	2	-0,2	0,527472527	1224,79	0,627
F41893 ILA_ARATH Protein ILITYHIA OS=Arabidopsis thaliana GN=ILA PE=1 SV=1	4	-0,164	0,528471528	1227,11	0,627
Q8H0V3 LGUL_ARATH Lactoylgutathione lyase OS=Arabidopsis thaliana GN=At1g08110 PE=2 SV=1	3	-0,157	0,527472527	1224,79	0,627
Q84L30 RD23D_ARATH Ubiquitin receptor RAD23d OS=Arabidopsis thaliana GN=RAD23D PE=1 SV=2	1	-0,279	0,53046953	1231,75	0,628
Q9SU13 FLA2_ARATH Fasciclin-like arabinogalactan protein 2 OS=Arabidopsis thaliana GN=FLA2 PE=1 SV=1	1	0,364	0,53046953	1231,75	0,629
P29513 TBB5_ARATH Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1	2	-0,232	0,53046953	1231,75	0,629
Q8LAC4 URH2_ARATH Probable uridine nucleosidase 2 OS=Arabidopsis thaliana GN=URH2 PE=2 SV=1	2	-0,177	0,532467532	1236,39	0,629
A0A1P8B8B4 A0A1P8B8B4_ARATH TolB protein-like protein OS=Arabidopsis thaliana GN=At4g01870 PE=4 SV=1	5	-0,141	0,531468531	1234,07	0,629
O04151 CALR1_ARATH Calreticulin-1 OS=Arabidopsis thaliana GN=CRT1 PE=1 SV=1	6	0,118	0,531468531	1234,07	0,629
Q9FL13 Q9FL13_ARATH At5g40190 OS=Arabidopsis thaliana GN=MSN9.9 PE=2 SV=1	1	0,293	0,533466533	1238,71	0,63
Q94K73 SYFM_ARATH Phenylalanine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At3g58140 PE=1 SV=1	2	0,219	0,533466533	1238,71	0,63
Q9SHJ8 HIBC8_ARATH 3-hydroxyisobutryl-CoA hydrolase-like protein 5 OS=Arabidopsis thaliana GN=At1g06550 PE=1 SV=2	4	-0,15	0,532467532	1236,39	0,63
O48773 PDI23_ARATH Protein disulfide-isomerase 2-3 OS=Arabidopsis thaliana GN=PDIL2-3 PE=2 SV=1	5	0,146	0,532467532	1236,39	0,63
P42643 14331_ARATH 14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	0,249	0,535464535	1243,35	0,631
Q9FKC0 R13A4_ARATH 60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1	2	0,187	0,536463536	1245,67	0,631
Q9MBH2 AIG2B_ARATH Protein AIG2 B OS=Arabidopsis thaliana GN=AIG2B PE=2 SV=1	3	0,155	0,535464535	1243,35	0,631
Q9M5K2 DLDH2_ARATH Dihydrolipoyl dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=LPD2 PE=1 SV=1	6	0,123	0,534465534	1241,03	0,631
Q9FNE2 GRXC2_ARATH Glutaredoxin-C2 OS=Arabidopsis thaliana GN=GRXC2 PE=3 SV=1	1	-0,234	0,536463536	1245,67	0,632
Q38882 PLDA1_ARATH Phospholipase D alpha 1 OS=Arabidopsis thaliana GN=PLDALPHA1 PE=1 SV=2	5	0,134	0,537462537	1247,99	0,632
O49482 CADH5_ARATH Cinnamyl alcohol dehydrogenase 5 OS=Arabidopsis thaliana GN=CAD5 PE=1 SV=1	6	-0,119	0,536463536	1245,67	0,632
Q9SCV3 BGAL9_ARATH Beta-galactosidase 9 OS=Arabidopsis thaliana GN=BGAL9 PE=2 SV=1	1	0,28	0,54045954	1254,95	0,633
Q8VYG9 PIRL9_ARATH Plant intracellular Ras-group-related LRR protein 9 OS=Arabidopsis thaliana GN=PIRL9 PE=2 SV=1	2	-0,212	0,543456543	1261,91	0,633
Q9S7D8 APS4_ARATH ATP sulfurylase 4, chloroplastic OS=Arabidopsis thaliana GN=APS4 PE=2 SV=1	2	0,2	0,539460539	1252,63	0,633
Q9M9W1 RL222_ARATH 60S ribosomal protein L22-2 OS=Arabidopsis thaliana GN=RPL22B PE=2 SV=1	2	0,172	0,538461538	1250,31	0,633
Q8GYL5 RS253_ARATH 40S ribosomal protein S25-3 OS=Arabidopsis thaliana GN=RPS25D PE=3 SV=2	3	0,144	0,539460539	1252,63	0,633
P42759 ERD10_ARATH Dehydrin ERD10 OS=Arabidopsis thaliana GN=ERD10 PE=1 SV=1	5	-0,125	0,54045954	1254,95	0,633
P21238 CPNA1_ARATH Chaperonin 60 subunit alpha 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60A1 PE=1 SV=2	21	-0,094	0,538461538	1250,31	0,633
Q9ZPH2 GRS17_ARATH Monothiol glutaredoxin-S17 OS=Arabidopsis thaliana GN=GRXS17 PE=1 SV=1	1	0,348	0,544455544	1264,23	0,634
Q84P21 4CLL5_ARATH 4-coumarate--CoA ligase-like 5 OS=Arabidopsis thaliana GN=4CLL5 PE=1 SV=2	1	-0,272	0,543456543	1261,91	0,634
O65719 HSP7C_ARATH Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	1	0,216	0,543456543	1261,91	0,634
Q8RWG8 RBP1B_ARATH Ran-binding protein 1 homolog b OS=Arabidopsis thaliana GN=RANBP1B PE=1 SV=2	2	0,189	0,542457542	1259,59	0,634
Q9SIQ9 ALFC6_ARATH Fructose-bisphosphate aldolase 6, cytosolic OS=Arabidopsis thaliana GN=FBA6 PE=1 SV=1	7	-0,115	0,539460539	1252,63	0,634
Q9SYP2 PFP1_ARATH Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 1 OS=Arabidopsis thaliana GN=PFP-ALPHA1 PE=2 SV=	7	0,114	0,543456543	1261,91	0,634
Q38882 PLDA1_ARATH Phospholipase D alpha 1 OS=Arabidopsis thaliana GN=PLDALPHA1 PE=1 SV=2	17	-0,098	0,54045954	1254,95	0,634

O22813 O22813_ARATH At2g33630/F4P9.40 OS=Arabidopsis thaliana GN=At2g33630 PE=2 SV=1	1	-0,253	0,545454545	1266,55	0,635
Q9SK74 C3H21_ARATH Zinc finger CCCH domain-containing protein 21 OS=Arabidopsis thaliana GN=At2g20280 PE=4 SV=1	1	-0,249	0,543456543	1261,91	0,635
Q9M314 Q9M314_ARATH AT3g61540/F2A19_140 OS=Arabidopsis thaliana GN=F2A19.140 PE=1 SV=1	3	-0,186	0,542457542	1259,59	0,635
Q9SK22 RS161_ARATH 40S ribosomal protein S16-1 OS=Arabidopsis thaliana GN=RPS16A PE=2 SV=1	5	0,123	0,542457542	1259,59	0,635
P46309 GSH1_ARATH Glutamate--cysteine ligase, chloroplastic OS=Arabidopsis thaliana GN=GSH1 PE=1 SV=2	9	-0,114	0,543456543	1261,91	0,635
Q9SF16 TCPH_ARATH T-complex protein 1 subunit eta OS=Arabidopsis thaliana GN=CCT7 PE=1 SV=1	17	0,091	0,542457542	1259,59	0,635
Q9SJM9 Q9SJM9_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g36290 PE=4 SV=1	2	-0,185	0,546453546	1268,87	0,636
Q9SA34 IMDH2_ARATH Inosine-5'-monophosphate dehydrogenase 2 OS=Arabidopsis thaliana GN=At1g16350 PE=1 SV=1	4	-0,141	0,547452547	1271,18	0,636
Q9LX65 VATH_ARATH V-type proton ATPase subunit H OS=Arabidopsis thaliana GN=VHA-H PE=1 SV=1	7	-0,119	0,546453546	1268,87	0,636
P34066 PSA1A_ARATH Proteasome subunit alpha type-1-A OS=Arabidopsis thaliana GN=PAF1 PE=1 SV=3	8	-0,119	0,547452547	1271,18	0,636
Q9CAF2 NUD26_ARATH Nudix hydrolase 26, chloroplastic OS=Arabidopsis thaliana GN=NUDT26 PE=1 SV=1	1	-0,378	0,55044955	1278,14	0,637
P29513 TBB5_ARATH Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1	1	-0,239	0,551448551	1280,46	0,637
Q9S7C0 HSP70_ARATH Heat shock 70 kDa protein 14 OS=Arabidopsis thaliana GN=HSP70-14 PE=1 SV=1	1	0,215	0,551448551	1280,46	0,637
Q9FMR5 VA714_ARATH Vesicle-associated membrane protein 714 OS=Arabidopsis thaliana GN=VAMP714 PE=1 SV=1	2	0,211	0,55044955	1278,14	0,637
Q9M8R9 RRAA1_ARATH Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 1 OS=Arabidopsis thaliana GN=At3g02770 PE=2 SV=1	2	-0,196	0,547452547	1271,18	0,637
Q9LMC9 GLT2_ARATH Germin-like protein subfamily T member 2 OS=Arabidopsis thaliana GN=At1g18980 PE=2 SV=1	4	-0,128	0,552447552	1282,78	0,637
Q8GUL2 MOS14_ARATH Transportin MOS14 OS=Arabidopsis thaliana GN=MOS14 PE=1 SV=1	1	0,354	0,55044955	1278,14	0,638
P92557 RT07_ARATH Ribosomal protein S7, mitochondrial OS=Arabidopsis thaliana GN=RPS7 PE=2 SV=1	1	0,338	0,552447552	1282,78	0,638
F4I0I6 F4I0I6_ARATH BSD domain-containing protein OS=Arabidopsis thaliana GN=At1g69030 PE=1 SV=1	1	-0,236	0,549450549	1275,82	0,638
Q94AM1 OOPDA_ARATH Organellar oligopeptidase A, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OOP PE=1 SV=1	2	-0,194	0,55044955	1278,14	0,638
Q42344 HMGB4_ARATH High mobility group B protein 4 OS=Arabidopsis thaliana GN=HMGB4 PE=1 SV=1	2	0,174	0,55044955	1278,14	0,638
Q9C9K3 PFP2_ARATH Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2 OS=Arabidopsis thaliana GN=PFP-ALPHA2 PE=2 SV=	2	0,164	0,549450549	1275,82	0,638
Q8VZ19 RL302_ARATH 60S ribosomal protein L30-2 OS=Arabidopsis thaliana GN=RPL30B PE=3 SV=1	3	0,13	0,551448551	1280,46	0,638
P93032 IDH2_ARATH Isocitrate dehydrogenase [NAD] regulatory subunit 2, mitochondrial OS=Arabidopsis thaliana GN=IDH2 PE=1 SV=2	5	-0,129	0,552447552	1282,78	0,638
Q9FGI6 NDUS1_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial OS=Arabidopsis thaliana GN=EMB1467 PE=1 SV=2	11	-0,107	0,551448551	1280,46	0,638
Q9LM92 SMD3B_ARATH Small nuclear ribonucleoprotein SmD3b OS=Arabidopsis thaliana GN=SMD3B PE=2 SV=1	1	0,252	0,554445554	1287,42	0,639
Q8L8W6 RL392_ARATH 60S ribosomal protein L39-2 OS=Arabidopsis thaliana GN=RPL39B PE=3 SV=1	1	0,233	0,554445554	1287,42	0,639
Q39043 MD37F_ARATH Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2	2	0,179	0,555444555	1289,74	0,639
Q9LRA7 TPS9_ARATH Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 OS=Arabidopsis thaliana GN=TPS9 PE=2 SV=1	1	0,363	0,56043956	1301,34	0,64
F4HUK6 AAE1_ARATH Probable acyl-activating enzyme 1, peroxisomal OS=Arabidopsis thaliana GN=AAE1 PE=2 SV=1	1	0,271	0,556443556	1292,06	0,64
P41568 SUI11_ARATH Protein translation factor SUI1 homolog 1 OS=Arabidopsis thaliana GN=At4g27130 PE=1 SV=2	1	0,237	0,559440559	1299,02	0,64
A1L4Y4 A1L4Y4_ARATH At5g61510 OS=Arabidopsis thaliana GN=At5g61510 PE=2 SV=1	3	-0,209	0,56043956	1301,34	0,64
Q8VZ95 VAP11_ARATH Vesicle-associated protein 1-1 OS=Arabidopsis thaliana GN=PVA11 PE=1 SV=1	2	-0,174	0,555444555	1289,74	0,64
Q5XF75 EFTS_ARATH Elongation factor Ts, mitochondrial OS=Arabidopsis thaliana GN=EFTS PE=1 SV=1	1	0,344	0,561438561	1303,66	0,641
Q8RYE9 GPPL3_ARATH Haloacid dehalogenase-like hydrolase domain-containing protein At2g33255 OS=Arabidopsis thaliana GN=At2g33255 PE=1 SV=1	1	-0,249	0,562437562	1305,98	0,641
F4I3M3 F4I3M3_ARATH Kinase with tetratricopeptide repeat domain-containing protein OS=Arabidopsis thaliana GN=BSK7 PE=4 SV=1	1	0,24	0,558441558	1296,7	0,641
Q8H104 SYDC1_ARATH Aspartate--tRNA ligase 1, cytoplasmic OS=Arabidopsis thaliana GN=At4g26870 PE=2 SV=1	1	0,24	0,562437562	1305,98	0,641
Q9LHS5 Q9LHS5_ARATH Cell division related protein-like OS=Arabidopsis thaliana GN=At5g06110 PE=4 SV=1	1	0,235	0,564435564	1310,62	0,641
O22822 U74F2_ARATH UDP-glycosyltransferase 74F2 OS=Arabidopsis thaliana GN=UGT74F2 PE=1 SV=1	1	-0,227	0,561438561	1303,66	0,641
Q9LUT2 METK4_ARATH S-adenosylmethionine synthase 4 OS=Arabidopsis thaliana GN=METK4 PE=1 SV=1	1	0,209	0,558441558	1296,7	0,641
O65655 O65655_ARATH SAP domain-containing protein OS=Arabidopsis thaliana GN=At4g39680 PE=1 SV=1	1	-0,203	0,557442557	1294,38	0,641
Q9CA59 NRP1_ARATH NRP1-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=1 SV=1	1	0,191	0,559440559	1299,02	0,641
O23138 CYC1_ARATH Cytochrome c-1 OS=Arabidopsis thaliana GN=CYTC-1 PE=1 SV=1	2	-0,183	0,56043956	1301,34	0,641
O05000 NU2M_ARATH NADH-ubiquinone oxidoreductase chain 2 OS=Arabidopsis thaliana GN=ND2 PE=2 SV=2	1	0,182	0,563436563	1308,3	0,641
P82874 TO203_ARATH Mitochondrial import receptor subunit TOM20-3 OS=Arabidopsis thaliana GN=TOM20-3 PE=1 SV=1	2	-0,171	0,559440559	1299,02	0,641
O04313 JAL31_ARATH PYK10-binding protein 2 OS=Arabidopsis thaliana GN=PBP2 PE=1 SV=1	3	-0,144	0,562437562	1305,98	0,641
Q9LVA0 BAG7_ARATH BAG family molecular chaperone regulator 7 OS=Arabidopsis thaliana GN=BAG7 PE=1 SV=1	5	-0,137	0,56043956	1301,34	0,641
Q9ZWC4 Q9ZWC4_ARATH At1g04040/F21M11_2 OS=Arabidopsis thaliana GN=F21M11.2 PE=2 SV=1	2	0,137	0,562437562	1305,98	0,641
F4IC59 F4IC59_ARATH Aldolase superfamily protein OS=Arabidopsis thaliana GN=At1g12230 PE=4 SV=1	3	-0,135	0,558441558	1296,7	0,641
F4JFN3 HS906_ARATH Heat shock protein 90-6, mitochondrial OS=Arabidopsis thaliana GN=HSP90-6 PE=2 SV=1	7	0,109	0,557442557	1294,38	0,641
Q9SRV5 METE2_ARATH 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 OS=Arabidopsis thaliana GN=MS2 PE=1 SV=1	10	0,098	0,559440559	1299,02	0,641

Q9LYR4 Q9LYR4_ARATH Aldolase-type TIM barrel family protein OS=Arabidopsis thaliana GN=TRA2 PE=2 SV=1	14	0,094	0,559440559	1299,02	0,641
Q39211 NRPB3_ARATH DNA-directed RNA polymerases II, IV and V subunit 3 OS=Arabidopsis thaliana GN=NRPB3 PE=1 SV=1	1	-0,251	0,564435564	1310,62	0,642
Q9FHR8 DCI1_ARATH Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, peroxisomal OS=Arabidopsis thaliana GN=DCI1 PE=2 SV=1	1	-0,25	0,564435564	1310,62	0,642
Q9C5U8 HIS8_ARATH Histidinol dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=HISN8 PE=2 SV=1	2	-0,195	0,567432567	1317,58	0,642
Q8LPF1 PP387_ARATH Pentatricopeptide repeat-containing protein At5g15980, mitochondrial OS=Arabidopsis thaliana GN=At5g15980 PE=2 SV=1	2	0,194	0,566433566	1315,26	0,642
Q9LFJ8 U78D2_ARATH UDP-glycosyltransferase 78D2 OS=Arabidopsis thaliana GN=UGT78D2 PE=2 SV=1	2	-0,175	0,567432567	1317,58	0,642
Q9SJ81 FLA7_ARATH Fasciclin-like arabinogalactan protein 7 OS=Arabidopsis thaliana GN=FLA7 PE=1 SV=1	2	0,17	0,564435564	1310,62	0,642
Q9SF21 Q9SF21_ARATH At3g11770 OS=Arabidopsis thaliana GN=F26K24.6 PE=1 SV=1	3	-0,142	0,565434565	1312,94	0,642
P93736 SVVM1_ARATH Valine--tRNA ligase, mitochondrial 1 OS=Arabidopsis thaliana GN=TNW2 PE=1 SV=2	8	-0,106	0,566433566	1315,26	0,642
Q9C5M0 DTC_ARATH Mitochondrial dicarboxylate/tricarboxylate transporter DTC OS=Arabidopsis thaliana GN=DTC PE=1 SV=1	10	-0,097	0,565434565	1312,94	0,642
Q9LNU4 PSD3A_ARATH 26S proteasome non-ATPase regulatory subunit 3 homolog A OS=Arabidopsis thaliana GN=RPN3A PE=1 SV=3	11	-0,096	0,558441558	1296,7	0,642
F4JJ02 F4JJ02_ARATH RING/U-box superfamily protein OS=Arabidopsis thaliana GN=At4g33565 PE=4 SV=1	1	-0,355	0,567432567	1317,58	0,643
Q8RXK6 RH8_ARATH DEAD-box ATP-dependent RNA helicase 8 OS=Arabidopsis thaliana GN=RH8 PE=2 SV=1	1	-0,243	0,568431568	1319,9	0,643
Q84WU8 FTSH3_ARATH ATP-dependent zinc metalloprotease FTSH 3, mitochondrial OS=Arabidopsis thaliana GN=FTSH3 PE=1 SV=1	1	-0,235	0,571428571	1326,86	0,643
A0A1P8AUZ9 A0A1P8AUZ9_ARATH reversed Nuclear matrix constituent protein-like protein OS=Arabidopsis thaliana GN=LINC2 PE=1 SV=1	1	-0,231	0,57042957	1324,54	0,643
O04421 SRP14_ARATH Signal recognition particle 14 kDa protein OS=Arabidopsis thaliana GN=SRP14 PE=2 SV=2	1	0,224	0,571428571	1326,86	0,643
P42643 14331_ARATH 14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	10	0,105	0,566433566	1315,26	0,643
O24616 PSA7B_ARATH Proteasome subunit alpha type-7-B OS=Arabidopsis thaliana GN=PAD2 PE=1 SV=2	6	-0,105	0,568431568	1319,9	0,643
Q8GUL8 UGP11_ARATH Uncharacterized GPI-anchored protein At5g19230 OS=Arabidopsis thaliana GN=At5g19230 PE=1 SV=1	1	-0,353	0,573426573	1331,5	0,644
Q9M0M4 MO25M_ARATH Putative MO25-like protein At4g17270 OS=Arabidopsis thaliana GN=At4g17270 PE=2 SV=1	1	0,231	0,571428571	1326,86	0,644
O49636 MPC4_ARATH Mitochondrial pyruvate carrier 4 OS=Arabidopsis thaliana GN=MPC4 PE=3 SV=1	1	-0,227	0,57042957	1324,54	0,644
Q9SHH7 GSTUP_ARATH Glutathione S-transferase U25 OS=Arabidopsis thaliana GN=GSTU25 PE=1 SV=1	1	0,214	0,572427572	1329,18	0,644
Q9Z591 MSRB5_ARATH Peptide methionine sulfoxide reductase B5 OS=Arabidopsis thaliana GN=MSRB5 PE=1 SV=1	3	-0,156	0,57042957	1324,54	0,644
Q9LIR4 ILVD_ARATH Dihydroxy-acid dehydratase, chloroplastic OS=Arabidopsis thaliana GN=DHAD PE=1 SV=1	6	-0,106	0,571428571	1326,86	0,644
Q94A40 COPA1_ARATH Coatamer subunit alpha-1 OS=Arabidopsis thaliana GN=At1g62020 PE=2 SV=2	20	0,093	0,57042957	1324,54	0,644
Q9FFV2 Q9FFV2_ARATH Trafficking protein particle complex subunit OS=Arabidopsis thaliana GN=MBG8.1 PE=2 SV=1	1	0,355	0,573426573	1331,5	0,645
Q9SHJ6 PMD2_ARATH Peroxisomal and mitochondrial division factor 2 OS=Arabidopsis thaliana GN=PMD2 PE=1 SV=1	1	-0,348	0,575424575	1336,14	0,645
P46086 KIME_ARATH Mevalonate kinase OS=Arabidopsis thaliana GN=At5g27450 PE=2 SV=1	2	0,18	0,574425574	1333,82	0,645
Q9S230 HIS4_ARATH Imidazole glycerol phosphate synthase hisHF, chloroplastic OS=Arabidopsis thaliana GN=HISN4 PE=2 SV=1	2	-0,174	0,574425574	1333,82	0,645
P34791 CP20C_ARATH Peptidyl-prolyl cis-trans isomerase CYP20-3, chloroplastic OS=Arabidopsis thaliana GN=CYP20-3 PE=1 SV=1	3	-0,143	0,574425574	1333,82	0,645
Q9LZ66 SIR_ARATH Assimilatory sulfite reductase (ferredoxin), chloroplastic OS=Arabidopsis thaliana GN=SIR PE=1 SV=1	12	0,089	0,57042957	1324,54	0,645
Q9LHT0 TRNHF_ARATH Tropinone reductase homolog At5g06060 OS=Arabidopsis thaliana GN=At5g06060 PE=2 SV=1	1	-0,345	0,576423576	1338,46	0,646
Q9ZVH7 FAX3_ARATH Protein FATTY ACID EXPORT 3, chloroplastic OS=Arabidopsis thaliana GN=FAX3 PE=2 SV=2	1	0,223	0,577422577	1340,78	0,647
Q9CAU9 Q9CAU9_ARATH Contains similarity to O-linked GlcNAc transferases OS=Arabidopsis thaliana GN=At3g04830 PE=2 SV=1	2	0,179	0,578421578	1343,09	0,648
Q9STT3 Q9STT3_ARATH Aldose 1-epimerase OS=Arabidopsis thaliana GN=T23J7.130 PE=2 SV=1	1	-0,328	0,58041958	1347,73	0,65
Q9SJ44 UEV1C_ARATH Ubiquitin-conjugating enzyme E2 variant 1C OS=Arabidopsis thaliana GN=UEV1C PE=1 SV=1	1	0,243	0,581418581	1350,05	0,65
Q80983 FTSH4_ARATH ATP-dependent zinc metalloprotease FTSH 4, mitochondrial OS=Arabidopsis thaliana GN=FTSH4 PE=1 SV=2	2	0,192	0,58041958	1347,73	0,65
P51427 RS52_ARATH 40S ribosomal protein S5-2 OS=Arabidopsis thaliana GN=RP55B PE=1 SV=2	4	-0,16	0,581418581	1350,05	0,65
Q9SVP6 PILR2_ARATH Pinorelinol reductase 2 OS=Arabidopsis thaliana GN=PRR2 PE=1 SV=1	2	0,167	0,583416583	1354,69	0,652
P51407 RLA21_ARATH 60S acidic ribosomal protein P2-1 OS=Arabidopsis thaliana GN=RPP2A PE=3 SV=2	4	0,115	0,586413586	1361,65	0,652
Q9LVC8 COQ5_ARATH 2-methoxy-6-polypropenyl-1,4-benzoquinol methylase, mitochondrial OS=Arabidopsis thaliana GN=COQ5 PE=2 SV=1	1	0,346	0,588411588	1366,29	0,653
Q9LDU6 ST7R_ARATH 7-dehydrocholesterol reductase OS=Arabidopsis thaliana GN=DWF5 PE=1 SV=1	1	-0,293	0,585414585	1359,33	0,653
Q9FNI2 Q9FNI2_ARATH Similarity to unknown protein OS=Arabidopsis thaliana GN=MHF15.22 PE=2 SV=1	1	-0,248	0,585414585	1359,33	0,653
PODI74 S61G1_ARATH Protein transport protein Sec61 subunit gamma-1 OS=Arabidopsis thaliana GN=SEC61G1 PE=1 SV=1	1	0,248	0,586413586	1361,65	0,653
Q93YW5 P2C58_ARATH Probable protein phosphatase 2C 58 OS=Arabidopsis thaliana GN=At4g28400 PE=2 SV=1	1	-0,229	0,588411588	1366,29	0,653
Q9M338 AKRCB_ARATH Aldo-keto reductase family 4 member C11 OS=Arabidopsis thaliana GN=AKR4C11 PE=1 SV=1	1	-0,225	0,587412587	1363,97	0,653
F4J4V1 F4J4V1_ARATH Ankyrin repeat family protein OS=Arabidopsis thaliana GN=TPR10 PE=4 SV=1	1	-0,209	0,587412587	1363,97	0,653
Q9ZRT5 GSTT1_ARATH Glutathione S-transferase T1 OS=Arabidopsis thaliana GN=GSTT1 PE=2 SV=1	2	0,169	0,586413586	1361,65	0,653
Q96518 PER16_ARATH Peroxidase 16 OS=Arabidopsis thaliana GN=PER16 PE=1 SV=2	2	0,15	0,588411588	1366,29	0,653
P52410 KASC1_ARATH 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic OS=Arabidopsis thaliana GN=KAS1 PE=1 SV=2	5	-0,121	0,586413586	1361,65	0,653
Q8GWG0 GPAT9_ARATH Glycerol-3-phosphate acyltransferase 9 OS=Arabidopsis thaliana GN=GPAT9 PE=1 SV=1	1	0,338	0,585414585	1359,33	0,654

F4JQ90 F4JQ90_ARATH FGGY family of carbohydrate kinase OS=Arabidopsis thaliana GN=At4g30310 PE=1 SV=1	1	0,33	0,585414585	1359,33	0,654
Q4V3D1 Q4V3D1_ARATH At1g48620 OS=Arabidopsis thaliana GN=HON5 PE=1 SV=1	1	-0,237	0,59040959	1370,93	0,654
Q93V62 Q93V62_ARATH At4g27450/F27G19_50 OS=Arabidopsis thaliana GN=At4g27450 PE=1 SV=1	2	-0,165	0,588411588	1366,29	0,654
Q8LPJ4 AB2E_ARATH ABC transporter E family member 2 OS=Arabidopsis thaliana GN=ABCE2 PE=2 SV=1	3	-0,142	0,586413586	1361,65	0,654
Q9LMS7 Q9LMS7_ARATH T10F20.8 protein OS=Arabidopsis thaliana GN=At1g18070 PE=1 SV=1	9	0,106	0,589410589	1368,61	0,654
Q94KE3 Q94KE3_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=At3g52990 PE=2 SV=1	8	0,095	0,59040959	1370,93	0,654
F4JNE0 F4JNE0_ARATH Poly(U)-specific endoribonuclease-B protein OS=Arabidopsis thaliana GN=At4g17100 PE=4 SV=1	1	-0,238	0,591408591	1373,25	0,655
Q8L9E3 Q8L9E3_ARATH At5g61220 OS=Arabidopsis thaliana GN=MAF19.16 PE=2 SV=1	2	0,187	0,592407592	1375,57	0,655
Q93Z53 PKP3_ARATH Plastidial pyruvate kinase 3, chloroplastic OS=Arabidopsis thaliana GN=PKP3 PE=1 SV=1	2	-0,182	0,592407592	1375,57	0,655
O80798 O80798_ARATH AT1G65270 protein OS=Arabidopsis thaliana GN=At1g65270 PE=2 SV=1	2	0,171	0,593406593	1377,89	0,655
O82628 VATG1_ARATH V-type proton ATPase subunit G1 OS=Arabidopsis thaliana GN=VHA-G1 PE=1 SV=1	4	-0,12	0,594405594	1380,21	0,655
Q8LBN0 TCPZB_ARATH T-complex protein 1 subunit zeta 2 OS=Arabidopsis thaliana GN=CCT6B PE=1 SV=1	12	-0,094	0,591408591	1373,25	0,655
Q9ZVD0 SRRT_ARATH Serrate RNA effector molecule OS=Arabidopsis thaliana GN=SE PE=1 SV=2	1	-0,333	0,595404595	1382,53	0,656
Q9SR10 Q9SR10_ARATH reversed At3g04640 OS=Arabidopsis thaliana GN=At3g04640 PE=2 SV=1	1	-0,235	0,594405594	1380,21	0,656
Q9LSX7 PEX22_ARATH Peroxisome biogenesis protein 22 OS=Arabidopsis thaliana GN=PEX22 PE=1 SV=1	1	-0,23	0,593406593	1377,89	0,656
Q9SSL0 Q9SSL0_ARATH At1g70820 OS=Arabidopsis thaliana GN=At1g70820 PE=2 SV=1	1	0,197	0,593406593	1377,89	0,656
Q8LBB2 KING1_ARATH SNF1-related protein kinase regulatory subunit gamma-1 OS=Arabidopsis thaliana GN=KING1 PE=1 SV=2	2	0,155	0,594405594	1380,21	0,656
Q93Y22 COPD_ARATH Coatomer subunit delta OS=Arabidopsis thaliana GN=At5g05010 PE=1 SV=2	8	-0,094	0,595404595	1382,53	0,656
Q9C8I6 IOS1_ARATH LRR receptor-like serine/threonine-protein kinase IOS1 OS=Arabidopsis thaliana GN=IOS1 PE=1 SV=1	1	0,35	0,596403596	1384,85	0,657
O64818 Y2309_ARATH Uncharacterized protein At2g23090 OS=Arabidopsis thaliana GN=At2g23090 PE=1 SV=1	1	0,222	0,605394605	1405,73	0,657
Q9SLC8 Q9SLC8_ARATH ESSS subunit of NADH:ubiquinone oxidoreductase (Complex I) protein OS=Arabidopsis thaliana GN=MHK10.3 PE=2 SV=1	2	0,183	0,597402597	1387,17	0,657
Q9M2L4 ACA11_ARATH Putative calcium-transporting ATPase 11, plasma membrane-type OS=Arabidopsis thaliana GN=ACA11 PE=1 SV=1	4	-0,152	0,609390609	1415	0,657
Q9SHC8 VAP12_ARATH Vesicle-associated protein 1-2 OS=Arabidopsis thaliana GN=PVA12 PE=1 SV=1	3	-0,143	0,605394605	1405,73	0,657
Q9LXP4 Q9LXP4_ARATH At3g44190 OS=Arabidopsis thaliana GN=F26G5_140 PE=2 SV=1	4	-0,118	0,605394605	1405,73	0,657
Q8VZW3 CFI3_ARATH Probable chalcone--flavonone isomerase 3 OS=Arabidopsis thaliana GN=CHI3 PE=1 SV=1	5	-0,101	0,608391608	1412,69	0,657
Q24JL3 STR2_ARATH Thiosulfate/3-mercaptopyruvate sulfurtransferase 2 OS=Arabidopsis thaliana GN=STR2 PE=1 SV=1	1	-0,298	0,603396603	1401,09	0,658
O04482 UCH2_ARATH Ubiquitin carboxyl-terminal hydrolase 2 OS=Arabidopsis thaliana GN=UCH2 PE=1 SV=1	1	-0,269	0,608391608	1412,69	0,658
Q9LQW4 CAP15_ARATH Putative clathrin assembly protein At1g14686 OS=Arabidopsis thaliana GN=At1g14686 PE=3 SV=1	1	-0,226	0,607392607	1410,37	0,658
F4HQZ1 F4HQZ1_ARATH Regulator of chromosome condensation (RCC1) family protein OS=Arabidopsis thaliana GN=At1g19880 PE=1 SV=1	1	0,219	0,607392607	1410,37	0,658
P56820 EIF3D_ARATH Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=TIF3D1 PE=1 SV=1	1	-0,218	0,607392607	1410,37	0,658
F4IBH5 F4IBH5_ARATH LETM1-like protein OS=Arabidopsis thaliana GN=LETM2 PE=4 SV=1	1	0,202	0,604395604	1403,41	0,658
P51818 HS903_ARATH Heat shock protein 90-3 OS=Arabidopsis thaliana GN=HSP90-3 PE=1 SV=2	2	-0,161	0,608391608	1412,69	0,658
Q9SEU8 TRXM2_ARATH Thioredoxin M2, chloroplastic OS=Arabidopsis thaliana GN=At4g03520 PE=1 SV=2	2	-0,152	0,602397602	1398,77	0,658
Q9SK39 SBP3_ARATH Probable steroid-binding protein 3 OS=Arabidopsis thaliana GN=MP3 PE=1 SV=1	2	0,138	0,598401598	1389,49	0,658
P22953 MD37E_ARATH Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3	2	0,132	0,598401598	1389,49	0,658
Q9FI56 CLPC1_ARATH Chaperone protein ClpC1, chloroplastic OS=Arabidopsis thaliana GN=CLPC1 PE=1 SV=1	4	-0,13	0,609390609	1415	0,658
A0A1P8ATN7 A0A1P8ATN7_ARATH Prolyl oligopeptidase family protein OS=Arabidopsis thaliana GN=At1g50380 PE=4 SV=1	4	0,129	0,605394605	1405,73	0,658
Q9FNP8 RS193_ARATH 40S ribosomal protein S19-3 OS=Arabidopsis thaliana GN=RPS19C PE=2 SV=1	4	0,122	0,609390609	1415	0,658
Q9FFP6 Q9FFP6_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=MBK5.16 PE=3 SV=1	5	0,117	0,605394605	1405,73	0,658
P25858 G3PC1_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	2	0,116	0,6003996	1394,13	0,658
P54888 P5CS2_ARATH Delta-1-pyrroline-5-carboxylate synthase B OS=Arabidopsis thaliana GN=P5CSB PE=2 SV=1	5	0,111	0,602397602	1398,77	0,658
Q23722 MVD1_ARATH Diphenylmethanone decarboxylase MVD1, peroxisomal OS=Arabidopsis thaliana GN=MVD1 PE=1 SV=1	6	-0,111	0,606393606	1408,05	0,658
O48676 U74B1_ARATH UDP-glycosyltransferase 74B1 OS=Arabidopsis thaliana GN=UGT74B1 PE=1 SV=1	4	-0,11	0,608391608	1412,69	0,658
Q38929 IDI1_ARATH Isopentenyl-diphosphate Delta-isomerase I, chloroplastic OS=Arabidopsis thaliana GN=IPP1 PE=2 SV=3	3	0,105	0,609390609	1415	0,658
P47999 CYSKP_ARATH Cysteine synthase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=OASB PE=1 SV=2	7	-0,102	0,605394605	1405,73	0,658
P48523 CADH4_ARATH Cinnamyl alcohol dehydrogenase 4 OS=Arabidopsis thaliana GN=CAD4 PE=1 SV=1	7	0,095	0,604395604	1403,41	0,658
Q1JPL7 PME18_ARATH Pectinesterase/pectinesterase inhibitor 18 OS=Arabidopsis thaliana GN=PME18 PE=1 SV=3	14	-0,085	0,61038961	1417,32	0,658
Q9LXA8 BXL6_ARATH Probable beta-D-xyllosidase 6 OS=Arabidopsis thaliana GN=BXL6 PE=2 SV=1	1	-0,335	0,608391608	1412,69	0,659
F4II29 F4II29_ARATH Kinase family with ARM repeat domain-containing protein OS=Arabidopsis thaliana GN=CTEXP PE=1 SV=1	1	-0,327	0,603396603	1401,09	0,659
Q9ZSI6 Q9ZSI6_ARATH At4g01700 OS=Arabidopsis thaliana GN=At4g01700 PE=2 SV=1	1	0,319	0,602397602	1398,77	0,659
F4J5M9 CLC3_ARATH Clathrin light chain 3 OS=Arabidopsis thaliana GN=At3g51890 PE=1 SV=1	1	0,233	0,6003996	1394,13	0,659

P92964 SR531_ARATH Serine/arginine-rich splicing factor RS31 OS=Arabidopsis thaliana GN=RS31 PE=1 SV=2	1	0,226	0,602397602	1398,77	0,659
Q9M8X9 RS162_ARATH 40S ribosomal protein S16-2 OS=Arabidopsis thaliana GN=RPS16B PE=1 SV=1	1	0,204	0,612387612	1421,96	0,659
Q9LJ85 Q9LJ85_ARATH Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At3g2262	1	-0,2	0,604395604	1403,41	0,659
P0D119 PHF5A_ARATH PHD finger-like domain-containing protein 5A OS=Arabidopsis thaliana GN=At2g30000 PE=3 SV=1	1	0,181	0,612387612	1421,96	0,659
O23207 FQRL2_ARATH Probable NAD(P)H dehydrogenase (quinone) FQR1-like 2 OS=Arabidopsis thaliana GN=At4g36750 PE=1 SV=1	2	0,175	0,612387612	1421,96	0,659
Q93VP3 IF5A2_ARATH Eukaryotic translation initiation factor 5A-2 OS=Arabidopsis thaliana GN=ELF5A-2 PE=1 SV=1	4	-0,133	0,601398601	1396,45	0,659
Q9AV97 KDSA1_ARATH 2-dehydro-3-deoxyphosphooctonate aldolase 1 OS=Arabidopsis thaliana GN=KDSA1 PE=1 SV=2	4	-0,131	0,604395604	1403,41	0,659
P60040 RL72_ARATH 60S ribosomal protein L7-2 OS=Arabidopsis thaliana GN=RPL7B PE=1 SV=1	5	0,125	0,6003996	1394,13	0,659
Q8VZB9 R10A1_ARATH 60S ribosomal protein L10a-1 OS=Arabidopsis thaliana GN=RPL10AA PE=1 SV=1	4	0,12	0,601398601	1396,45	0,659
Q38951 2AAG_ARATH Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A gamma isoform OS=Arabidopsis thaliana GN=PP2AA3 PE=1	4	0,12	0,611388611	1419,64	0,659
Q9SKR2 SYT1_ARATH Synaptotagmin-1 OS=Arabidopsis thaliana GN=SYT1 PE=1 SV=2	6	-0,117	0,605394605	1405,73	0,659
P14671 TRPB1_ARATH Tryptophan synthase beta chain 1, chloroplastic OS=Arabidopsis thaliana GN=TSB1 PE=2 SV=1	5	0,115	0,602397602	1398,77	0,659
Q8LFC0 IDH1_ARATH Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial OS=Arabidopsis thaliana GN=IDH1 PE=1 SV=2	5	0,107	0,6003996	1394,13	0,659
Q941A6 SDH6_ARATH Succinate dehydrogenase subunit 6, mitochondrial OS=Arabidopsis thaliana GN=SDH6 PE=1 SV=1	4	-0,104	0,613386613	1424,28	0,659
Q9ZNT1 NB5R1_ARATH NADH--cytochrome b5 reductase 1 OS=Arabidopsis thaliana GN=CBR1 PE=1 SV=1	8	-0,096	0,604395604	1403,41	0,659
Q94K05 TCPQ_ARATH T-complex protein 1 subunit theta OS=Arabidopsis thaliana GN=CCT8 PE=1 SV=1	11	0,094	0,6003996	1394,13	0,659
Q9SAJ4 PGKY3_ARATH Phosphoglycerate kinase 3, cytosolic OS=Arabidopsis thaliana GN=PGK3 PE=1 SV=1	18	0,076	0,602397602	1398,77	0,659
Q9T003 Q9T003_ARATH O-methyltransferase family protein OS=Arabidopsis thaliana GN=At4g35160 PE=2 SV=1	1	0,318	0,615384615	1428,92	0,66
Q9SKZ1 PUR_ARATH Transcription factor Pur-alpha 1 OS=Arabidopsis thaliana GN=PURA1 PE=1 SV=2	3	-0,161	0,6003996	1394,13	0,66
Q8RX87 RFS6_ARATH Probable galactinol--sucrose galactosyltransferase 6 OS=Arabidopsis thaliana GN=RFS6 PE=2 SV=2	2	-0,156	0,612387612	1421,96	0,66
Q9LUQ6 RL192_ARATH 60S ribosomal protein L19-2 OS=Arabidopsis thaliana GN=RPL19B PE=2 SV=1	2	-0,152	0,614385614	1426,6	0,66
O23593 RGGB_ARATH RGG repeats nuclear RNA binding protein B OS=Arabidopsis thaliana GN=RGGB PE=1 SV=1	2	-0,121	0,614385614	1426,6	0,66
Q9ZU52 ALFP3_ARATH Fructose-bisphosphate aldolase 3, chloroplastic OS=Arabidopsis thaliana GN=FBA3 PE=1 SV=1	12	-0,083	0,615384615	1428,92	0,66
O49629 PAP2_ARATH Probable plastid-lipid-associated protein 2, chloroplastic OS=Arabidopsis thaliana GN=PAP2 PE=1 SV=1	2	-0,157	0,615384615	1428,92	0,661
Q9LJX4 PUM5_ARATH Pumilio homolog 5 OS=Arabidopsis thaliana GN=APUM5 PE=1 SV=2	2	0,127	0,617382617	1433,56	0,661
P00761 TRYP_PIG Trypsin OS=Sus scrofa PE=1 SV=1	2	-0,122	0,616383616	1431,24	0,661
Q940P8 TCPB_ARATH T-complex protein 1 subunit beta OS=Arabidopsis thaliana GN=CCT2 PE=1 SV=1	10	0,092	0,617382617	1433,56	0,661
Q8LD89 Q8LD89_ARATH ER lumen protein retaining receptor family protein OS=Arabidopsis thaliana GN=At4g38790 PE=2 SV=1	1	-0,285	0,617382617	1433,56	0,662
Q9FKW8 STR18_ARATH Thiosulfate sulfurtransferase 18 OS=Arabidopsis thaliana GN=STR18 PE=1 SV=1	4	0,121	0,618381618	1435,88	0,662
Q9SRQ6 NPC3_ARATH Non-specific phospholipase C3 OS=Arabidopsis thaliana GN=NPC3 PE=2 SV=1	3	-0,189	0,62037962	1440,52	0,664
P56761 PSBD_ARATH Photosystem II D2 protein OS=Arabidopsis thaliana GN=psbD PE=1 SV=3	2	-0,156	0,621378621	1442,84	0,664
P28186 RAE1C_ARATH Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1	3	0,119	0,622377622	1445,16	0,665
Q9SL67 PRS4B_ARATH 26S proteasome regulatory subunit 4 homolog B OS=Arabidopsis thaliana GN=RPT2B PE=1 SV=1	7	0,093	0,623376623	1447,48	0,666
Q8L9C4 KCR1_ARATH Very-long-chain 3-oxoacyl-CoA reductase 1 OS=Arabidopsis thaliana GN=KCR1 PE=1 SV=1	4	0,11	0,625374625	1452,12	0,667
Q9SJ8 MBF1A_ARATH Multiprotein-bridging factor 1a OS=Arabidopsis thaliana GN=MBF1A PE=2 SV=1	3	0,126	0,626373626	1454,44	0,668
Q9M7Q7 PCNA1_ARATH Proliferating cellular nuclear antigen 1 OS=Arabidopsis thaliana GN=PCNA PE=1 SV=2	5	-0,106	0,625374625	1452,12	0,668
P94017 CAP9_ARATH Putative clathrin assembly protein At1g14910 OS=Arabidopsis thaliana GN=At1g14910 PE=2 SV=2	1	-0,278	0,627372627	1456,76	0,669
O48588 O48588_ARATH Molybdenum cofactor sulfurase family protein OS=Arabidopsis thaliana GN=T19K24.17 PE=2 SV=1	2	0,211	0,628371628	1459,08	0,67
Q8LP51 LACS6_ARATH Long chain acyl-CoA synthetase 6, peroxisomal OS=Arabidopsis thaliana GN=LACS6 PE=1 SV=1	3	-0,133	0,629370629	1461,4	0,67
P0CJ46 ACT1_ARATH Actin-1 OS=Arabidopsis thaliana GN=ACT1 PE=1 SV=1	4	0,123	0,63036963	1463,72	0,67
Q56XG6 RH15_ARATH DEAD-box ATP-dependent RNA helicase 15 OS=Arabidopsis thaliana GN=RH15 PE=1 SV=3	9	0,088	0,629370629	1461,4	0,67
Q8W4Q1 Q8W4Q1_ARATH At4g35360/F23E12_80 OS=Arabidopsis thaliana GN=At4g35360 PE=1 SV=1	1	-0,31	0,631368631	1466,04	0,671
Q94A09 Q94A09_ARATH AT1G36310 protein OS=Arabidopsis thaliana GN=At1g36310 PE=1 SV=1	1	-0,28	0,63036963	1463,72	0,671
A8MSC5 A8MSC5_ARATH AT2G47470 protein OS=Arabidopsis thaliana GN=UNE5 PE=2 SV=1	1	0,189	0,639360639	1484,6	0,671
P20431 PMA3_ARATH ATPase 3, plasma membrane-type OS=Arabidopsis thaliana GN=AHA3 PE=1 SV=2	1	-0,172	0,631368631	1466,04	0,671
Q8LFJ5 T112A_ARATH Multifunctional methyltransferase subunit TRM112-like protein At1g22270 OS=Arabidopsis thaliana GN=At1g22270 PE=2 SV=1	2	-0,169	0,632367632	1468,36	0,671
O80526 ACLA3_ARATH ATP-citrate synthase alpha chain protein 3 OS=Arabidopsis thaliana GN=ACLA-3 PE=2 SV=1	2	-0,164	0,637362637	1479,96	0,671
P49967 SR543_ARATH Signal recognition particle 54 kDa protein 3 OS=Arabidopsis thaliana GN=SRP-54C PE=2 SV=2	3	-0,142	0,633366633	1470,68	0,671
Q9M0V3 DDB1A_ARATH DNA damage-binding protein 1a OS=Arabidopsis thaliana GN=DDB1A PE=1 SV=1	3	-0,14	0,633366633	1470,68	0,671
Q9SI8 DSK2B_ARATH Ubiquitin domain-containing protein DSK2b OS=Arabidopsis thaliana GN=DSK2B PE=1 SV=1	4	-0,115	0,632367632	1468,36	0,671
Q84XU2 PPP5_ARATH Serine/threonine-protein phosphatase 5 OS=Arabidopsis thaliana GN=PAPP5 PE=1 SV=1	4	0,113	0,633366633	1470,68	0,671

P53492 ACT7_ARATH Actin-7 OS=Arabidopsis thaliana GN=ACT7 PE=1 SV=1	2	0,112	0,63036963	1463,72	0,671
P17745 EFTU_ARATH Elongation factor Tu, chloroplastic OS=Arabidopsis thaliana GN=TUFA PE=1 SV=1	4	-0,111	0,639360639	1484,6	0,671
Q9ASY9 TENAE_ARATH Bifunctional TENA-E protein OS=Arabidopsis thaliana GN=TENA_E PE=1 SV=3	1	-0,282	0,64035964	1486,92	0,672
Q0WPA5 MSR2_ARATH Protein MANNAN SYNTHESIS-RELATED 2 OS=Arabidopsis thaliana GN=MSR2 PE=2 SV=1	1	0,274	0,636363636	1477,64	0,672
Q8LCY2 ISAM2_ARATH Iron-sulfur assembly protein IscA-like 2, mitochondrial OS=Arabidopsis thaliana GN=At5g03905 PE=1 SV=2	1	-0,213	0,635364635	1475,32	0,672
Q9FFW8 Q9FFW8_ARATH Tryptophan synthase beta chain OS=Arabidopsis thaliana GN=TSBtype2 PE=2 SV=1	1	0,213	0,637362637	1479,96	0,672
Q944A7 Y4523_ARATH Probable serine/threonine-protein kinase At4g35230 OS=Arabidopsis thaliana GN=At4g35230 PE=1 SV=1	1	-0,204	0,641358641	1489,23	0,672
Q8W458 Q8W458_ARATH PLAC8 family protein OS=Arabidopsis thaliana GN=F16G20.170:F16G20.180 PE=2 SV=1	1	-0,201	0,633366633	1470,68	0,672
Q500Z1 Q500Z1_ARATH At5g51220 OS=Arabidopsis thaliana GN=MWD22.17 PE=2 SV=1	1	0,198	0,637362637	1479,96	0,672
A0A1P8AUB6 A0A1P8AUB6_ARATH reversed Cyclin family protein OS=Arabidopsis thaliana GN=SDS PE=3 SV=1	1	0,196	0,637362637	1479,96	0,672
Q9FHX0 Q9FHX0_ARATH Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=MJC20.26 PE=2 SV=1	1	0,192	0,639360639	1484,6	0,672
Q9FNM0 Q9FNM0_ARATH 28 kDa heat/acid-stable phosphoprotein-like protein OS=Arabidopsis thaliana GN=MCL19.6 PE=1 SV=1	1	-0,19	0,636363636	1477,64	0,672
Q9LQ04 RMLCD_ARATH Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana GN=NRS/t	1	0,149	0,635364635	1475,32	0,672
Q9LSK7 Q9LSK7_ARATH At3g18035 OS=Arabidopsis thaliana GN=HON4 PE=1 SV=1	2	-0,14	0,64035964	1486,92	0,672
Q9LSP5 Q9LSP5_ARATH AT3g17020/K14A17_14 OS=Arabidopsis thaliana GN=At3g17020 PE=2 SV=1	3	-0,128	0,638361638	1482,28	0,672
Q501F7 Q501F7_ARATH At1g21440 OS=Arabidopsis thaliana GN=At1g21440 PE=2 SV=1	5	0,126	0,639360639	1484,6	0,672
Q9SZV4 Q9SZV4_ARATH AT4g30010/F6G3_40 OS=Arabidopsis thaliana GN=At4g30010 PE=2 SV=1	3	-0,1	0,635364635	1475,32	0,672
P55737 HS902_ARATH Heat shock protein 90-2 OS=Arabidopsis thaliana GN=HSP90-2 PE=1 SV=1	4	-0,099	0,639360639	1484,6	0,672
Q9SGW3 PSD8A_ARATH 26S proteasome non-ATPase regulatory subunit 8 homolog A OS=Arabidopsis thaliana GN=RPN12A PE=1 SV=1	6	-0,097	0,633366633	1470,68	0,672
Q9LTB2 MMT1_ARATH Methionine S-methyltransferase OS=Arabidopsis thaliana GN=MMT1 PE=1 SV=1	7	-0,086	0,636363636	1477,64	0,672
Q42403 TRXH3_ARATH Thioredoxin H3 OS=Arabidopsis thaliana GN=TRX3 PE=1 SV=1	13	0,079	0,638361638	1482,28	0,672
Q9FGN0 Q9FGN0_ARATH Conserved oligomeric Golgi complex component-related / COG complex component-like protein OS=Arabidopsis thaliana GN=	1	-0,297	0,644355644	1496,19	0,673
Q9LU05 PCAP2_ARATH Plasma membrane-associated cation-binding protein 2 OS=Arabidopsis thaliana GN=PCAP2 PE=1 SV=1	1	-0,192	0,645354645	1498,51	0,673
F4HQD4 HSP7P_ARATH Heat shock 70 kDa protein 15 OS=Arabidopsis thaliana GN=HSP70-15 PE=1 SV=1	3	0,145	0,636363636	1477,64	0,673
Q9SZA3 EIF3K_ARATH Eukaryotic translation initiation factor 3 subunit K OS=Arabidopsis thaliana GN=TIF3K1 PE=2 SV=1	4	0,117	0,643356643	1493,87	0,673
Q42472 DCE2_ARATH Glutamate decarboxylase 2 OS=Arabidopsis thaliana GN=GAD2 PE=1 SV=1	7	-0,094	0,643356643	1493,87	0,673
Q24457 ODPA3_ARATH Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic OS=Arabidopsis thaliana GN=PDH-E1 ALPHA PE=2 SV=1	7	-0,091	0,639360639	1484,6	0,673
O64517 MCA4_ARATH Metacaspase-4 OS=Arabidopsis thaliana GN=AMC4 PE=1 SV=1	6	0,084	0,644355644	1496,19	0,673
P93042 RHD3_ARATH Protein ROOT HAIR DEFECTIVE 3 OS=Arabidopsis thaliana GN=RHD3 PE=1 SV=1	9	0,082	0,643356643	1493,87	0,673
Q93VS8 Q93VS8_ARATH ARM repeat superfamily protein OS=Arabidopsis thaliana GN=emb2734 PE=2 SV=1	13	-0,075	0,642357642	1491,55	0,673
Q9FIQ0 AGD9_ARATH Probable ADP-ribosylation factor GTPase-activating protein AGD9 OS=Arabidopsis thaliana GN=AGD9 PE=1 SV=1	3	0,161	0,645354645	1498,51	0,674
Q8LGI2 QSPDL_ARATH Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410 OS=Arabidopsis thaliana GN=At5g39410 PE=	5	-0,114	0,643356643	1493,87	0,674
Q8RYE7 DF196_ARATH Defensin-like protein 196 OS=Arabidopsis thaliana GN=ATTI4 PE=3 SV=1	2	0,113	0,643356643	1493,87	0,674
Q9M081 SC24B_ARATH Protein transport protein Sec24-like At4g32640 OS=Arabidopsis thaliana GN=At4g32640 PE=3 SV=3	1	0,187	0,647352647	1503,15	0,675
Q8LBN7 COSA_ARATH Costars family protein At4g33640 OS=Arabidopsis thaliana GN=At4g33640 PE=1 SV=1	1	0,204	0,649350649	1507,79	0,676
Q9SZI2 NAP1A_ARATH Nucleosome assembly protein 1;1 OS=Arabidopsis thaliana GN=NAP1;1 PE=1 SV=1	1	0,143	0,648351648	1505,47	0,676
Q9C4Z6 GPLPB_ARATH Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1	2	0,137	0,648351648	1505,47	0,676
Q9SIE1 PAT_ARATH Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase OS=Arabidopsis thaliana GN=PAT P	4	0,119	0,651348651	1512,43	0,676
Q9FJI5 G6PD6_ARATH Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform 2 OS=Arabidopsis thaliana GN=ACG12 PE=2 SV=1	5	-0,109	0,649350649	1507,79	0,676
Q9SXS7 CYSD2_ARATH Bifunctional L-3-cyanoalanine synthase/cysteine synthase D2 OS=Arabidopsis thaliana GN=CYSD2 PE=1 SV=1	1	0,196	0,652347652	1514,75	0,677
Q9SB50 AP4M_ARATH AP-4 complex subunit mu OS=Arabidopsis thaliana GN=AP4M PE=2 SV=1	2	-0,176	0,651348651	1512,43	0,677
Q9L246 H2A4_ARATH Probable histone H2A.4 OS=Arabidopsis thaliana GN=At5g02560 PE=1 SV=1	1	-0,169	0,65034965	1510,11	0,677
O23034 UBA5_ARATH Ubiquitin-like modifier-activating enzyme 5 OS=Arabidopsis thaliana GN=At1g05350 PE=3 SV=2	2	-0,137	0,652347652	1514,75	0,677
Q9SP02 CP20A_ARATH Peptidyl-prolyl cis-trans isomerase CYP20-1 OS=Arabidopsis thaliana GN=CYP20-1 PE=1 SV=1	4	-0,103	0,65034965	1510,11	0,677
O81845 PUMP1_ARATH Mitochondrial uncoupling protein 1 OS=Arabidopsis thaliana GN=PUMP1 PE=1 SV=1	8	0,078	0,651348651	1512,43	0,677
F4ISU2 F4ISU2_ARATH Early endosome antigen OS=Arabidopsis thaliana GN=At2g32240 PE=1 SV=1	20	0,065	0,651348651	1512,43	0,677
Q9LYC9 Q9LYC9_ARATH Uncharacterized protein T20010_20 OS=Arabidopsis thaliana GN=T20010_20 PE=4 SV=1	1	0,286	0,657342657	1526,35	0,678
Q8VXZ9 R47BP_ARATH Polyadenylate-binding protein RBP47B' OS=Arabidopsis thaliana GN=RBP47B' PE=2 SV=1	1	-0,266	0,654345654	1519,39	0,678
Q39232 SUC1_ARATH Sucrose transport protein SUC1 OS=Arabidopsis thaliana GN=SUC1 PE=1 SV=1	1	-0,197	0,654345654	1519,39	0,678
O81629 KLCR1_ARATH Protein KINESIN LIGHT CHAIN-RELATED 1 OS=Arabidopsis thaliana GN=KLCR1 PE=1 SV=1	1	0,186	0,658341658	1528,67	0,678
O48724 WEB1_ARATH Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 OS=Arabidopsis thaliana GN=WEB1 PE=1 SV=1	1	-0,176	0,66033966	1533,31	0,678

Q39099 XTH4_ARATH Xyloglucan endotransglucosylase/hydrolase protein 4 OS=Arabidopsis thaliana GN=XTH4 PE=1 SV=1	1	0,171	0,66033966	1533,31	0,678
Q39255 SKP1A_ARATH SKP1-like protein 1A OS=Arabidopsis thaliana GN=SKP1A PE=1 SV=1	3	-0,142	0,658341658	1528,67	0,678
F4HYF3 DCYD1_ARATH Bifunctional D-cysteine desulfhydrase/1-aminocyclopropane-1-carboxylate deaminase, mitochondrial OS=Arabidopsis thaliana G	4	-0,117	0,657342657	1526,35	0,678
Q9LFG2 DAPF_ARATH Diaminopimelate epimerase, chloroplastic OS=Arabidopsis thaliana GN=DAPF PE=1 SV=1	4	0,107	0,656343656	1524,03	0,678
Q9FFEO RRAA2_ARATH Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 OS=Arabidopsis thaliana GN=At5g16450 PE=1 SV=1	3	-0,104	0,655344655	1521,71	0,678
P93031 GMD2_ARATH GDP-mannose 4,6 dehydratase 2 OS=Arabidopsis thaliana GN=MUR1 PE=1 SV=3	4	-0,102	0,656343656	1524,03	0,678
Q82663 SDHA1_ARATH Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial OS=Arabidopsis thaliana GN=SDH1-1 PE=1 SV=1	10	-0,076	0,661338661	1535,63	0,678
Q8H114 Q8H114_ARATH Appr-1-p processing enzyme family protein OS=Arabidopsis thaliana GN=At2g40600 PE=1 SV=1	1	0,265	0,656343656	1524,03	0,679
Q96293 ACT8_ARATH Actin-8 OS=Arabidopsis thaliana GN=ACT8 PE=1 SV=2	1	0,256	0,66033966	1533,31	0,679
Q9LIM9 Q9LIM9_ARATH Major latex protein-like OS=Arabidopsis thaliana GN=At3g26460 PE=4 SV=1	1	-0,206	0,657342657	1526,35	0,679
Q9M1W4 HMT2_ARATH Homocysteine S-methyltransferase 2 OS=Arabidopsis thaliana GN=HMT-2 PE=1 SV=1	1	0,185	0,656343656	1524,03	0,679
P21240 CPNB1_ARATH Chaperonin 60 subunit beta 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60B1 PE=1 SV=3	2	0,154	0,654345654	1519,39	0,679
Q8GW53 Q8GW53_ARATH At4g24340 OS=Arabidopsis thaliana GN=At4g24340 PE=2 SV=1	2	-0,139	0,655344655	1521,71	0,679
A8MS68 PLPD1_ARATH Dihydrolipoyl dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=LPD1 PE=2 SV=1	3	-0,127	0,656343656	1524,03	0,679
Q9LT78 RD21C_ARATH Probable cysteine protease RD21C OS=Arabidopsis thaliana GN=RD21C PE=1 SV=1	2	-0,114	0,658341658	1528,67	0,679
Q38929 IDI1_ARATH Isopentenyl-diphosphate Delta-isomerase I, chloroplastic OS=Arabidopsis thaliana GN=IPP1 PE=2 SV=3	4	0,1	0,661338661	1535,63	0,679
B9DGC0 B9DGC0_ARATH AT2G34560 protein OS=Arabidopsis thaliana GN=CCP1 PE=1 SV=1	4	-0,099	0,66033966	1533,31	0,679
O04450 TCPE_ARATH T-complex protein 1 subunit epsilon OS=Arabidopsis thaliana GN=CCT5 PE=1 SV=1	8	-0,081	0,658341658	1528,67	0,679
C02361 CPNB3_ARATH Chaperonin 60 subunit beta 3, chloroplastic OS=Arabidopsis thaliana GN=CPN60B3 PE=1 SV=1	10	-0,077	0,661338661	1535,63	0,679
Q9SAJ6 G3PP1_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic OS=Arabidopsis thaliana GN=GAPCP1 PE=1 SV=1	8	0,073	0,66033966	1533,31	0,679
O23254 GLYC4_ARATH Serine hydroxymethyltransferase 4 OS=Arabidopsis thaliana GN=SHM4 PE=1 SV=1	13	-0,068	0,662337662	1537,95	0,679
Q07473 CB4A_ARATH Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1	2	-0,162	0,664335664	1542,59	0,68
O23264 SEBP1_ARATH Selenium-binding protein 1 OS=Arabidopsis thaliana GN=SBP1 PE=1 SV=1	4	0,097	0,663336663	1540,27	0,68
Q944H0 PEAM2_ARATH Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2	14	0,072	0,66033966	1533,31	0,68
Q9MAT5 ANM10_ARATH Protein arginine N-methyltransferase PRMT10 OS=Arabidopsis thaliana GN=PRMT10 PE=1 SV=1	1	0,296	0,665334665	1544,91	0,681
P30182 TOP2_ARATH DNA topoisomerase 2 OS=Arabidopsis thaliana GN=TOP2 PE=2 SV=2	1	0,254	0,668331668	1551,87	0,682
Q9SU94 ANM11_ARATH Protein arginine N-methyltransferase 1.1 OS=Arabidopsis thaliana GN=PRMT11 PE=1 SV=1	1	0,252	0,667332667	1549,55	0,682
C02361 CPNB3_ARATH Chaperonin 60 subunit beta 3, chloroplastic OS=Arabidopsis thaliana GN=CPN60B3 PE=1 SV=1	3	0,122	0,669330669	1554,19	0,682
O23717 PSB5A_ARATH Proteasome subunit beta type-5-A OS=Arabidopsis thaliana GN=PBE1 PE=1 SV=1	4	-0,099	0,667332667	1549,55	0,682
P41376 IF4A1_ARATH Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	9	-0,072	0,667332667	1549,55	0,682
Q9ZRA2 HGD_ARATH Homogentisate 1,2-dioxygenase OS=Arabidopsis thaliana GN=HGO PE=2 SV=2	1	0,271	0,68031968	1579,7	0,683
Q9SN79 Q9SN79_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=F1P2.140 PE=2 SV=1	1	0,258	0,675324675	1568,1	0,683
O22151 GOS12_ARATH Golgi SNAP receptor complex member 1-2 OS=Arabidopsis thaliana GN=GOS12 PE=1 SV=2	1	0,254	0,68031968	1579,7	0,683
Q9SHE8 PSAF_ARATH Photosystem I reaction center subunit III, chloroplastic OS=Arabidopsis thaliana GN=PSAF PE=1 SV=1	1	-0,245	0,676323676	1570,42	0,683
Q41951 TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2	1	0,23	0,68031968	1579,7	0,683
Q0WQF4 VP53A_ARATH Vacuolar protein sorting-associated protein 53 A OS=Arabidopsis thaliana GN=VP53 PE=1 SV=1	1	-0,171	0,669330669	1554,19	0,683
O48832 ERD7_ARATH Protein EARLY-RESPONSIVE TO DEHYDRATION 7, chloroplastic OS=Arabidopsis thaliana GN=ERD7 PE=1 SV=1	1	-0,161	0,674325674	1565,78	0,683
Q9SU40 SKU5_ARATH Monocopper oxidase-like protein SKU5 OS=Arabidopsis thaliana GN=SKU5 PE=1 SV=1	2	-0,142	0,669330669	1554,19	0,683
O81146 PSA6A_ARATH Proteasome subunit alpha type-6-A OS=Arabidopsis thaliana GN=PAA1 PE=1 SV=2	2	0,141	0,681318681	1582,02	0,683
O49313 NDADB_ARATH NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B OS=Arabidopsis thaliana GN=At2g33220 PE=2 SV=1	2	-0,14	0,67032967	1556,51	0,683
A0A1I9LMH9 A0A1I9LMH9_ARATH reversed Haloacid dehalogenase-like hydrolase (HAD) superfamily protein OS=Arabidopsis thaliana GN=At3g29760 P	1	0,136	0,669330669	1554,19	0,683
Q9LPT6 Q9LPT6_ARATH F11F12.1 protein OS=Arabidopsis thaliana GN=F11F12.1 PE=1 SV=1	2	0,134	0,673326673	1563,46	0,683
Q9ZNT0 VPS4_ARATH Protein SUPPRESSOR OF K(+) TRANSPORT GROWTH DEFECT 1 OS=Arabidopsis thaliana GN=SKD1 PE=1 SV=1	3	0,132	0,672327672	1561,14	0,683
Q945K7 IDH5_ARATH Isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial OS=Arabidopsis thaliana GN=IDH5 PE=1 SV=1	3	-0,109	0,667332667	1549,55	0,683
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	1	0,105	0,679320679	1577,38	0,683
Q9C5Z2 EIF3H_ARATH Eukaryotic translation initiation factor 3 subunit H OS=Arabidopsis thaliana GN=TIF3H1 PE=1 SV=2	4	0,099	0,667332667	1549,55	0,683
Q9M0E2 RL282_ARATH F05 ribosomal protein L28-2 OS=Arabidopsis thaliana GN=RPL28C PE=2 SV=1	3	0,094	0,679320679	1577,38	0,683
P05466 AROA_ARATH 3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic OS=Arabidopsis thaliana GN=At2g45300 PE=2 SV=3	5	-0,088	0,675324675	1568,1	0,683
Q93ZN9 DAPAT_ARATH LL-diaminopimelate aminotransferase, chloroplastic OS=Arabidopsis thaliana GN=DAP PE=1 SV=1	7	-0,087	0,676323676	1570,42	0,683
Q38867 CP19C_ARATH Peptidyl-prolyl cis-trans isomerase CYP19-3 OS=Arabidopsis thaliana GN=CYP19-3 PE=2 SV=2	5	0,087	0,679320679	1577,38	0,683
Q949U7 PRX2E_ARATH Peroxiredoxin-2E, chloroplastic OS=Arabidopsis thaliana GN=PRXII PE=1 SV=2	8	-0,071	0,676323676	1570,42	0,683

Q96533 ADHX_ARATH Alcohol dehydrogenase class-3 OS=Arabidopsis thaliana GN=ADH2 PE=1 SV=2	8	-0,07	0,681318681	1582,02	0,683
Q8LER3 XTH7_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 7 OS=Arabidopsis thaliana GN=XTH7 PE=2 SV=2	1	0,255	0,672327672	1561,14	0,684
Q8LPK4 AP2A2_ARATH AP-2 complex subunit alpha-2 OS=Arabidopsis thaliana GN=ALPHAC-AD PE=1 SV=1	1	-0,253	0,678321678	1575,06	0,684
Q8GXH2 Q8GXH2_ARATH Apoptosis inhibitory protein 5 (API5) OS=Arabidopsis thaliana GN=At1g29030 PE=2 SV=1	1	-0,239	0,674325674	1565,78	0,684
Q9SVD1 Q9SVD1_ARATH At3g52500 OS=Arabidopsis thaliana GN=F22O6_120 PE=2 SV=1	1	0,216	0,68031968	1579,7	0,684
Q9CA75 XXT5_ARATH Probable xyloglucan 6-xylosyltransferase 5 OS=Arabidopsis thaliana GN=XXT5 PE=1 SV=1	2	-0,183	0,672327672	1561,14	0,684
Q9LHA7 PER31_ARATH Peroxidase 31 OS=Arabidopsis thaliana GN=PER31 PE=2 SV=1	1	-0,175	0,677322677	1572,74	0,684
O04663 IF4E4_ARATH Eukaryotic translation initiation factor isoform 4E OS=Arabidopsis thaliana GN=EIF(ISO)4E PE=1 SV=2	1	-0,168	0,673326673	1563,46	0,684
A0A1P8AQ86 A0A1P8AQ86_ARATH reversed Uncharacterized protein OS=Arabidopsis thaliana GN=At1g65349 PE=4 SV=1	1	-0,159	0,672327672	1561,14	0,684
Q8LC83 RS242_ARATH 40S ribosomal protein S24-2 OS=Arabidopsis thaliana GN=RPS24B PE=2 SV=2	1	0,159	0,675324675	1568,1	0,684
Q9FMR0 PER60_ARATH Peroxidase 60 OS=Arabidopsis thaliana GN=PER60 PE=1 SV=1	1	0,159	0,678321678	1575,06	0,684
Q9FFC0 H2B10_ARATH Histone H2B.10 OS=Arabidopsis thaliana GN=At5g22880 PE=1 SV=3	1	0,153	0,683316683	1586,66	0,684
Q84JQ4 PRK2_ARATH reversed Pollen receptor-like kinase 2 OS=Arabidopsis thaliana GN=PRK2 PE=1 SV=1	1	-0,151	0,672327672	1561,14	0,684
Q9LYN2 FRI3_ARATH Ferritin-3, chloroplastic OS=Arabidopsis thaliana GN=FER3 PE=2 SV=1	2	0,144	0,673326673	1563,46	0,684
Q9LPU5 IGMT1_ARATH Indole glucosinolate O-methyltransferase 1 OS=Arabidopsis thaliana GN=IGMT1 PE=1 SV=1	1	-0,136	0,675324675	1568,1	0,684
P49211 RL321_ARATH 60S ribosomal protein L32-1 OS=Arabidopsis thaliana GN=RPL32A PE=2 SV=2	1	0,134	0,679320679	1577,38	0,684
O80526 ACLA3_ARATH ATP-citrate synthase alpha chain protein 3 OS=Arabidopsis thaliana GN=ACLA-3 PE=2 SV=1	2	-0,124	0,676323676	1570,42	0,684
Q9M0V6 FNRR1_ARATH Ferredoxin--NADP reductase, root isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=RFNR1 PE=2 SV=2	2	-0,109	0,678321678	1575,06	0,684
Q93W22 RL103_ARATH 60S ribosomal protein L10-3 OS=Arabidopsis thaliana GN=RPL10C PE=2 SV=1	3	0,106	0,675324675	1568,1	0,684
B9DGD6 ACS_ARATH Acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal OS=Arabidopsis thaliana GN=ACS PE=1 SV=1	4	0,105	0,679320679	1577,38	0,684
Q9FY49 LKHA4_ARATH Leukotriene A-4 hydrolase homolog OS=Arabidopsis thaliana GN=LKHA4 PE=2 SV=1	4	-0,103	0,674325674	1565,78	0,684
P93285 COX2_ARATH Cytochrome c oxidase subunit 2 OS=Arabidopsis thaliana GN=COX2 PE=1 SV=2	3	-0,098	0,671328671	1558,83	0,684
O24412 PSD7A_ARATH 26S proteasome non-ATPase regulatory subunit 7 homolog A OS=Arabidopsis thaliana GN=RPN8A PE=1 SV=1	5	0,085	0,682317682	1584,34	0,684
Q9LDA4 PER38_ARATH Peroxidase 38 OS=Arabidopsis thaliana GN=PER38 PE=3 SV=1	5	-0,078	0,679320679	1577,38	0,684
Q8VWF6 SSL3_ARATH Protein STRICTOSIDINE SYNTHASE-LIKE 3 OS=Arabidopsis thaliana GN=SSL3 PE=2 SV=1	1	-0,263	0,684315684	1588,98	0,685
Q9FN41 MTBC_ARATH Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 OS=Arabidopsis thaliana GN=At5g5	2	-0,174	0,685314685	1591,3	0,686
Q9S725 4CL2_ARATH 4-coumarate--CoA ligase 2 OS=Arabidopsis thaliana GN=4CL2 PE=1 SV=2	1	-0,161	0,686313686	1593,62	0,686
Q39221 STLP2_ARATH SEC12-like protein 2 OS=Arabidopsis thaliana GN=STLP2 PE=1 SV=4	1	-0,155	0,687312687	1595,94	0,686
Q94AZ5 Q94AZ5_ARATH Alanine-tRNA ligase OS=Arabidopsis thaliana GN=At2g45060 PE=1 SV=1	3	0,133	0,687312687	1595,94	0,686
Q8VZC0 UXS1_ARATH UDP-glucuronic acid decarboxylase 1 OS=Arabidopsis thaliana GN=UXS1 PE=1 SV=1	2	0,132	0,685314685	1591,3	0,686
Q9C7S3 Q9C7S3_ARATH Inner membrane localized protein OS=Arabidopsis thaliana GN=At1g42960 PE=2 SV=1	2	0,132	0,687312687	1595,94	0,686
O80585 MTHR2_ARATH Methylenetetrahydrofolate reductase 2 OS=Arabidopsis thaliana GN=MTHFR2 PE=1 SV=2	5	0,092	0,686313686	1593,62	0,686
P19366 ATPB_ARATH ATP synthase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=atpB PE=1 SV=2	8	-0,079	0,687312687	1595,94	0,686
Q9LV19 DPYD_ARATH Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic OS=Arabidopsis thaliana GN=PYD1 PE=1 SV=1	5	-0,078	0,688311688	1598,26	0,686
P42043 HEMH1_ARATH Ferrochelatase-1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=FC1 PE=2 SV=1	1	0,253	0,691308691	1605,22	0,687
O04951 PP2A5_ARATH Serine/threonine-protein phosphatase PP2A-5 catalytic subunit OS=Arabidopsis thaliana GN=PP2A5 PE=1 SV=1	1	0,235	0,694305694	1612,18	0,687
Q9C7F7 LTPG1_ARATH Non-specific lipid transfer protein GPI-anchored 1 OS=Arabidopsis thaliana GN=LTPG1 PE=1 SV=1	1	-0,173	0,689310689	1600,58	0,687
Q9SXJ7 CLPC2_ARATH Chaperone protein ClpC2, chloroplastic OS=Arabidopsis thaliana GN=CLPC2 PE=1 SV=1	2	-0,144	0,689310689	1600,58	0,687
A0A1P8B667 A0A1P8B667_ARATH Aminopeptidase P1 OS=Arabidopsis thaliana GN=APP1 PE=1 SV=1	4	-0,112	0,687312687	1595,94	0,687
P92974 UBE12_ARATH Ubiquitin-activating enzyme E1 2 OS=Arabidopsis thaliana GN=UBA2 PE=1 SV=1	2	-0,099	0,691308691	1605,22	0,687
Q42418 PROF2_ARATH Profilin-2 OS=Arabidopsis thaliana GN=PRO2 PE=2 SV=1	3	-0,082	0,694305694	1612,18	0,687
Q9FME2 Q9FME2_ARATH AT5g60980/MSL3_100 OS=Arabidopsis thaliana GN=MSL3.12 PE=1 SV=1	6	0,076	0,694305694	1612,18	0,687
Q9FWY7 IMPA6_ARATH Importin subunit alpha-6 OS=Arabidopsis thaliana GN=IMPA6 PE=2 SV=1	1	-0,261	0,691308691	1605,22	0,688
Q9XEC4 APA3_ARATH Aspartic proteinase A3 OS=Arabidopsis thaliana GN=APA3 PE=2 SV=1	1	-0,244	0,697302697	1619,14	0,688
Q9M024 TAAC_ARATH Thylakoid ADP,ATP carrier protein, chloroplastic OS=Arabidopsis thaliana GN=TAAC PE=1 SV=1	1	-0,169	0,696303696	1616,82	0,688
Q940G0 TMN1_ARATH Transmembrane 9 superfamily member 1 OS=Arabidopsis thaliana GN=TMN1 PE=1 SV=1	2	0,148	0,693306693	1609,86	0,688
Q9SIH0 RS141_ARATH 40S ribosomal protein S14-1 OS=Arabidopsis thaliana GN=RPS14A PE=1 SV=1	1	0,14	0,691308691	1605,22	0,688
Q9ZR12 GRH1_ARATH GRR1-like protein 1 OS=Arabidopsis thaliana GN=GRH1 PE=1 SV=1	2	0,125	0,693306693	1609,86	0,688
O23714 PSB2A_ARATH Proteasome subunit beta type-2-A OS=Arabidopsis thaliana GN=PBD1 PE=1 SV=1	2	-0,116	0,696303696	1616,82	0,688
P40940 ARF3_ARATH ADP-ribosylation factor 3 OS=Arabidopsis thaliana GN=ARF3 PE=1 SV=2	2	0,108	0,697302697	1619,14	0,688
Q9ZRD6 YKT61_ARATH VAMP-like protein YKT61 OS=Arabidopsis thaliana GN=YKT61 PE=2 SV=1	2	0,106	0,691308691	1605,22	0,688

Q9LHH7 FOLD2_ARATH Bifunctional protein FOLD 2 OS=Arabidopsis thaliana GN=FOLD2 PE=2 SV=1	5	-0,09	0,694305694	1612,18	0,688
P56765 ACCD_ARATH Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=accD PE=1 SV=2	4	-0,087	0,695304695	1614,5	0,688
Q9LD55 EIF3A_ARATH Eukaryotic translation initiation factor 3 subunit A OS=Arabidopsis thaliana GN=TIF3A1 PE=1 SV=1	8	-0,078	0,694305694	1612,18	0,688
Q96255 SERB1_ARATH Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1	6	0,078	0,694305694	1612,18	0,688
Q9C6T1 PMK_ARATH Phosphomevalonate kinase, peroxisomal OS=Arabidopsis thaliana GN=PMK PE=1 SV=1	2	-0,134	0,698301698	1621,46	0,689
Q9LHG9 NACA1_ARATH Nascent polypeptide-associated complex subunit alpha-like protein 1 OS=Arabidopsis thaliana GN=At3g12390 PE=1 SV=1	2	0,107	0,697302697	1619,14	0,689
Q9SAK4 SSDH_ARATH Succinate-semialdehyde dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=ALDH5F1 PE=1 SV=2	4	-0,094	0,693306693	1609,86	0,689
Q9C525 BGL21_ARATH Beta-glucosidase 21 OS=Arabidopsis thaliana GN=BGLU21 PE=1 SV=1	7	-0,08	0,693306693	1609,86	0,689
O80501 RAH1B_ARATH Ras-related protein RABH1b OS=Arabidopsis thaliana GN=RABH1B PE=1 SV=1	8	0,077	0,694305694	1612,18	0,689
Q9LW52 Q9LW52_ARATH Transmembrane protein OS=Arabidopsis thaliana GN=At3g23450 PE=4 SV=1	1	0,15	0,703296703	1633,05	0,69
Q05728 PUR5_ARATH Phosphoribosylformylglycinamidine cyclo-ligase, chloroplastic OS=Arabidopsis thaliana GN=PUR5 PE=1 SV=2	2	-0,127	0,7002997	1626,1	0,69
Q9LKL2 APRR1_ARATH reversed Two-component response regulator-like APRR1 OS=Arabidopsis thaliana GN=APRR1 PE=1 SV=1	1	-0,109	0,702297702	1630,74	0,69
Q9SIP7 RS31_ARATH 40S ribosomal protein S3-1 OS=Arabidopsis thaliana GN=RPS3A PE=1 SV=1	3	-0,094	0,701298701	1628,42	0,69
Q9SEE5 GALK1_ARATH Galactokinase OS=Arabidopsis thaliana GN=GAL1 PE=1 SV=2	5	0,092	0,7002997	1626,1	0,69
Q9FT52 ATP5H_ARATH ATP synthase subunit d, mitochondrial OS=Arabidopsis thaliana GN=At3g52300 PE=1 SV=3	10	0,058	0,699300699	1623,78	0,69
P56779 PSBE_ARATH Cytochrome b559 subunit alpha OS=Arabidopsis thaliana GN=psbE PE=1 SV=4	1	0,246	0,701298701	1628,42	0,691
P28188 RAD2A_ARATH Ras-related protein RABD2a OS=Arabidopsis thaliana GN=RABD2A PE=1 SV=3	1	0,229	0,705294705	1637,69	0,691
Q43731 PER50_ARATH Peroxidase 50 OS=Arabidopsis thaliana GN=PER50 PE=1 SV=1	1	-0,225	0,706293706	1640,01	0,691
O64740 SC13B_ARATH Protein transport protein SEC13 homolog B OS=Arabidopsis thaliana GN=SEC13B PE=1 SV=1	1	-0,139	0,705294705	1637,69	0,691
Q5M729 ODP23_ARATH Dihydropyridyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial OS=Arabidopsis	1	-0,137	0,702297702	1630,74	0,691
F4KDN4 F4KDN4_ARATH CHCH domain protein OS=Arabidopsis thaliana GN=MSJ1.24 PE=4 SV=1	2	-0,131	0,706293706	1640,01	0,691
F4J6A1 F4J6A1_ARATH Eukaryotic translation initiation factor 3 subunit G OS=Arabidopsis thaliana GN=EIF3G1 PE=3 SV=1	4	-0,102	0,703296703	1633,05	0,691
Q9LZH9 RL7A2_ARATH 60S ribosomal protein L7a-2 OS=Arabidopsis thaliana GN=RPL7AB PE=2 SV=1	2	0,09	0,702297702	1630,74	0,691
F4IW47 TKTC2_ARATH Transketolase-2, chloroplastic OS=Arabidopsis thaliana GN=TKL-2 PE=1 SV=1	4	-0,089	0,704295704	1635,37	0,691
P48347 14310_ARATH 14-3-3-like protein GF14 epsilon OS=Arabidopsis thaliana GN=GRF10 PE=1 SV=1	9	0,068	0,703296703	1633,05	0,691
P20115 CISY4_ARATH Citrate synthase 4, mitochondrial OS=Arabidopsis thaliana GN=CSY4 PE=1 SV=3	12	0,06	0,706293706	1640,01	0,691
Q8H107 ODO2B_ARATH Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial OS=Ara	1	-0,21	0,709290709	1646,97	0,692
Q9LZ16 NDS5B_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B OS=Arabidopsis thaliana GN=At3g62790 PE=3 SV=1	1	-0,157	0,707292707	1642,33	0,692
Q42479 CDPK3_ARATH Calcium-dependent protein kinase 3 OS=Arabidopsis thaliana GN=CPK3 PE=1 SV=1	1	0,155	0,711288711	1651,61	0,692
Q38820 TI232_ARATH Mitochondrial import inner membrane translocase subunit TIM23-2 OS=Arabidopsis thaliana GN=TIM23-2 PE=1 SV=1	2	-0,149	0,711288711	1651,61	0,692
O82790 O82790_ARATH AT2G45990 protein OS=Arabidopsis thaliana GN=At2g45990 PE=1 SV=1	1	0,145	0,708291708	1644,65	0,692
F4IFY8 SYHC_ARATH Histidine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At3g02760 PE=2 SV=1	2	-0,12	0,705294705	1637,69	0,692
Q8LAD2 SUC2A_ARATH reversed Succinate--CoA ligase [ADP-forming] subunit alpha-2, mitochondrial OS=Arabidopsis thaliana GN=At5g23250 PE=1 SV=1	1	-0,116	0,711288711	1651,61	0,692
P11829 ACP1_ARATH Acyl carrier protein 1, chloroplastic OS=Arabidopsis thaliana GN=ACP1 PE=1 SV=1	2	-0,107	0,709290709	1646,97	0,692
Q9C5G5 SAC7_ARATH Phosphoinositide phosphatase SAC7 OS=Arabidopsis thaliana GN=SAC7 PE=2 SV=1	3	-0,103	0,71028971	1649,29	0,692
Q94C74 GLYM2_ARATH Serine hydroxymethyltransferase 2, mitochondrial OS=Arabidopsis thaliana GN=SHM2 PE=1 SV=2	4	0,1	0,708291708	1644,65	0,692
Q9TOK7 HIBC6_ARATH 3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial OS=Arabidopsis thaliana GN=At4g13360 PE=1 SV=2	3	0,098	0,708291708	1644,65	0,692
Q8LBK6 GRS15_ARATH Monothiol glutaredoxin-S15, mitochondrial OS=Arabidopsis thaliana GN=GRXS15 PE=1 SV=2	3	0,093	0,712287712	1653,93	0,692
Q9LD57 PGKH1_ARATH Phosphoglycerate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=PGK1 PE=1 SV=1	4	-0,083	0,712287712	1653,93	0,692
Q8GUN1 Q8GUN1_ARATH AT4G31340 protein OS=Arabidopsis thaliana GN=At4g31340 PE=2 SV=1	5	-0,082	0,711288711	1651,61	0,692
P34893 CH10_ARATH 10 kDa chaperonin, mitochondrial OS=Arabidopsis thaliana GN=CPN10 PE=1 SV=1	6	-0,069	0,706293706	1640,01	0,692
Q9FJ15 G6PD6_ARATH Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform 2 OS=Arabidopsis thaliana GN=ACG12 PE=2 SV=1	1	-0,24	0,714285714	1658,57	0,693
Q56WD9 THIK2_ARATH 3-ketoacyl-CoA thiolase 2, peroxisomal OS=Arabidopsis thaliana GN=PED1 PE=1 SV=2	1	0,22	0,718281718	1667,85	0,693
Q94F08 HIPL2_ARATH HIPL2 protein OS=Arabidopsis thaliana GN=HIPL2 PE=1 SV=2	1	0,142	0,711288711	1651,61	0,693
Q9LT75 PTN2A_ARATH Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN2A OS=Arabidopsis thaliana GN=	1	-0,141	0,717282717	1665,53	0,693
Q9FM77 Q9FM77_ARATH Isopentenyl-diphosphate delta-isomerase OS=Arabidopsis thaliana GN=MDF20.5 PE=2 SV=1	2	-0,12	0,713286713	1656,25	0,693
Q9ZUG4 MTNA_ARATH Methylthioribose-1-phosphate isomerase OS=Arabidopsis thaliana GN=At2g05830 PE=1 SV=2	3	0,096	0,71028971	1649,29	0,693
Q9M9M9 NDUAC_ARATH Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Arabidopsis thaliana GN=At3g03100 PE=1 SV=1	5	-0,083	0,718281718	1667,85	0,693
Q38884 EIF3I_ARATH Eukaryotic translation initiation factor 3 subunit I OS=Arabidopsis thaliana GN=TIF3I1 PE=2 SV=2	4	-0,073	0,714285714	1658,57	0,693
Q01525 14332_ARATH 14-3-3-like protein GF14 omega OS=Arabidopsis thaliana GN=GRF2 PE=2 SV=2	9	0,073	0,718281718	1667,85	0,693
Q9XGM1 VATD_ARATH V-type proton ATPase subunit D OS=Arabidopsis thaliana GN=VHA-D PE=1 SV=2	15	-0,052	0,711288711	1651,61	0,693

Q94A97 UBC35_ARATH Ubiquitin-conjugating enzyme E2 35 OS=Arabidopsis thaliana GN=UBC35 PE=1 SV=1	1	0,228	0,719280719	1670,17	0,694
Q9FYQ8 TMN11_ARATH Transmembrane 9 superfamily member 11 OS=Arabidopsis thaliana GN=TMN11 PE=2 SV=1	1	0,216	0,72027972	1672,49	0,694
Q9LEA7 GL18_ARATH Germin-like protein subfamily 1 member 8 OS=Arabidopsis thaliana GN=GLP9 PE=2 SV=2	1	-0,204	0,722277722	1677,13	0,694
Q39243 TRXB1_ARATH Thioredoxin reductase 1, mitochondrial OS=Arabidopsis thaliana GN=NTR1 PE=1 SV=3	1	-0,164	0,718281718	1667,85	0,694
Q9T0G2 CYC2_ARATH Cytochrome c-2 OS=Arabidopsis thaliana GN=CYTC-2 PE=1 SV=1	2	0,154	0,717282717	1665,53	0,694
O65506 O65506_ARATH Disease resistance protein (TIR-NBS-LRR class) OS=Arabidopsis thaliana GN=At4g36140 PE=4 SV=1	1	0,152	0,716283716	1663,21	0,694
Q8GXE7 Q8GXE7_ARATH ATP synthase E chain OS=Arabidopsis thaliana GN=At5g15320 PE=2 SV=1	1	-0,151	0,72027972	1672,49	0,694
P35510 PAL1_ARATH Phenylalanine ammonia-lyase 1 OS=Arabidopsis thaliana GN=PAL1 PE=1 SV=3	1	0,148	0,722277722	1677,13	0,694
O04551 O04551_ARATH Plant/protein OS=Arabidopsis thaliana GN=At1g27020 PE=2 SV=1	1	-0,135	0,718281718	1667,85	0,694
Q9T024 Q9T024_ARATH AT4g39150/T22F8_50 OS=Arabidopsis thaliana GN=At4g39150 PE=2 SV=1	2	0,133	0,716283716	1663,21	0,694
O22912 CX5C1_ARATH Probable cytochrome c oxidase subunit 5C-1 OS=Arabidopsis thaliana GN=At2g47380 PE=1 SV=1	1	-0,129	0,716283716	1663,21	0,694
O65660 PLAT1_ARATH PLAT domain-containing protein 1 OS=Arabidopsis thaliana GN=PLAT1 PE=1 SV=1	1	-0,125	0,722277722	1677,13	0,694
Q9FX60 H3L1_ARATH Histone H3-like 1 OS=Arabidopsis thaliana GN=At1g13370 PE=2 SV=3	1	0,115	0,721278721	1674,81	0,694
P36210 RK121_ARATH 50S ribosomal protein L12-1, chloroplastic OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=1	2	-0,096	0,72027972	1672,49	0,694
Q9LQ55 DRP2B_ARATH Dynamin-2B OS=Arabidopsis thaliana GN=DRP2B PE=1 SV=2	4	-0,083	0,717282717	1665,53	0,694
Q0WLB5 CLAH2_ARATH Clathrin heavy chain 2 OS=Arabidopsis thaliana GN=CHC2 PE=1 SV=1	5	-0,083	0,721278721	1674,81	0,694
Q9SYM5 RHM1_ARATH Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase R	8	0,069	0,717282717	1665,53	0,694
O23255 SAHH1_ARATH Adenosylhomocysteinase 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1	10	0,065	0,721278721	1674,81	0,694
Q9FH46 Q9FH46_ARATH Signal recognition particle subunit SRP68 OS=Arabidopsis thaliana GN=At5g61970 PE=2 SV=1	2	0,123	0,716283716	1663,21	0,695
P42697 DRP1A_ARATH Dynamin-related protein 1A OS=Arabidopsis thaliana GN=DRP1A PE=1 SV=3	13	0,061	0,717282717	1665,53	0,695
Q9XI62 APY3_ARATH Probable apyrase 3 OS=Arabidopsis thaliana GN=APY3 PE=2 SV=1	1	-0,22	0,725274725	1684,09	0,696
Q9LF21 Q9LF21_ARATH Eukaryotic translation initiation factor 3 subunit M OS=Arabidopsis thaliana GN=At5g15610 PE=1 SV=1	1	-0,16	0,725274725	1684,09	0,696
Q9ZPI6 AIM1_ARATH Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 OS=Arabidopsis thaliana GN=AIM1 PE=1 SV=1	9	-0,066	0,725274725	1684,09	0,696
P36428 SYA_ARATH Alanine--tRNA ligase OS=Arabidopsis thaliana GN=ALATS PE=1 SV=3	12	-0,057	0,726273726	1686,41	0,696
Q9SJ44 UEV1C_ARATH Ubiquitin-conjugating enzyme E2 variant 1C OS=Arabidopsis thaliana GN=UEV1C PE=1 SV=1	1	-0,215	0,726273726	1686,41	0,697
P56778 PSBC_ARATH Photosystem II CP43 reaction center protein OS=Arabidopsis thaliana GN=psbC PE=1 SV=3	1	-0,201	0,727272727	1688,73	0,697
O22860 RL38_ARATH 60S ribosomal protein L38 OS=Arabidopsis thaliana GN=RPL38A PE=3 SV=1	3	0,086	0,727272727	1688,73	0,697
Q9SIW3 SPR1_ARATH Protein SPIRAL1 OS=Arabidopsis thaliana GN=SPR1 PE=2 SV=1	2	0,098	0,731268731	1698,01	0,698
O65719 HSP7C_ARATH Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	1	-0,153	0,73026973	1695,69	0,699
P28188 RAD2A_ARATH Ras-related protein RABD2a OS=Arabidopsis thaliana GN=RABD2A PE=1 SV=3	1	0,139	0,732267732	1700,33	0,699
Q9FM65 FLA1_ARATH Fasciclin-like arabinogalactan protein 1 OS=Arabidopsis thaliana GN=FLA1 PE=1 SV=1	1	-0,137	0,731268731	1698,01	0,699
Q9FUP0 OPR3_ARATH 12-oxophytodienoate reductase 3 OS=Arabidopsis thaliana GN=OPR3 PE=1 SV=2	2	0,122	0,733266733	1702,65	0,699
Q9LW35 Q9LW35_ARATH Alcohol dehydrogenase-like protein OS=Arabidopsis thaliana GN=At3g26760 PE=2 SV=1	2	0,115	0,731268731	1698,01	0,699
Q9LZ83 Q9LZ83_ARATH AT5G04420 protein OS=Arabidopsis thaliana GN=T32M21_20 PE=1 SV=1	2	-0,099	0,73026973	1695,69	0,699
P92985 RBP1C_ARATH Ran-binding protein 1 homolog c OS=Arabidopsis thaliana GN=RANBP1C PE=2 SV=1	2	0,092	0,73026973	1695,69	0,699
Q8LPJ5 ICDHP_ARATH Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At5g14590 PE=1 SV=1	5	0,086	0,731268731	1698,01	0,699
Q9LZ19 GSTFD_ARATH Glutathione S-transferase F13 OS=Arabidopsis thaliana GN=GSTF13 PE=3 SV=1	1	-0,18	0,733266733	1702,65	0,7
Q8H107 ODO2B_ARATH Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial OS=Ara	3	-0,097	0,734265734	1704,97	0,7
F41B94 JAL8_ARATH Jacalin-related lectin 8 OS=Arabidopsis thaliana GN=JAL8 PE=3 SV=1	3	0,09	0,734265734	1704,97	0,7
Q9SIM4 RL141_ARATH 60S ribosomal protein L14-1 OS=Arabidopsis thaliana GN=RPL14A PE=2 SV=1	5	0,067	0,733266733	1702,65	0,7
Q8LD03 RS73_ARATH 40S ribosomal protein S7-3 OS=Arabidopsis thaliana GN=RPS7C PE=1 SV=2	2	-0,094	0,736263736	1709,6	0,701
Q9FFR3 6PGD2_ARATH 6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV=1	1	0,112	0,738261738	1714,24	0,703
P46646 AAT4_ARATH Aspartate aminotransferase, cytoplasmic isozyme 2 OS=Arabidopsis thaliana GN=ASP4 PE=2 SV=2	2	0,093	0,739260739	1716,56	0,703
Q8W4F3 SYQ_ARATH Glutamine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=OVA9 PE=2 SV=1	2	-0,091	0,738261738	1714,24	0,703
O81644 VIL12_ARATH Villin-2 OS=Arabidopsis thaliana GN=VLN2 PE=1 SV=2	1	-0,202	0,742257742	1723,52	0,705
Q94JQ7 Q94JQ7_ARATH At1g07830/F24B9_7 OS=Arabidopsis thaliana GN=At1g07830 PE=1 SV=1	1	-0,201	0,743256743	1725,84	0,705
P19366 ATPB_ARATH ATP synthase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=atpB PE=1 SV=2	1	0,102	0,742257742	1723,52	0,705
Q9SVA6 DRG3_ARATH Developmentally-regulated G-protein 3 OS=Arabidopsis thaliana GN=DRG3 PE=1 SV=1	3	0,093	0,742257742	1723,52	0,705
P49688 RS23_ARATH 40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2	5	0,061	0,742257742	1723,52	0,705
Q9STX5 ENPL_ARATH Endoplasmic reticulum protein OS=Arabidopsis thaliana GN=HSP90-7 PE=1 SV=1	17	0,05	0,743256743	1725,84	0,705
Q56WF8 SCP48_ARATH Serine carboxypeptidase-like 48 OS=Arabidopsis thaliana GN=SCPL48 PE=2 SV=2	1	-0,202	0,744255744	1728,16	0,706

P50287 ASPGA_ARATH Isoaspartyl peptidase/L-asparaginase 1 OS=Arabidopsis thaliana GN=At5g08100 PE=1 SV=2	1	-0,202	0,749250749	1739,76	0,706
F4KCL7 OE64M_ARATH Outer envelope protein 64, mitochondrial OS=Arabidopsis thaliana GN=OM64 PE=1 SV=1	1	-0,201	0,746253746	1732,8	0,706
Q8VZB1 Q8VZB1_ARATH NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=EMB2799 PE=1 SV=1	1	0,146	0,745254745	1730,48	0,706
Q9SUT9 RTNLB_ARATH Reticulon-like protein B2 OS=Arabidopsis thaliana GN=RTNLB2 PE=1 SV=1	1	0,138	0,745254745	1730,48	0,706
Q9C9P3 Q9C9P3_ARATH ADP-glucose pyrophosphorylase family protein OS=Arabidopsis thaliana GN=F9E10.24 PE=1 SV=1	1	-0,121	0,746253746	1732,8	0,706
P41376 IF4A1_ARATH Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1	5	-0,075	0,75024975	1742,08	0,706
Q94A94 DCDA2_ARATH Diaminopimelate decarboxylase 2, chloroplastic OS=Arabidopsis thaliana GN=LYSA2 PE=1 SV=1	5	-0,073	0,746253746	1732,8	0,706
Q9C522 ACLB1_ARATH ATP-citrate synthase beta chain protein 1 OS=Arabidopsis thaliana GN=ACLB-1 PE=2 SV=1	8	0,056	0,746253746	1732,8	0,706
Q9ZT91 EFTM_ARATH Elongation factor Tu, mitochondrial OS=Arabidopsis thaliana GN=TUFA PE=1 SV=1	12	-0,052	0,742257742	1723,52	0,706
Q9SAZ5 AHP3_ARATH Histidine-containing phosphotransfer protein 3 OS=Arabidopsis thaliana GN=AHP3 PE=1 SV=2	1	0,169	0,751248751	1744,4	0,707
F4JKY6 F4JKY6_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At4g15960 PE=4 SV=1	1	0,143	0,749250749	1739,76	0,707
Q8W207 CSN2_ARATH COP9 signalosome complex subunit 2 OS=Arabidopsis thaliana GN=CSN2 PE=1 SV=1	1	0,134	0,752247752	1746,72	0,707
Q43870 APS2_ARATH ATP sulfurylase 2 OS=Arabidopsis thaliana GN=APS2 PE=1 SV=1	1	0,133	0,748251748	1737,44	0,707
Q9SIA7 SOX_ARATH Probable sarcosine oxidase OS=Arabidopsis thaliana GN=At2g24580 PE=2 SV=1	1	0,133	0,751248751	1744,4	0,707
Q9SR33 ORP3B_ARATH Oxysterol-binding protein-related protein 3B OS=Arabidopsis thaliana GN=ORP3B PE=2 SV=1	1	-0,13	0,748251748	1737,44	0,707
Q8RV04 TIM141_ARATH Mitochondrial import inner membrane translocase subunit TIM14-1 OS=Arabidopsis thaliana GN=TIM14-1 PE=1 SV=1	1	-0,12	0,75024975	1742,08	0,707
Q9LKA4 UBA2C_ARATH UBP1-associated protein 2C OS=Arabidopsis thaliana GN=UBA2C PE=2 SV=1	2	0,12	0,75024975	1742,08	0,707
Q9LJE5 Q9LJE5_ARATH AT3g13460/MRP15_10 OS=Arabidopsis thaliana GN=ECT2 PE=1 SV=1	2	0,106	0,748251748	1737,44	0,707
Q9M401 BCAT3_ARATH Branched-chain-amino-acid aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=BCAT3 PE=1 SV=1	3	0,101	0,749250749	1739,76	0,707
P42731 PABP2_ARATH Polyadenylate-binding protein 2 OS=Arabidopsis thaliana GN=PAB2 PE=1 SV=1	9	0,066	0,749250749	1739,76	0,707
Q9ZU25 MPPA1_ARATH Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At1g51980 PE=1 SV=	12	-0,055	0,746253746	1732,8	0,707
Q8H166 ALEU_ARATH Thiol protease aleurain OS=Arabidopsis thaliana GN=ALEU PE=1 SV=2	2	-0,11	0,754245754	1751,36	0,708
Q9FLT9 Q9FLT9_ARATH AT5g24650/K18P6_19 OS=Arabidopsis thaliana GN=HP30-2 PE=2 SV=1	3	0,117	0,755244755	1753,68	0,709
P28186 RAE1C_ARATH Ras-related protein RAB1c OS=Arabidopsis thaliana GN=RAB1C PE=1 SV=1	1	-0,113	0,754245754	1751,36	0,709
F4K000 F4K000_ARATH Metal-dependent protein hydrolase OS=Arabidopsis thaliana GN=MJC20.7 PE=1 SV=1	2	-0,099	0,756243756	1756	0,709
Q8RWF0 PS13A_ARATH 26S proteasome non-ATPase regulatory subunit 13 homolog A OS=Arabidopsis thaliana GN=RPN9A PE=1 SV=1	3	-0,083	0,755244755	1753,68	0,709
Q94AA4 PFKA3_ARATH ATP-dependent 6-phosphofructokinase 3 OS=Arabidopsis thaliana GN=PFK3 PE=1 SV=1	4	0,08	0,756243756	1756	0,709
Q9SPE6 SNAA2_ARATH Alpha-soluble NSF attachment protein 2 OS=Arabidopsis thaliana GN=ASNAP2 PE=1 SV=1	3	-0,076	0,754245754	1751,36	0,709
Q8VYI4 Q8VYI4_ARATH Aspartate-semialdehyde dehydrogenase, putative OS=Arabidopsis thaliana GN=At1g14810 PE=2 SV=1	5	0,076	0,755244755	1753,68	0,709
Q940G5 Q940G5_ARATH Glucose-6-phosphate 1-epimerase OS=Arabidopsis thaliana GN=At4g25900 PE=2 SV=1	5	-0,064	0,757242757	1758,32	0,709
Q9M328 Q9M328_ARATH AT3G53990 protein OS=Arabidopsis thaliana GN=F5K20_290 PE=2 SV=1	8	-0,053	0,757242757	1758,32	0,709
Q9M063 GEML3_ARATH Putative GEM-like protein 3 OS=Arabidopsis thaliana GN=At4g04100 PE=3 SV=2	1	0,18	0,763236763	1772,24	0,71
Q9SR15 SYWC_ARATH Tryptophan--trNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At3g04600 PE=2 SV=1	1	0,14	0,759240759	1762,96	0,71
P50318 PGKH2_ARATH Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=1 SV=3	2	0,099	0,757242757	1758,32	0,71
A2RVM0 TIC32_ARATH Short-chain dehydrogenase TIC 32, chloroplastic OS=Arabidopsis thaliana GN=TIC32 PE=2 SV=1	3	-0,097	0,76023976	1765,28	0,71
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	2	-0,072	0,758241758	1760,64	0,71
Q9FKA5 Y5957_ARATH Uncharacterized protein At5g39570 OS=Arabidopsis thaliana GN=At5g39570 PE=1 SV=1	5	0,06	0,762237762	1769,92	0,71
Q9FF55 PDI14_ARATH Protein disulfide isomerase-like 1-4 OS=Arabidopsis thaliana GN=PDIL1-4 PE=1 SV=1	12	-0,046	0,763236763	1772,24	0,71
Q9ZUN8 Q9ZUN8_ARATH Putative WD-40 repeat protein OS=Arabidopsis thaliana GN=heat stress tolerant DWD 1 PE=1 SV=1	1	-0,192	0,762237762	1769,92	0,711
Q9FH13 RAA3_ARATH Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3 OS=Arabidopsis thaliana GN=At5g56260 PE=1 SV=1	1	-0,17	0,763236763	1772,24	0,711
Q94F09 PDI52_ARATH Protein disulfide-isomerase 5-2 OS=Arabidopsis thaliana GN=PDIL5-2 PE=1 SV=1	1	0,123	0,762237762	1769,92	0,711
Q9SCL7 NAGK_ARATH Acetylglutamate kinase, chloroplastic OS=Arabidopsis thaliana GN=NAGK PE=1 SV=1	2	-0,108	0,762237762	1769,92	0,711
Q9SX85 SEC3A_ARATH Exocyst complex component SEC3A OS=Arabidopsis thaliana GN=SEC3A PE=1 SV=1	2	-0,086	0,765234765	1776,88	0,711
A7WM73 HEXO1_ARATH Beta-hexosaminidase 1 OS=Arabidopsis thaliana GN=HEXO1 PE=1 SV=1	3	0,083	0,761238761	1767,6	0,711
Q94BY3 Q94BY3_ARATH Translocon-associated protein subunit beta OS=Arabidopsis thaliana GN=MUA22.2 PE=2 SV=1	2	0,083	0,762237762	1769,92	0,711
O48844 PSD1A_ARATH 26S proteasome non-ATPase regulatory subunit 1 homolog A OS=Arabidopsis thaliana GN=RPN2A PE=1 SV=1	5	-0,066	0,763236763	1772,24	0,711
Q9C5Z1 EIF3B_ARATH Eukaryotic translation initiation factor 3 subunit B OS=Arabidopsis thaliana GN=TIF3B1 PE=1 SV=1	7	0,06	0,761238761	1767,6	0,711
O49299 PGMC1_ARATH Probable phosphoglucomutase, cytoplasmic 1 OS=Arabidopsis thaliana GN=At1g23190 PE=2 SV=2	8	0,049	0,76023976	1765,28	0,711
P28769 TCPA_ARATH T-complex protein 1 subunit alpha OS=Arabidopsis thaliana GN=CCT1 PE=1 SV=1	19	-0,049	0,76023976	1765,28	0,711
Q9SYB5 OST3B_ARATH Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3B OS=Arabidopsis thaliana GN=OST3B PE=2 SV=1	1	0,122	0,766233766	1779,19	0,712
Q2PE59 Q2PE59_ARATH Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=AtXYP14	1	0,11	0,765234765	1776,88	0,712

Q94BT0 SPSA1_ARATH Sucrose-phosphate synthase 1 OS=Arabidopsis thaliana GN=SPS1 PE=1 SV=1	2	0,108	0,767232767	1781,51	0,712
P49211 RL321_ARATH 60S ribosomal protein L32-1 OS=Arabidopsis thaliana GN=RPL32A PE=2 SV=2	3	0,078	0,767232767	1781,51	0,712
Q8L8Y0 RS21_ARATH 40S ribosomal protein S2-1 OS=Arabidopsis thaliana GN=RPS2A PE=2 SV=2	4	0,07	0,766233766	1779,19	0,712
Q8L611 SC31B_ARATH Protein transport protein SEC31 homolog B OS=Arabidopsis thaliana GN=SEC31B PE=1 SV=1	7	-0,064	0,767232767	1781,51	0,712
Q9M250 GMPP2_ARATH Probable mannose-1-phosphate guanylyltransferase 2 OS=Arabidopsis thaliana GN=At3g55590 PE=2 SV=1	1	0,175	0,773226773	1795,43	0,713
Q9LFL3 TOL1_ARATH TOM1-like protein 1 OS=Arabidopsis thaliana GN=TOL1 PE=1 SV=1	2	0,086	0,769230769	1786,15	0,713
Q9ZPW5 Q9ZPW5_ARATH AAA-type ATPase family protein OS=Arabidopsis thaliana GN=At2g18330 PE=2 SV=2	2	-0,085	0,769230769	1786,15	0,713
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	3	0,081	0,769230769	1786,15	0,713
P34790 CP18C_ARATH Peptidyl-prolyl cis-trans isomerase CYP18-3 OS=Arabidopsis thaliana GN=CYP18-3 PE=1 SV=1	7	-0,051	0,77022977	1788,47	0,713
Q9SD85 F3PH_ARATH Flavonoid 3'-monooxygenase OS=Arabidopsis thaliana GN=CYP75B1 PE=1 SV=1	1	0,204	0,772227772	1793,11	0,714
Q8GW78 CLPT2_ARATH ATP-dependent Clp protease ATP-binding subunit CLPT2, chloroplastic OS=Arabidopsis thaliana GN=CLPT2 PE=1 SV=1	1	0,118	0,773226773	1795,43	0,714
Q9M0N1 PUX10_ARATH Plant UBX domain-containing protein 10 OS=Arabidopsis thaliana GN=PUX10 PE=2 SV=1	1	-0,115	0,772227772	1793,11	0,714
O04496 AED3_ARATH Aspartyl protease AED3 OS=Arabidopsis thaliana GN=AED3 PE=1 SV=1	1	0,113	0,773226773	1795,43	0,714
P05466 AROA_ARATH 3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic OS=Arabidopsis thaliana GN=At2g45300 PE=2 SV=3	2	-0,11	0,775224775	1800,07	0,714
Q94A82 NUD19_ARATH Nudix hydrolase 19, chloroplastic OS=Arabidopsis thaliana GN=NUDT19 PE=1 SV=1	1	-0,107	0,774225774	1797,75	0,714
Q84XV2 GTE1_ARATH Transcription factor GTE1 OS=Arabidopsis thaliana GN=GTE1 PE=2 SV=1	1	0,092	0,772227772	1793,11	0,714
Q9FFT4 PDC2_ARATH Pyruvate decarboxylase 2 OS=Arabidopsis thaliana GN=PDC2 PE=2 SV=1	4	-0,082	0,772227772	1793,11	0,714
O49453 Y4844_ARATH Uncharacterized protein At4g28440 OS=Arabidopsis thaliana GN=At4g28440 PE=1 SV=1	3	-0,072	0,773226773	1795,43	0,714
Q9SR5Y GSTF7_ARATH Glutathione S-transferase F7 OS=Arabidopsis thaliana GN=GSTF7 PE=2 SV=3	4	-0,068	0,776223776	1802,39	0,714
Q9FIE8 UXS3_ARATH UDP-glucuronic acid decarboxylase 3 OS=Arabidopsis thaliana GN=UXS3 PE=1 SV=1	8	-0,056	0,775224775	1800,07	0,714
Q9FVT2 EF1G2_ARATH Probable elongation factor 1-gamma 2 OS=Arabidopsis thaliana GN=At1g57720 PE=1 SV=1	8	0,052	0,771228771	1790,79	0,714
P93306 NDUS2_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 2 OS=Arabidopsis thaliana GN=NAD7 PE=1 SV=2	9	0,05	0,775224775	1800,07	0,714
Q9FI44 SDAF2_ARATH Succinate dehydrogenase assembly factor 2, mitochondrial OS=Arabidopsis thaliana GN=SDHAF2 PE=1 SV=1	1	0,176	0,777222777	1804,71	0,715
Q94JV5 NILP2_ARATH Nitrilase-like protein 2 OS=Arabidopsis thaliana GN=NLP2 PE=2 SV=1	1	-0,124	0,772227772	1793,11	0,715
Q9FUS6 GSTUD_ARATH Glutathione S-transferase U13 OS=Arabidopsis thaliana GN=GSTU13 PE=2 SV=1	4	0,064	0,775224775	1800,07	0,715
P33207 FABG_ARATH 3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic OS=Arabidopsis thaliana GN=At1g24360 PE=1 SV=2	7	0,05	0,778221778	1807,03	0,715
P42644 14333_ARATH 14-3-3-like protein GRF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2	1	0,171	0,778221778	1807,03	0,716
Q9SVD7 UEV1D_ARATH Ubiquitin-conjugating enzyme E2 variant 1D OS=Arabidopsis thaliana GN=UEV1D PE=1 SV=1	2	-0,093	0,779220779	1809,35	0,716
Q9M0V6 FNRR1_ARATH Ferredoxin--NADP reductase, root isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=RFNR1 PE=2 SV=2	3	0,07	0,78021978	1811,67	0,716
Q9ASY8 TOM71_ARATH Mitochondrial import receptor subunit TOM7-1 OS=Arabidopsis thaliana GN=TOM7-1 PE=1 SV=1	1	0,118	0,78021978	1811,67	0,717
Q7PC86 AB35G_ARATH ABC transporter G family member 35 OS=Arabidopsis thaliana GN=ABCG35 PE=2 SV=1	2	0,078	0,781218781	1813,99	0,717
Q38845 2AAA_ARATH Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Arabidopsis thaliana GN=PP2AA1 PE=1 S	5	0,059	0,782217782	1816,31	0,717
Q9C713 SYRC_ARATH Arginine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At1g66530 PE=1 SV=1	1	-0,163	0,783216783	1818,63	0,718
O82629 VATG2_ARATH V-type proton ATPase subunit G2 OS=Arabidopsis thaliana GN=VHA-G2 PE=1 SV=2	5	0,06	0,782217782	1816,31	0,718
Q9CA40 NUDT1_ARATH Nudix hydrolase 1 OS=Arabidopsis thaliana GN=NUDT1 PE=1 SV=1	1	0,111	0,786213786	1825,59	0,719
O04486 RAA2A_ARATH Ras-related protein RABA2a OS=Arabidopsis thaliana GN=RABA2A PE=2 SV=1	1	0,103	0,784215784	1820,95	0,719
Q9LPC5 BIG3_ARATH Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Arabidopsis thaliana GN=BIG3 PE=1 SV=1	2	0,088	0,786213786	1825,59	0,719
Q9FYA6 BCAT5_ARATH Branched-chain-amino-acid aminotransferase 5, chloroplastic OS=Arabidopsis thaliana GN=BCAT5 PE=1 SV=1	2	0,075	0,788211788	1830,23	0,719
Q43873 PER73_ARATH Peroxidase 73 OS=Arabidopsis thaliana GN=PER73 PE=1 SV=1	1	0,122	0,786213786	1825,59	0,72
O04023 SRC2_ARATH Protein SRC2 homolog OS=Arabidopsis thaliana GN=SRC2 PE=1 SV=1	1	-0,115	0,79020979	1834,87	0,72
Q9LK29 CYC1A_ARATH Cytochrome c1 1, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC11 PE=1 SV=1	1	0,098	0,788211788	1830,23	0,72
Q9TOI8 MTN1_ARATH 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1 OS=Arabidopsis thaliana GN=MTN1 PE=1 SV=1	3	0,072	0,788211788	1830,23	0,72
Q9ZUB3 SPD1_ARATH Spermidine synthase 1 OS=Arabidopsis thaliana GN=SPDSYN1 PE=1 SV=1	3	-0,07	0,788211788	1830,23	0,72
Q38858 CALR2_ARATH Calreticulin-2 OS=Arabidopsis thaliana GN=CRT2 PE=1 SV=3	5	-0,06	0,786213786	1825,59	0,72
Q9FJZ7 Q9FJZ7_ARATH AT5G66420 protein OS=Arabidopsis thaliana GN=At5g66420 PE=2 SV=1	5	-0,058	0,786213786	1825,59	0,72
Q93VT9 RL101_ARATH 60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1	4	0,055	0,79020979	1834,87	0,72
Q940G3 Q940G3_ARATH 39S ribosomal protein OS=Arabidopsis thaliana GN=MIJ24.9 PE=2 SV=1	1	0,174	0,79020979	1834,87	0,721
Q9SKX0 AB13C_ARATH ABC transporter C family member 13 OS=Arabidopsis thaliana GN=ABCC13 PE=2 SV=3	1	-0,119	0,802197802	1862,7	0,721
Q8VYV0 Q8VYV0_ARATH At1g43690/F2J6_4 OS=Arabidopsis thaliana GN=At1g43690 PE=1 SV=1	1	-0,11	0,801198801	1860,38	0,721
Q9ZW16 TRNHA_ARATH Tropinone reductase homolog At2g29330 OS=Arabidopsis thaliana GN=TRI PE=1 SV=1	1	0,101	0,79020979	1834,87	0,721
P50883 RL121_ARATH 60S ribosomal protein L12-1 OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=2	1	0,096	0,803196803	1865,02	0,721

Q9SX65 DNAT1_ARATH 1,4-dihydroxy-2-naphthoyl-CoA thioesterase 1 OS=Arabidopsis thaliana GN=DHNAT1 PE=1 SV=1	2	0,089	0,801198801	1860,38	0,721
Q9FMF7 DIT21_ARATH Dicarboxylate transporter 2.1, chloroplastic OS=Arabidopsis thaliana GN=DIT2-1 PE=1 SV=1	2	-0,088	0,801198801	1860,38	0,721
Q949P2 COPDA_ARATH Probable cytosolic oligopeptidase A OS=Arabidopsis thaliana GN=CYOP PE=1 SV=1	3	0,082	0,796203796	1848,79	0,721
Q9MAT0 PSD1B_ARATH 26S proteasome non-ATPase regulatory subunit 1 homolog B OS=Arabidopsis thaliana GN=RPN2B PE=1 SV=1	2	-0,079	0,792207792	1839,51	0,721
Q9CAA0 COB21_ARATH Coatomer subunit beta'-1 OS=Arabidopsis thaliana GN=At1g79990 PE=2 SV=2	2	-0,077	0,802197802	1862,7	0,721
Q9SR73 RS281_ARATH 40S ribosomal protein S28-1 OS=Arabidopsis thaliana GN=RPS28A PE=3 SV=1	3	-0,056	0,798201798	1853,42	0,721
Q8L953 RS273_ARATH 40S ribosomal protein S27-3 OS=Arabidopsis thaliana GN=RPS27D PE=2 SV=2	3	-0,052	0,8001998	1858,06	0,721
Q8LD03 RS73_ARATH 40S ribosomal protein S7-3 OS=Arabidopsis thaliana GN=RPS7C PE=1 SV=2	8	-0,05	0,8001998	1858,06	0,721
Q95748 NDUS3_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 OS=Arabidopsis thaliana GN=NAD9 PE=1 SV=2	9	-0,047	0,798201798	1853,42	0,721
Q8H1Y0 ODPA2_ARATH Pyruvate dehydrogenase E1 component subunit alpha-2, mitochondrial OS=Arabidopsis thaliana GN=IAR4 PE=1 SV=2	10	-0,045	0,796203796	1848,79	0,721
Q8VZM1 NAA15_ARATH N-terminal acetyltransferase A complex auxiliary subunit NAA15 OS=Arabidopsis thaliana GN=NAA15 PE=1 SV=1	10	-0,044	0,8001998	1858,06	0,721
O80852 GSTF9_ARATH Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1	8	0,042	0,799200799	1855,74	0,721
P31414 AVP1_ARATH Pyrophosphate-energized vacuolar membrane proton pump 1 OS=Arabidopsis thaliana GN=AVP1 PE=1 SV=1	10	0,042	0,799200799	1855,74	0,721
Q0WLB5 CLAH2_ARATH Clathrin heavy chain 2 OS=Arabidopsis thaliana GN=CHC2 PE=1 SV=1	33	-0,036	0,788211788	1830,23	0,721
Q681K2 ATS3A_ARATH Embryo-specific protein ATS3A OS=Arabidopsis thaliana GN=ATS3A PE=1 SV=1	1	-0,164	0,793206793	1841,83	0,722
Q96242 CP74A_ARATH Allene oxide synthase, chloroplastic OS=Arabidopsis thaliana GN=CYP74A PE=1 SV=3	1	0,153	0,795204795	1846,47	0,722
Q9FI94 DHYS_ARATH Deoxyhypusine synthase OS=Arabidopsis thaliana GN=DHS PE=2 SV=1	1	0,15	0,798201798	1853,42	0,722
P92949 FRO2_ARATH Ferric reduction oxidase 2 OS=Arabidopsis thaliana GN=FRO2 PE=1 SV=2	1	-0,145	0,798201798	1853,42	0,722
Q9LFX8 Q9LFX8_ARATH Glycine-rich protein OS=Arabidopsis thaliana GN=At1g27090 PE=1 SV=1	2	-0,118	0,796203796	1848,79	0,722
Q9LYU8 AK1_ARATH Aspartokinase 1, chloroplastic OS=Arabidopsis thaliana GN=AK1 PE=1 SV=1	1	0,116	0,793206793	1841,83	0,722
A8MRX0 GSOX5_ARATH Flavin-containing monooxygenase FMO GS-OX5 OS=Arabidopsis thaliana GN=FMOGS-OX5 PE=1 SV=2	2	0,107	0,795204795	1846,47	0,722
Q9SMN0 CXE12_ARATH Probable carboxylesterase 12 OS=Arabidopsis thaliana GN=CXE12 PE=1 SV=1	1	-0,101	0,795204795	1846,47	0,722
Q9FJB4 Q9FJB4_ARATH AT5g35460/MOK9_4 OS=Arabidopsis thaliana GN=MOK9.4 PE=1 SV=1	1	-0,098	0,799200799	1855,74	0,722
O64764 TRXO1_ARATH Thioredoxin O1, mitochondrial OS=Arabidopsis thaliana GN=At2g35010 PE=2 SV=1	2	0,097	0,8001998	1858,06	0,722
Q84W89 RH37_ARATH DEAD-box ATP-dependent RNA helicase 37 OS=Arabidopsis thaliana GN=RH37 PE=2 SV=2	2	0,093	0,792207792	1839,51	0,722
Q84M96 ALKR2_ARATH Probable aldo-keto reductase 2 OS=Arabidopsis thaliana GN=AGD2 PE=2 SV=1	3	0,087	0,798201798	1853,42	0,722
Q9SG77 PME24_ARATH Putative pectinesterase/pectinesterase inhibitor 24 OS=Arabidopsis thaliana GN=PME24 PE=3 SV=1	2	0,081	0,799200799	1855,74	0,722
O49543 MNIF1_ARATH Cysteine desulfurase, mitochondrial OS=Arabidopsis thaliana GN=NIFS1 PE=1 SV=1	3	0,076	0,803196803	1865,02	0,722
Q9LZV9 NLTPA_ARATH Non-specific lipid-transfer protein 10 OS=Arabidopsis thaliana GN=LTP10 PE=3 SV=1	2	0,071	0,797202797	1851,1	0,722
Q9LKA3 MDHM2_ARATH Malate dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=At3g15020 PE=1 SV=1	2	0,065	0,794205794	1844,15	0,722
Q8LPJ7 RS262_ARATH 40S ribosomal protein S26-2 OS=Arabidopsis thaliana GN=RPS26B PE=2 SV=2	3	0,059	0,794205794	1844,15	0,722
Q9LZG0 ADK2_ARATH Adenosine kinase 2 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1	5	0,055	0,804195804	1867,34	0,722
P49205 RS171_ARATH 40S ribosomal protein S17-1 OS=Arabidopsis thaliana GN=RPS17A PE=2 SV=3	6	0,048	0,796203796	1848,79	0,722
F417I0 ALAT1_ARATH Alanine aminotransferase 1, mitochondrial OS=Arabidopsis thaliana GN=ALAAT1 PE=1 SV=1	12	-0,039	0,796203796	1848,79	0,722
P25858 G3PC1_ARATH Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2	19	-0,038	0,795204795	1846,47	0,722
Q56Z27 PLST4_ARATH Plastidic glucose transporter 4 OS=Arabidopsis thaliana GN=At5g16150 PE=1 SV=2	1	-0,159	0,795204795	1846,47	0,723
Q38942 RAE1_ARATH Protein RAE1 OS=Arabidopsis thaliana GN=RAE1 PE=1 SV=2	1	0,148	0,806193806	1871,98	0,723
Q43127 GLNA2_ARATH Glutamine synthetase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLN2 PE=1 SV=1	3	-0,065	0,806193806	1871,98	0,723
Q9LDA4 PER38_ARATH Peroxidase 38 OS=Arabidopsis thaliana GN=PER38 PE=3 SV=1	2	-0,073	0,806193806	1871,98	0,724
Q9SN86 MDHP_ARATH Malate dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=At3g47520 PE=1 SV=1	13	-0,041	0,807192807	1874,3	0,724
P25696 ENO2_ARATH Bifunctional enolase 2/transcriptional activator OS=Arabidopsis thaliana GN=ENO2 PE=1 SV=1	18	-0,033	0,809190809	1878,94	0,725
Q0WML1 Q0WML1_ARATH ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g08947 PE=2 SV=1	1	0,145	0,813186813	1888,22	0,726
Q9SQR4 ADRC3_ARATH NADPH-dependent aldehyde reductase-like protein, chloroplastic OS=Arabidopsis thaliana GN=At3g03980 PE=3 SV=1	1	-0,14	0,812187812	1885,9	0,726
Q9C550 LEU12_ARATH 2-isopropylmalate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=IPMS2 PE=1 SV=1	1	0,136	0,817182817	1897,5	0,726
O81488 ALFL4_ARATH PHD finger protein ALFIN-LIKE 4 OS=Arabidopsis thaliana GN=AL4 PE=1 SV=2	1	-0,099	0,815184815	1892,86	0,726
Q9M2Z4 MSBP2_ARATH Membrane steroid-binding protein 2 OS=Arabidopsis thaliana GN=MSBP2 PE=1 SV=1	2	-0,097	0,812187812	1885,9	0,726
Q8RW90 FAH_ARATH Fumarylacetoacetase OS=Arabidopsis thaliana GN=FAH PE=1 SV=1	1	0,088	0,818181818	1899,82	0,726
Q9FKV6 Q9FKV6_ARATH Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=At5g44320 PE=2 SV=1	2	0,075	0,817182817	1897,5	0,726
Q9SGE9 SYFB_ARATH Phenylalanine--tRNA ligase beta subunit, cytoplasmic OS=Arabidopsis thaliana GN=At1g72550 PE=2 SV=1	2	0,072	0,811188811	1883,58	0,726
O65378 ACCO3_ARATH 1-aminocyclopropane-1-carboxylate oxidase 3 OS=Arabidopsis thaliana GN=At1g12010 PE=2 SV=1	3	0,071	0,817182817	1897,5	0,726
Q9FFP6 Q9FFP6_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=MBK5.16 PE=3 SV=1	4	0,069	0,818181818	1899,82	0,726

P49689 RS30_ARATH 40S ribosomal protein S30 OS=Arabidopsis thaliana GN=RPS30A PE=3 SV=3	2	0,069	0,819180819	1902,14	0,726
Q8LA13 RH11_ARATH DEAD-box ATP-dependent RNA helicase 11 OS=Arabidopsis thaliana GN=RH11 PE=1 SV=1	3	-0,066	0,81018981	1881,26	0,726
A0A1P8AZN3 A0A1P8AZN3_ARATH Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g32520 PE=4 SV=1	5	-0,052	0,818181818	1899,82	0,726
P27323 HS901_ARATH Heat shock protein 90-1 OS=Arabidopsis thaliana GN=HSP90-1 PE=1 SV=3	5	-0,051	0,811188811	1883,58	0,726
Q9LUV2 POP3_ARATH Stress-response A/B barrel domain-containing protein HS1 OS=Arabidopsis thaliana GN=HS1 PE=1 SV=1	6	0,042	0,813186813	1888,22	0,726
Q9M1R2 SYPC_ARATH Proline--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At3g62120 PE=1 SV=1	9	0,041	0,812187812	1885,9	0,726
Q8S4Y1 THIC1_ARATH Acetyl-CoA acetyltransferase, cytosolic 1 OS=Arabidopsis thaliana GN=AAT1 PE=1 SV=1	13	-0,036	0,814185814	1890,54	0,726
P29197 CH60A_ARATH Chaperonin CPN60, mitochondrial OS=Arabidopsis thaliana GN=CPN60 PE=1 SV=2	10	0,035	0,816183816	1895,18	0,726
Q8VXY9 UAH_ARATH Ureidoglycolate hydrolase OS=Arabidopsis thaliana GN=UAH PE=1 SV=1	2	-0,108	0,813186813	1888,22	0,727
Q9FRL3 ERDL6_ARATH Sugar transporter ERD6-like 6 OS=Arabidopsis thaliana GN=At1g75220 PE=1 SV=1	1	0,093	0,814185814	1890,54	0,727
Q9LZD3 E70A1_ARATH Exocyst complex component EXO70A1 OS=Arabidopsis thaliana GN=EXO70A1 PE=1 SV=1	2	0,087	0,816183816	1895,18	0,727
Q96290 MSSP1_ARATH Monosaccharide-sensing protein 1 OS=Arabidopsis thaliana GN=MSSP1 PE=1 SV=2	2	-0,077	0,812187812	1885,9	0,727
Q9FE58 RL223_ARATH 60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1	2	-0,069	0,815184815	1892,86	0,727
P52901 ODPA1_ARATH Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=E1 ALPHA PE=1 SV=2	3	0,069	0,818181818	1899,82	0,727
O64768 O64768_ARATH Kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing protein OS=Arabidopsis thaliana GN=At2g35050 PE=:	1	-0,068	0,817182817	1897,5	0,727
O22791 O22791_ARATH Putative RNA-binding protein OS=Arabidopsis thaliana GN=At2g33410 PE=2 SV=1	3	0,066	0,817182817	1897,5	0,727
P40941 ADT2_ARATH ADP, ATP carrier protein 2, mitochondrial OS=Arabidopsis thaliana GN=AAC2 PE=1 SV=2	4	-0,052	0,815184815	1892,86	0,727
P83291 NB5R2_ARATH NADH-cytochrome b5 reductase-like protein OS=Arabidopsis thaliana GN=CBR2 PE=1 SV=2	9	0,047	0,82017982	1904,46	0,727
O23715 PSA3_ARATH Proteasome subunit alpha type-3 OS=Arabidopsis thaliana GN=PAG1 PE=1 SV=2	8	-0,034	0,816183816	1895,18	0,727
Q9SRD4 IGMT5_ARATH Indole glucosinolate O-methyltransferase 5 OS=Arabidopsis thaliana GN=IGMT5 PE=2 SV=1	7	-0,045	0,822177822	1909,1	0,728
Q9SYG4 UBP1A_ARATH Oligouridylate-binding protein 1A OS=Arabidopsis thaliana GN=UBP1A PE=1 SV=1	2	-0,089	0,824175824	1913,74	0,729
P29976 AROF_ARATH Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2	11	-0,039	0,824175824	1913,74	0,729
Q9SJT9 COPA2_ARATH Coatomer subunit alpha-2 OS=Arabidopsis thaliana GN=At2g21390 PE=2 SV=1	8	-0,037	0,823176823	1911,42	0,729
P46248 AAT5_ARATH Aspartate aminotransferase, chloroplastic OS=Arabidopsis thaliana GN=ASP5 PE=1 SV=2	15	0,035	0,823176823	1911,42	0,729
P57741 PFD3_ARATH Probable prefoldin subunit 3 OS=Arabidopsis thaliana GN=At5g49510 PE=1 SV=1	1	0,094	0,827172827	1920,7	0,73
Q8LF05 RBL19_ARATH Rhomboid-like protein 19 OS=Arabidopsis thaliana GN=RBL19 PE=2 SV=1	1	-0,093	0,827172827	1920,7	0,73
F419G7 F419G7_ARATH TLR4 regulator/MIR-interacting MSAP protein OS=Arabidopsis thaliana GN=At1g42480 PE=4 SV=1	1	-0,092	0,826173826	1918,38	0,73
Q42605 UGE1_ARATH Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 OS=Arabidopsis thaliana GN=UGE1 PE=1 SV=2	1	0,09	0,829170829	1925,33	0,73
Q93ZV7 LA1_ARATH La protein 1 OS=Arabidopsis thaliana GN=LA1 PE=1 SV=1	1	-0,086	0,83016983	1927,65	0,73
Q3EBM1 Q3EBM1_ARATH Transcriptional activator (DUF662) OS=Arabidopsis thaliana GN=At2g36410 PE=2 SV=1	1	0,08	0,827172827	1920,7	0,73
Q9LLC1 BCCP2_ARATH Biotin carboxyl carrier protein of acetyl-CoA carboxylase 2, chloroplastic OS=Arabidopsis thaliana GN=BCCP2 PE=1 SV=1	2	0,065	0,828171828	1923,01	0,73
Q9LSA3 RL303_ARATH 60S ribosomal protein L30-3 OS=Arabidopsis thaliana GN=RPL30C PE=3 SV=1	3	0,058	0,826173826	1918,38	0,73
Q9SZB3 Q9SZB3_ARATH NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=FLDH PE=2 SV=1	4	0,049	0,83016983	1927,65	0,73
Q9FJN8 RAA4A_ARATH Ras-related protein RABA4a OS=Arabidopsis thaliana GN=RABA4A PE=1 SV=1	3	-0,047	0,829170829	1925,33	0,73
Q9LXU5 Q9LXU5_ARATH Leucine-rich repeat (LRR) family protein OS=Arabidopsis thaliana GN=At5g12940 PE=2 SV=1	6	0,044	0,828171828	1923,01	0,73
POCJ46 ACT1_ARATH Actin-1 OS=Arabidopsis thaliana GN=ACT1 PE=1 SV=1	7	0,034	0,825174825	1916,06	0,73
Q82662 SUCB_ARATH Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Arabidopsis thaliana GN=At2g20420 PE=1 SV=1	13	0,03	0,828171828	1923,01	0,73
F41IU4 AIR9_ARATH 187-kDa microtubule-associated protein AIR9 OS=Arabidopsis thaliana GN=AIR9 PE=1 SV=1	1	0,118	0,833166833	1934,61	0,731
Q6NLQ6 CDPKW_ARATH Calcium-dependent protein kinase 32 OS=Arabidopsis thaliana GN=CPK32 PE=1 SV=1	1	0,103	0,833166833	1934,61	0,731
Q96253 ATP5E_ARATH ATP synthase subunit epsilon, mitochondrial OS=Arabidopsis thaliana GN=At1g51650 PE=1 SV=3	1	-0,086	0,832167832	1932,29	0,731
Q53YF3 SPC3B_ARATH Signal peptidase complex subunit 3B OS=Arabidopsis thaliana GN=At5g27430 PE=2 SV=1	1	0,085	0,831168831	1929,97	0,731
Q82656 PTP1_ARATH Protein-tyrosine-phosphatase PTP1 OS=Arabidopsis thaliana GN=PTP1 PE=1 SV=1	2	-0,074	0,83016983	1927,65	0,731
A8MS32 A8MS32_ARATH AT5G64130 protein OS=Arabidopsis thaliana GN=MHJ24.11 PE=1 SV=1	1	0,07	0,827172827	1920,7	0,731
O65719 HSP7C_ARATH Heat shock 70 kDa protein 3 OS=Arabidopsis thaliana GN=HSP70-3 PE=1 SV=1	2	0,067	0,832167832	1932,29	0,731
Q8LAS8 SFGH_ARATH S-formylglutathione hydrolase OS=Arabidopsis thaliana GN=SFGH PE=1 SV=2	5	-0,053	0,832167832	1932,29	0,731
Q9SEI4 PRS6B_ARATH 26S proteasome regulatory subunit 6B homolog OS=Arabidopsis thaliana GN=RPT3 PE=1 SV=1	6	-0,044	0,832167832	1932,29	0,731
P19456 PMA2_ARATH ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	5	0,039	0,833166833	1934,61	0,731
Q8RWN5 RZ1C_ARATH Glycine-rich RNA-binding protein RZ1C OS=Arabidopsis thaliana GN=RZ1C PE=1 SV=1	1	-0,092	0,837162837	1943,89	0,732
Q42029 PSBP1_ARATH Oxygen-evolving enhancer protein 2-1, chloroplastic OS=Arabidopsis thaliana GN=PSBP1 PE=1 SV=2	1	0,085	0,836163836	1941,57	0,732
P51419 RL273_ARATH 60S ribosomal protein L27-3 OS=Arabidopsis thaliana GN=RPL27C PE=2 SV=2	1	0,069	0,836163836	1941,57	0,732
Q9FFG3 Q9FFG3_ARATH Outer membrane OMP85 family protein OS=Arabidopsis thaliana GN=MOP10.6 PE=2 SV=1	2	0,069	0,836163836	1941,57	0,732

Q9FNC9 TOM92_ARATH Mitochondrial import receptor subunit TOM9-2 OS=Arabidopsis thaliana GN=TOM9-2 PE=1 SV=3	2	0,064	0,835164835	1939,25	0,732
P82873 TO202_ARATH Mitochondrial import receptor subunit TOM20-2 OS=Arabidopsis thaliana GN=TOM20-2 PE=1 SV=2	3	-0,05	0,837162837	1943,89	0,732
Q38842 Q38842_ARATH ATOZ11 protein OS=Arabidopsis thaliana GN=ATOZ11 PE=2 SV=1	3	-0,049	0,837162837	1943,89	0,732
Q42525 HXX1_ARATH Hexokinase-1 OS=Arabidopsis thaliana GN=HXX1 PE=1 SV=2	7	0,044	0,836163836	1941,57	0,732
Q9FWA3 6GPD3_ARATH 6-phosphogluconate dehydrogenase, decarboxylating 3 OS=Arabidopsis thaliana GN=At3g02360 PE=2 SV=1	14	-0,031	0,838161838	1946,21	0,732
Q22203 C98A3_ARATH Cytochrome P450 98A3 OS=Arabidopsis thaliana GN=CYP98A3 PE=1 SV=1	3	-0,059	0,84015984	1950,85	0,733
Q9SY33 PER7_ARATH Peroxidase 7 OS=Arabidopsis thaliana GN=PER7 PE=2 SV=1	3	0,058	0,84015984	1950,85	0,733
Q8L7R2 KHSE_ARATH Homoserine kinase OS=Arabidopsis thaliana GN=HSK PE=1 SV=1	2	0,057	0,836163836	1941,57	0,733
Q9M8R4 DJ1D_ARATH Protein DJ-1 homolog D OS=Arabidopsis thaliana GN=DJ1D PE=1 SV=1	1	0,098	0,84015984	1950,85	0,734
Q9LUS7 RLF23_ARATH Rapid alkalization factor 23 OS=Arabidopsis thaliana GN=RALF23 PE=1 SV=1	1	0,085	0,841158841	1953,17	0,734
Q9M885 RS72_ARATH 40S ribosomal protein S7-2 OS=Arabidopsis thaliana GN=RPS7B PE=2 SV=1	3	0,057	0,842157842	1955,49	0,734
Q9STT2 VPS29_ARATH Vacuolar protein sorting-associated protein 29 OS=Arabidopsis thaliana GN=VPS29 PE=2 SV=1	2	-0,053	0,844155844	1960,13	0,734
Q9FVC8 DAPA2_ARATH 4-hydroxy-tetrahydridipicolinate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=DHGPS2 PE=1 SV=2	1	0,134	0,846153846	1964,77	0,735
Q9L2Q0 CX5C2_ARATH Cytochrome c oxidase subunit 5C-2 OS=Arabidopsis thaliana GN=At3g62400 PE=3 SV=1	1	0,128	0,844155844	1960,13	0,735
F4JLY4 F4JLY4_ARATH Cytochrome P450, family 706, subfamily A, polypeptide 1 OS=Arabidopsis thaliana GN=CYP706A1 PE=3 SV=1	1	-0,113	0,845154845	1962,45	0,735
O80915 PR1B4_ARATH PRA1 family protein B4 OS=Arabidopsis thaliana GN=PRA1B4 PE=1 SV=1	1	0,092	0,846153846	1964,77	0,735
B4F7N8 B4F7N8_ARATH At5g18420 OS=Arabidopsis thaliana GN=At5g18420 PE=2 SV=1	1	-0,086	0,843156843	1957,81	0,735
Q8H124 Y2446_ARATH reversed Uncharacterized protein At2g34460, chloroplastic OS=Arabidopsis thaliana GN=At2g34460 PE=1 SV=1	1	-0,067	0,843156843	1957,81	0,735
Q9SKI2 VPS2A_ARATH Vacuolar protein sorting-associated protein 2 homolog 1 OS=Arabidopsis thaliana GN=VPS2.1 PE=1 SV=2	2	0,066	0,844155844	1960,13	0,735
Q8RU07 Q8RU07_ARATH EMBRYO DEFECTIVE 3147 OS=Arabidopsis thaliana GN=EMB3147 PE=2 SV=1	4	0,041	0,844155844	1960,13	0,735
Q93ZN2 ALKR4_ARATH Probable aldo-keto reductase 4 OS=Arabidopsis thaliana GN=At1g60710 PE=2 SV=1	5	-0,037	0,847152847	1967,09	0,735
Q9LQF2 CINV1_ARATH Alkaline/neutral invertase CINV1 OS=Arabidopsis thaliana GN=CINV1 PE=1 SV=1	6	0,035	0,848151848	1969,41	0,735
Q8LCG7 NFYC2_ARATH Nuclear transcription factor Y subunit C-2 OS=Arabidopsis thaliana GN=NFYC2 PE=1 SV=2	1	0,086	0,846153846	1964,77	0,736
Q9M2Q4 NT102_ARATH reversed RNA cytidine acetyltransferase 2 OS=Arabidopsis thaliana GN=At3g57940 PE=2 SV=2	1	-0,076	0,852147852	1978,69	0,736
Q9LYT7 LEUD2_ARATH 3-isopropylmalate dehydratase small subunit 2 OS=Arabidopsis thaliana GN=IPM11 PE=1 SV=1	1	0,072	0,849150849	1971,73	0,736
P42814 RNS2_ARATH Ribonuclease 2 OS=Arabidopsis thaliana GN=RNS2 PE=2 SV=1	1	0,072	0,852147852	1978,69	0,736
O49686 PYR1_ARATH Abscissic acid receptor PYR1 OS=Arabidopsis thaliana GN=PYR1 PE=1 SV=1	2	-0,071	0,848151848	1969,41	0,736
O49513 RAA1E_ARATH Ras-related protein RABA1e OS=Arabidopsis thaliana GN=RABA1E PE=2 SV=1	1	0,068	0,847152847	1967,09	0,736
Q9ZV85 GGH3_ARATH Probable gamma-glutamyl hydrolase 3 OS=Arabidopsis thaliana GN=GGH3 PE=2 SV=1	3	-0,051	0,848151848	1969,41	0,736
Q9M292 Q9M292_ARATH Nicalin OS=Arabidopsis thaliana GN=T22K7_10 PE=2 SV=1	7	-0,042	0,853146853	1981,01	0,736
Q94C74 GLYM2_ARATH Serine hydroxymethyltransferase 2, mitochondrial OS=Arabidopsis thaliana GN=SHM2 PE=1 SV=2	5	0,041	0,851148851	1976,37	0,736
Q9FY99 G6PD2_ARATH Glucose-6-phosphate 1-dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=At5g13110 PE=1 SV=2	3	0,038	0,85014985	1974,05	0,736
Q9FI56 CLPC1_ARATH Chaperone protein ClpC1, chloroplastic OS=Arabidopsis thaliana GN=CLPC1 PE=1 SV=1	14	0,032	0,851148851	1976,37	0,736
P19456 PMA2_ARATH ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	12	0,03	0,851148851	1976,37	0,736
Q9ZVJ4 CYP22_ARATH Peptidyl-prolyl cis-trans isomerase CYP22 OS=Arabidopsis thaliana GN=CYP22 PE=2 SV=1	1	0,124	0,851148851	1976,37	0,737
Q9M1X0 RRFC_ARATH Ribosome-recycling factor, chloroplastic OS=Arabidopsis thaliana GN=RRF PE=2 SV=2	1	-0,107	0,859140859	1994,93	0,737
Q9LTH9 ZIP2_ARATH Zinc transporter 2 OS=Arabidopsis thaliana GN=ZIP2 PE=2 SV=1	1	-0,075	0,85014985	1974,05	0,737
Q84WJ9 PP1R7_ARATH Protein phosphatase 1 regulatory inhibitor subunit PPP1R7 homolog OS=Arabidopsis thaliana GN=At5g19680 PE=1 SV=1	1	0,075	0,857142857	1990,29	0,737
F4I3B3 RB47A_ARATH Polyadenylate-binding protein RBP47A OS=Arabidopsis thaliana GN=RBP47A PE=2 SV=1	1	0,072	0,856143856	1987,97	0,737
Q9LUC6 C7A14_ARATH Cytochrome P450 72A14 OS=Arabidopsis thaliana GN=CYP72A14 PE=2 SV=1	2	-0,068	0,855144855	1985,65	0,737
Q8GRX2 Q8GRX2_ARATH Eukaryotic translation initiation factor 3 subunit J OS=Arabidopsis thaliana GN=At5g37475 PE=1 SV=1	2	-0,066	0,854145854	1983,33	0,737
Q9C787 Q9C787_ARATH Uncharacterized protein At1g69510 OS=Arabidopsis thaliana GN=At1g69510 PE=1 SV=1	2	0,058	0,851148851	1976,37	0,737
F4KHD5 F4KHD5_ARATH A-kinase anchor-like protein OS=Arabidopsis thaliana GN=MPO12.160 PE=1 SV=1	2	-0,051	0,853146853	1981,01	0,737
F4JXW9 F4JXW9_ARATH Catalytics OS=Arabidopsis thaliana GN=At5g11560 PE=4 SV=1	6	0,041	0,855144855	1985,65	0,737
Q944Q6 Q944Q6_ARATH Expressed protein OS=Arabidopsis thaliana GN=At2g14835 PE=1 SV=1	1	-0,079	0,858141858	1992,61	0,738
O81098 RPB5A_ARATH DNA-directed RNA polymerases II and IV subunit 5A OS=Arabidopsis thaliana GN=NRPB5A PE=1 SV=1	1	0,076	0,856143856	1987,97	0,738
Q9LIL4 P24B3_ARATH Transmembrane emp24 domain-containing protein p24beta3 OS=Arabidopsis thaliana GN=At3g22845 PE=2 SV=1	1	-0,076	0,858141858	1992,61	0,738
O82221 RUXG_ARATH Probable small nuclear ribonucleoprotein G OS=Arabidopsis thaliana GN=At2g23930 PE=3 SV=1	2	-0,065	0,859140859	1994,93	0,738
Q9C5R8 BAS1B_ARATH 2-Cys peroxiredoxin BAS1-like, chloroplastic OS=Arabidopsis thaliana GN=At5g06290 PE=2 SV=3	2	-0,057	0,857142857	1990,29	0,738
Q9C8F1 IF5Y_ARATH Probable eukaryotic translation initiation factor 5-1 OS=Arabidopsis thaliana GN=At1g36730 PE=2 SV=1	2	0,055	0,857142857	1990,29	0,738
Q9FFQ4 FLS5_ARATH Probable flavonol synthase 5 OS=Arabidopsis thaliana GN=FLS5 PE=2 SV=1	3	0,051	0,859140859	1994,93	0,738

Q8LBZ7 SDHB1_ARATH Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 1, mitochondrial OS=Arabidopsis thaliana GN=SDH2-1 PE=1 SV=2	4	0,043	0,859140859	1994,93	0,738
O04499 PMG1_ARATH 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=PGM1 PE=2 SV=3	6	0,035	0,855144855	1985,65	0,738
Q9SI16 PER15_ARATH Peroxidase 15 OS=Arabidopsis thaliana GN=PER15 PE=2 SV=1	1	-0,106	0,862137862	2001,88	0,739
Q39247 2ABB_ARATH Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta isoform OS=Arabidopsis thaliana GN=PP2AB2 PE=1 SV	2	-0,064	0,861138861	1999,56	0,739
Q9ZWA8 FLA9_ARATH Fasciclin-like arabinogalactan protein 9 OS=Arabidopsis thaliana GN=FLA9 PE=1 SV=1	2	0,054	0,861138861	1999,56	0,739
Q9SUA1 Q9SUA1_ARATH DEK domain-containing chromatin associated protein OS=Arabidopsis thaliana GN=DEK3 PE=1 SV=1	3	0,039	0,863136863	2004,2	0,739
Q8RWY6 CLASP_ARATH CLIP-associated protein OS=Arabidopsis thaliana GN=CLASP PE=1 SV=1	1	-0,08	0,863136863	2004,2	0,74
Q9ZW85 LEUD3_ARATH 3-isopropylmalate dehydratase small subunit 3 OS=Arabidopsis thaliana GN=At2g43090 PE=1 SV=1	4	0,049	0,866133866	2011,16	0,74
Q949M9 Q949M9_ARATH ATPase ASNA1 homolog OS=Arabidopsis thaliana GN=At1g01910 PE=1 SV=1	4	0,039	0,866133866	2011,16	0,74
Q93V74 Q93V74_ARATH At4g34180/F28A23_60 OS=Arabidopsis thaliana GN=At4g34180 PE=2 SV=1	7	-0,038	0,865134865	2008,84	0,74
Q94F20 Q94F20_ARATH At5g25460 OS=Arabidopsis thaliana GN=DGR2 PE=2 SV=1	9	0,032	0,863136863	2004,2	0,74
Q93Z66 KPRS3_ARATH Ribose-phosphate pyrophosphokinase 3, chloroplastic OS=Arabidopsis thaliana GN=PRS3 PE=2 SV=1	1	0,1	0,871128871	2022,76	0,741
Q42538 SAT5_ARATH Serine acetyltransferase 5 OS=Arabidopsis thaliana GN=SAT5 PE=1 SV=1	1	0,093	0,866133866	2011,16	0,741
Q9FDZ2 Q9FDZ2_ARATH reversed At1g25025 OS=Arabidopsis thaliana GN=F4F7.40 PE=2 SV=1	1	0,08	0,868131868	2015,8	0,741
Q9SRL6 Q9SRL6_ARATH Outer membrane OMP85 family protein OS=Arabidopsis thaliana GN=F9F8.12 PE=1 SV=1	1	0,077	0,87012987	2020,44	0,741
Q84WK5 GID8_ARATH Protein GID8 homolog OS=Arabidopsis thaliana GN=GID8 PE=1 SV=1	2	0,06	0,868131868	2015,8	0,741
P53780 METC_ARATH Cystathionine beta-lyase, chloroplastic OS=Arabidopsis thaliana GN=At3g57050 PE=1 SV=1	2	-0,045	0,869130869	2018,12	0,741
P41377 IF4A2_ARATH Eukaryotic initiation factor 4A-2 OS=Arabidopsis thaliana GN=TIF4A-2 PE=1 SV=1	3	-0,044	0,866133866	2011,16	0,741
Q9LPG6 RHM2_ARATH Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RH	5	0,038	0,865134865	2008,84	0,741
Q56WN1 GLN11_ARATH Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2	5	0,035	0,872127872	2025,08	0,741
P50700 OSL3_ARATH Osmotin-like protein OSM34 OS=Arabidopsis thaliana GN=OSM34 PE=2 SV=2	4	0,029	0,871128871	2022,76	0,741
Q84K16 AP1G1_ARATH AP-1 complex subunit gamma-1 OS=Arabidopsis thaliana GN=GAMMA-ADR PE=1 SV=1	1	-0,076	0,87012987	2020,44	0,742
Q9FM97 Q9FM97_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=MCD7.8 PE=2 SV=1	1	-0,076	0,874125874	2029,72	0,742
Q9M2U2 TECR_ARATH Very-long-chain enoyl-CoA reductase OS=Arabidopsis thaliana GN=ECR PE=1 SV=1	1	-0,07	0,872127872	2025,08	0,742
Q84K82 Q84K82_ARATH 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein OS=Arabidopsis thaliana GN=At5g20400 PE=2 SV=1	1	0,068	0,871128871	2022,76	0,742
Q94AU3 Q94AU3_ARATH reversed Expressed protein OS=Arabidopsis thaliana GN=At2g21385 PE=2 SV=1	1	-0,067	0,871128871	2022,76	0,742
POCJ46 ACT1_ARATH Actin-1 OS=Arabidopsis thaliana GN=ACT1 PE=1 SV=1	4	0,035	0,869130869	2018,12	0,742
Q9M0D5 Q9M0D5_ARATH AT4g29480/F17A13_300 OS=Arabidopsis thaliana GN=At4g29480 PE=2 SV=1	2	-0,035	0,872127872	2025,08	0,742
Q41969 IF2B_ARATH Eukaryotic translation initiation factor 2 subunit beta OS=Arabidopsis thaliana GN=EIF2B PE=1 SV=3	5	0,032	0,87012987	2020,44	0,742
Q9SFB1 Q9SFB1_ARATH F17A17.37 protein OS=Arabidopsis thaliana GN=F17A17.37 PE=2 SV=1	7	0,029	0,874125874	2029,72	0,742
Q42560 ACO1_ARATH Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2	8	0,028	0,868131868	2015,8	0,742
Q7DLR9 PSB4_ARATH Proteasome subunit beta type-4 OS=Arabidopsis thaliana GN=PBG1 PE=1 SV=2	6	-0,032	0,874125874	2029,72	0,743
Q6NPM5 ATS3B_ARATH Embryo-specific protein ATS3B OS=Arabidopsis thaliana GN=ATS3B PE=1 SV=1	1	0,071	0,88011988	2043,64	0,744
Q9XI87 Q9XI87_ARATH At1g14000 OS=Arabidopsis thaliana GN=VH1-interacting kinase PE=2 SV=1	2	-0,068	0,878121878	2039	0,744
Q67YA0 Q67YA0_ARATH reversed RNA-binding (RRM/RBD/RNP motifs) family protein OS=Arabidopsis thaliana GN=At5g03495 PE=2 SV=1	1	0,067	0,877122877	2036,68	0,744
F4HY32 F4HY32_ARATH Calcium-binding EF hand family protein OS=Arabidopsis thaliana GN=At1g21630 PE=1 SV=1	1	-0,059	0,879120879	2041,32	0,744
Q39251 ADF2_ARATH Actin-depolymerizing factor 2 OS=Arabidopsis thaliana GN=ADF2 PE=1 SV=1	1	-0,053	0,877122877	2036,68	0,744
Q5HZ00 SPS3_ARATH Solanesyl diphosphate synthase 3, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=SPS3 PE=1 SV=1	2	0,048	0,876123876	2034,36	0,744
O80944 AKRC8_ARATH Aldo-keto reductase family 4 member C8 OS=Arabidopsis thaliana GN=AKR4C8 PE=1 SV=2	3	-0,04	0,879120879	2041,32	0,744
Q42262 R53A2_ARATH 40S ribosomal protein S3a-2 OS=Arabidopsis thaliana GN=RPS3AB PE=2 SV=3	6	-0,032	0,879120879	2041,32	0,744
Q9FZA2 AGP31_ARATH Non-classical arabinogalactan protein 31 OS=Arabidopsis thaliana GN=AGP31 PE=1 SV=1	5	0,03	0,877122877	2036,68	0,744
P39207 NDK1_ARATH Nucleoside diphosphate kinase 1 OS=Arabidopsis thaliana GN=NDK1 PE=1 SV=1	8	0,028	0,88011988	2043,64	0,744
Q8VXX9 BETL1_ARATH Bet1-like protein At4g14600 OS=Arabidopsis thaliana GN=At4g14600 PE=2 SV=1	1	0,075	0,879120879	2041,32	0,745
Q9LW57 PAP6_ARATH Plastid-lipid-associated protein 6, chloroplastic OS=Arabidopsis thaliana GN=PAP6 PE=1 SV=1	1	0,073	0,881118881	2045,96	0,745
Q9C505 IF5A3_ARATH Eukaryotic translation initiation factor 5A-3 OS=Arabidopsis thaliana GN=ELF5A-3 PE=2 SV=1	2	-0,053	0,882117882	2048,28	0,745
Q8LG11 Q8LG11_ARATH Proline-rich cell wall protein-like OS=Arabidopsis thaliana GN=At5g53330 PE=1 SV=1	1	0,061	0,883116883	2050,6	0,746
Q9C5G6 Q9C5G6_ARATH Peptidase C15, pyroglutamyl peptidase I-like protein OS=Arabidopsis thaliana GN=At1g23430 PE=2 SV=1	2	0,048	0,883116883	2050,6	0,746
P42644 14333_ARATH 14-3-3-like protein GF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2	5	0,031	0,889110889	2064,52	0,746
O49213 FCL1_ARATH GDP-L-fucose synthase 1 OS=Arabidopsis thaliana GN=GER1 PE=1 SV=3	1	0,084	0,885114885	2055,24	0,747
Q9ST43 PH1_ARATH Pleckstrin homology domain-containing protein 1 OS=Arabidopsis thaliana GN=PH1 PE=2 SV=2	1	0,084	0,889110889	2064,52	0,747
Q42093 AB2C_ARATH ABC transporter C family member 2 OS=Arabidopsis thaliana GN=ABCC2 PE=1 SV=2	1	0,062	0,889110889	2064,52	0,747

Q9FKS5 CYC1B_ARATH Cytochrome c1 2, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC12 PE=1 SV=1	1	0,061	0,885114885	2055,24	0,747
Q9ZUU3 PP190_ARATH Pentatricopeptide repeat-containing protein At2g37230 OS=Arabidopsis thaliana GN=At2g37230 PE=2 SV=1	1	-0,061	0,886113886	2057,56	0,747
Q9C9Z2 RER3_ARATH Protein RETICULATA-RELATED 3, chloroplastic OS=Arabidopsis thaliana GN=RER3 PE=1 SV=1	1	-0,061	0,887112887	2059,88	0,747
Q9SIY7 PR1B2_ARATH PRA1 family protein B2 OS=Arabidopsis thaliana GN=PRA1B2 PE=1 SV=1	2	0,055	0,887112887	2059,88	0,747
Q84K47 AB2A_ARATH ABC transporter A family member 2 OS=Arabidopsis thaliana GN=ABCA2 PE=2 SV=1	2	0,052	0,888111888	2062,2	0,747
Q23290 RL36A_ARATH 60S ribosomal protein L36a OS=Arabidopsis thaliana GN=RPL36AA PE=3 SV=3	2	-0,043	0,886113886	2057,56	0,747
Q9FNC4 Q9FNC4_ARATH HAD superfamily, subfamily IIIB acid phosphatase OS=Arabidopsis thaliana GN=MRH10.13 PE=2 SV=1	2	0,036	0,889110889	2064,52	0,747
O81146 PSA6A_ARATH Proteasome subunit alpha type-6-A OS=Arabidopsis thaliana GN=PAA1 PE=1 SV=2	4	-0,031	0,888111888	2062,2	0,747
Q38950 2AAB_ARATH Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Arabidopsis thaliana GN=PP2AA2 PE=1 SV	5	-0,031	0,889110889	2064,52	0,747
Q9SVG4 RETOL_ARATH Berberine bridge enzyme-like 19 OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2	7	-0,028	0,887112887	2059,88	0,747
Q93Z16 RPN2_ARATH Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Arabidopsis thaliana GN=RPN2 PE=1 SV=1	13	-0,025	0,886113886	2057,56	0,747
O22899 PRP43_ARATH Probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3 OS=Arabidopsis thaliana GN=At2g47250 PE=2 SV=1	1	0,078	0,896103896	2080,75	0,748
P92980 APR3_ARATH 5'-adenylsulfate reductase 3, chloroplastic OS=Arabidopsis thaliana GN=APR3 PE=2 SV=2	1	-0,07	0,9000999	2090,03	0,748
Q8S528 AL2B7_ARATH Aldehyde dehydrogenase family 2 member B7, mitochondrial OS=Arabidopsis thaliana GN=ALDH2B7 PE=1 SV=2	1	0,069	0,894105894	2076,11	0,748
F4K9G5 F4K9G5_ARATH Tautomerase/MIF superfamily protein OS=Arabidopsis thaliana GN=At5g01650 PE=4 SV=1	1	0,061	0,9000999	2090,03	0,748
P29515 TBB7_ARATH Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	1	0,059	0,893106893	2073,79	0,748
O22100 O22100_ARATH ATMRK1 OS=Arabidopsis thaliana GN=ATMRK1 PE=2 SV=1	1	0,059	0,899100899	2087,71	0,748
Q9SEE9 SR45_ARATH Serine/arginine-rich splicing factor SR45 OS=Arabidopsis thaliana GN=SR45 PE=1 SV=1	1	-0,058	0,893106893	2073,79	0,748
Q9SIQ8 Q9SIQ8_ARATH AT2G31490 protein OS=Arabidopsis thaliana GN=At2g31490 PE=2 SV=1	1	0,058	0,893106893	2073,79	0,748
O82352 RTNLE_ARATH Reticulon-like protein B5 OS=Arabidopsis thaliana GN=RTNLB5 PE=1 SV=1	1	0,054	0,894105894	2076,11	0,748
P24636 TBB4_ARATH Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2	1	0,052	0,907092907	2106,27	0,748
Q8VYI0 LSM8_ARATH Sm-like protein LSM8 OS=Arabidopsis thaliana GN=LSM8 PE=1 SV=1	2	-0,049	0,892107892	2071,47	0,748
F4I600 F4I600_ARATH Vacuolar ATP synthase catalytic subunit-related / V-ATPase-related / vacuolar proton pump-like protein OS=Arabidopsis thaliana	1	0,048	0,897102897	2083,07	0,748
Q9SZN7 HIP26_ARATH Heavy metal-associated isoprenylated plant protein 26 OS=Arabidopsis thaliana GN=HIP26 PE=1 SV=1	1	-0,047	0,894105894	2076,11	0,748
Q9S548 SDP6_ARATH Glycerol-3-phosphate dehydrogenase SDP6, mitochondrial OS=Arabidopsis thaliana GN=SDP6 PE=1 SV=1	2	-0,044	0,891108891	2069,15	0,748
Q9CAD1 Q9CAD1_ARATH At1g63660 OS=Arabidopsis thaliana GN=At1g63660 PE=2 SV=1	2	-0,041	0,9000999	2090,03	0,748
Q9SF85 ADK1_ARATH Adenosine kinase 1 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=1	4	0,034	0,891108891	2069,15	0,748
Q96529 PURA_ARATH Adenylosuccinate synthetase, chloroplastic OS=Arabidopsis thaliana GN=PURA PE=1 SV=1	5	0,031	0,892107892	2071,47	0,748
Q9FXA2 PABP8_ARATH Polyadenylate-binding protein 8 OS=Arabidopsis thaliana GN=PAB8 PE=1 SV=1	8	-0,03	0,893106893	2073,79	0,748
Q84W12 Q84W12_ARATH At4g16450 OS=Arabidopsis thaliana GN=At4g16450 PE=1 SV=1	4	-0,03	0,899100899	2087,71	0,748
O82204 RL281_ARATH 60S ribosomal protein L28-1 OS=Arabidopsis thaliana GN=RPL28A PE=1 SV=1	3	0,028	0,889110889	2064,52	0,748
Q8L7B5 CH60B_ARATH Chaperonin CPN60-like 1, mitochondrial OS=Arabidopsis thaliana GN=At2g33210 PE=1 SV=1	6	-0,024	0,897102897	2083,07	0,748
Q8LBI1 RL51_ARATH 60S ribosomal protein L5-1 OS=Arabidopsis thaliana GN=ATL5 PE=1 SV=2	9	0,023	0,895104895	2078,43	0,748
Q9SV20 COPB2_ARATH Coatomer subunit beta-2 OS=Arabidopsis thaliana GN=At4g31490 PE=2 SV=2	11	-0,019	0,901098901	2092,35	0,748
Q8LAA6 PIP15_ARATH Probable aquaporin PIP1-5 OS=Arabidopsis thaliana GN=PIP1-5 PE=1 SV=2	1	0,079	0,899100899	2087,71	0,749
Q8RXK6 RH8_ARATH DEAD-box ATP-dependent RNA helicase 8 OS=Arabidopsis thaliana GN=RH8 PE=2 SV=1	1	0,078	0,897102897	2083,07	0,749
Q9ZPY5 Q9ZPY5_ARATH At2g46540/F11C10.23 OS=Arabidopsis thaliana GN=At2g46540 PE=2 SV=2	1	0,054	0,899100899	2087,71	0,749
O23547 EXLB1_ARATH Expansin-like B1 OS=Arabidopsis thaliana GN=EXLB1 PE=2 SV=2	1	-0,053	0,906093906	2103,95	0,749
A0A19LMG4 A0A19LMG4_ARATH Uncharacterized protein OS=Arabidopsis thaliana GN=At3g48475 PE=4 SV=1	1	0,05	0,898101898	2085,39	0,749
Q9M9U3 Q9M9U3_ARATH At1g18720/F6A14_17 OS=Arabidopsis thaliana GN=At1g18720 PE=2 SV=1	1	-0,048	0,907092907	2106,27	0,749
Q9SAU2 Q9SAU2_ARATH D-ribulose-5-phosphate-3-epimerase OS=Arabidopsis thaliana GN=RPE PE=2 SV=1	1	0,045	0,905094905	2101,63	0,749
Q9FXC0 Q9FXC0_ARATH At1g56700 OS=Arabidopsis thaliana GN=At1g56700 PE=2 SV=1	2	0,04	0,896103896	2080,75	0,749
Q9SN68 RAF2B_ARATH Ras-related protein RABF2b OS=Arabidopsis thaliana GN=RABF2B PE=1 SV=1	2	0,04	0,9000999	2090,03	0,749
A0A1P8BAA4 A0A1P8BAA4_ARATH Cytidine/deoxycytidylate deaminase family protein OS=Arabidopsis thaliana GN=GSDA PE=4 SV=1	1	-0,039	0,898101898	2085,39	0,749
Q42338 Q42338_ARATH AT3G48140 protein OS=Arabidopsis thaliana GN=T24C20_20 PE=2 SV=1	1	0,036	0,899100899	2087,71	0,749
Q9FIW4 BGL42_ARATH Beta-glucosidase 42 OS=Arabidopsis thaliana GN=BGLU42 PE=2 SV=1	2	0,035	0,904095904	2099,31	0,749
Q9FFE0 RRAA2_ARATH Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 OS=Arabidopsis thaliana GN=At5g16450 PE=1 SV=1	3	0,034	0,907092907	2106,27	0,749
Q9LK96 Q9LK96_ARATH AT3g15090/K15M2_24 OS=Arabidopsis thaliana GN=At3g15090 PE=2 SV=1	4	0,033	0,897102897	2083,07	0,749
Q9S9P8-3 FNRR2_ARATH Isoform 3 of Ferredoxin--NADP reductase, root isozyme 2, chloroplastic OS=Arabidopsis thaliana GN=RFNR2	5	0,031	0,903096903	2096,99	0,749
Q9LQ55 DRP2B_ARATH Dynamin-2B OS=Arabidopsis thaliana GN=DRP2B PE=1 SV=2	8	-0,03	0,904095904	2099,31	0,749
F4I354 F4I354_ARATH Double-stranded DNA-binding family protein OS=Arabidopsis thaliana GN=At1g29850 PE=1 SV=2	3	0,03	0,905094905	2101,63	0,749

Q9SRG3 PDI12_ARATH Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1	9	0,024	0,902097902	2094,67	0,749
P56757 ATPA_ARATH ATP synthase subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=atpA PE=1 SV=1	7	0,024	0,909090909	2110,91	0,749
O04202 EIF3F_ARATH Eukaryotic translation initiation factor 3 subunit F OS=Arabidopsis thaliana GN=TIF3F1 PE=1 SV=1	8	0,022	0,904095904	2099,31	0,749
Q9S795 BADH1_ARATH Betaine aldehyde dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=ALDH10A8 PE=2 SV=1	5	-0,021	0,908091908	2108,59	0,749
Q9T0P4 GLTB2_ARATH Ferredoxin-dependent glutamate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=GLU2 PE=1 SV=2	18	-0,018	0,903096903	2096,99	0,749
P51414 RL261_ARATH 60S ribosomal protein L26-1 OS=Arabidopsis thaliana GN=RPL26A PE=2 SV=2	9	0,018	0,907092907	2106,27	0,749
P93819 MDHC1_ARATH Malate dehydrogenase 1, cytoplasmic OS=Arabidopsis thaliana GN=MDH1 PE=1 SV=2	14	-0,016	0,902097902	2094,67	0,749
Q84K90 Q84K90_ARATH Chromosome-associated kinesin OS=Arabidopsis thaliana GN=At4g26410 PE=2 SV=1	1	-0,05	0,912087912	2117,87	0,75
F41WK4 F41WK4_ARATH Sucrase/ferredoxin-like family protein OS=Arabidopsis thaliana GN=At3g27570 PE=1 SV=1	2	-0,047	0,905094905	2101,63	0,75
Q38906 TOC34_ARATH Translocase of chloroplast 34, chloroplastic OS=Arabidopsis thaliana GN=TOC34 PE=1 SV=2	2	-0,041	0,906093906	2103,95	0,75
Q9LKA5 MORF8_ARATH Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MORF8 PE=1 SV=1	2	0,037	0,909090909	2110,91	0,75
O23138 CYC1_ARATH Cytochrome c-1 OS=Arabidopsis thaliana GN=CYTC-1 PE=1 SV=1	2	-0,027	0,907092907	2106,27	0,75
Q0WJN6 CLAH1_ARATH Clathrin heavy chain 1 OS=Arabidopsis thaliana GN=CHC1 PE=1 SV=1	7	-0,023	0,907092907	2106,27	0,75
Q38814 THI4_ARATH Thiamine thiazole synthase, chloroplastic OS=Arabidopsis thaliana GN=THI1 PE=1 SV=1	1	0,057	0,912087912	2117,87	0,751
P43291 SRK2A_ARATH Serine/threonine-protein kinase SRK2A OS=Arabidopsis thaliana GN=SRK2A PE=1 SV=1	1	-0,049	0,912087912	2117,87	0,751
Q9SIR5 Q9SIR5_ARATH AmmeMemoRadiSam system protein B OS=Arabidopsis thaliana GN=At2g25280 PE=2 SV=1	1	-0,048	0,911088911	2115,55	0,751
Q84TE6 NAC22_ARATH reversed NAC domain-containing protein 21/22 OS=Arabidopsis thaliana GN=NAC021 PE=1 SV=2	1	0,043	0,915084915	2124,83	0,751
O23170 O23170_ARATH Pectinesterase like protein OS=Arabidopsis thaliana GN=C7A10.200 PE=4 SV=1	2	-0,039	0,913086913	2120,19	0,751
Q9LMU0 FCL2_ARATH Putative GDP-L-fucose synthase 2 OS=Arabidopsis thaliana GN=GER2 PE=1 SV=1	2	0,036	0,913086913	2120,19	0,751
P29517 TBB9_ARATH Tubulin beta-9 chain OS=Arabidopsis thaliana GN=TUBB9 PE=1 SV=1	2	0,035	0,913086913	2120,19	0,751
Q94K78 Q94K78_ARATH Transmembrane protein OS=Arabidopsis thaliana GN=At2g40765 PE=2 SV=1	2	-0,03	0,912087912	2117,87	0,751
Q70DU8 AL3H1_ARATH Aldehyde dehydrogenase family 3 member H1 OS=Arabidopsis thaliana GN=ALDH3H1 PE=1 SV=2	6	-0,023	0,914085914	2122,51	0,751
O65282 CH20_ARATH 20 kDa chaperonin, chloroplastic OS=Arabidopsis thaliana GN=CPN20 PE=1 SV=2	5	-0,022	0,915084915	2124,83	0,751
Q9M9K1 PMG2_ARATH Probable 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 2 OS=Arabidopsis thaliana GN=At3g08590 PE=1 SV=1	13	-0,02	0,915084915	2124,83	0,751
O49485 SERA1_ARATH D-3-phosphoglycerate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=PGDH1 PE=1 SV=1	18	0,016	0,916083916	2127,15	0,751
P57106 MDHC2_ARATH Malate dehydrogenase 2, cytoplasmic OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1	1	-0,051	0,915084915	2124,83	0,752
Q9FY64 RS154_ARATH 40S ribosomal protein S15-4 OS=Arabidopsis thaliana GN=RPS15D PE=2 SV=1	1	-0,034	0,918081918	2131,79	0,753
Q949U9 Q949U9_ARATH Mitochondrial substrate carrier family protein OS=Arabidopsis thaliana GN=F14F8_20 PE=2 SV=1	1	0,06	0,922077922	2141,06	0,754
Q38997 KIN10_ARATH SNF1-related protein kinase catalytic subunit alpha KIN10 OS=Arabidopsis thaliana GN=KIN10 PE=1 SV=2	1	0,057	0,921078921	2138,75	0,754
Q8L466 Q8L466_ARATH At1g24050/T23E23_11 OS=Arabidopsis thaliana GN=At1g24050 PE=1 SV=1	1	-0,049	0,922077922	2141,06	0,754
P0DH79 Y5064_ARATH CBS domain-containing protein CBSCBSPB5 OS=Arabidopsis thaliana GN=CBSCBSPB5 PE=1 SV=1	1	-0,039	0,922077922	2141,06	0,754
P58684 SPCS2_ARATH Probable signal peptidase complex subunit 2 OS=Arabidopsis thaliana GN=At2g39960 PE=2 SV=1	1	0,038	0,923076923	2143,38	0,754
Q93Z53 PKP3_ARATH Plastidial pyruvate kinase 3, chloroplastic OS=Arabidopsis thaliana GN=PKP3 PE=1 SV=1	2	0,032	0,923076923	2143,38	0,754
O80988 GCSF2_ARATH Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana GN=GLDP2 PE=1 SV=1	3	-0,025	0,921078921	2138,75	0,754
Q9LHL7 Q9LHL7_ARATH Aha1 domain-containing protein OS=Arabidopsis thaliana GN=T21B14.13 PE=1 SV=1	5	0,02	0,922077922	2141,06	0,754
Q9C8P0 ODP25_ARATH Dihydropyridyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic OS=Arabidopsis th	6	0,019	0,923076923	2143,38	0,754
Q03251 RBG8_ARATH Glycine-rich RNA-binding protein 8 OS=Arabidopsis thaliana GN=RBG8 PE=1 SV=1	8	-0,017	0,924075924	2145,7	0,754
Q84J81 Q84J81_ARATH Fes1A OS=Arabidopsis thaliana GN=Fes1A PE=2 SV=1	1	-0,054	0,926073926	2150,34	0,755
Q94F49 H2A5_ARATH Probable histone H2A.5 OS=Arabidopsis thaliana GN=At5g27670 PE=1 SV=1	2	-0,048	0,921078921	2138,75	0,755
Q9ZVF1 CAR10_ARATH Protein C2-DOMAIN ABA-RELATED 10 OS=Arabidopsis thaliana GN=CAR10 PE=2 SV=1	1	-0,035	0,921078921	2138,75	0,755
Q9FGF3 Q9FGF3_ARATH At5g64430 OS=Arabidopsis thaliana GN=At5g64430 PE=1 SV=1	1	0,034	0,926073926	2150,34	0,755
Q8S8T4 UXS4_ARATH UDP-glucuronic acid decarboxylase 4 OS=Arabidopsis thaliana GN=UXS4 PE=2 SV=1	2	0,028	0,925074925	2148,02	0,755
F4KIB2 TMN8_ARATH Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1	2	-0,026	0,926073926	2150,34	0,755
P51420 RL313_ARATH 60S ribosomal protein L31-3 OS=Arabidopsis thaliana GN=RPL31C PE=3 SV=2	1	-0,024	0,922077922	2141,06	0,755
Q93W30 Q93W30_ARATH Expressed protein OS=Arabidopsis thaliana GN=At2g35605 PE=2 SV=1	4	0,022	0,928071928	2154,98	0,755
Q9FLH2 Q9FLH2_ARATH 2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=MPA24.10 PE=2 SV=1	1	-0,06	0,929070929	2157,3	0,756
Q9LTW8 Q9LTW8_ARATH CTP synthase OS=Arabidopsis thaliana GN=T2E22.2 PE=2 SV=1	1	-0,037	0,928071928	2154,98	0,756
Q94AH6 CUL1_ARATH Cullin-1 OS=Arabidopsis thaliana GN=CUL1 PE=1 SV=1	2	0,03	0,928071928	2154,98	0,756
Q9LM21 Q9LM21_ARATH F16L1.2 protein OS=Arabidopsis thaliana GN=At1g22250 PE=2 SV=1	1	-0,03	0,931068931	2161,94	0,756
Q84M96 ALKR2_ARATH Probable aldo-keto reductase 2 OS=Arabidopsis thaliana GN=AGD2 PE=2 SV=1	3	-0,024	0,928071928	2154,98	0,756
O82462 SYEC_ARATH Glutamate--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At5g26710 PE=1 SV=1	6	-0,018	0,93006993	2159,62	0,756

Q9LTX9 HSP7G_ARATH Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana GN=HSP70-7 PE=2 SV=1	9	-0,012	0,929070929	2157,3	0,756
Q8LDP4 CP19D_ARATH Peptidyl-prolyl cis-trans isomerase CYP19-4 OS=Arabidopsis thaliana GN=CYP19-4 PE=1 SV=2	1	-0,034	0,933066933	2166,58	0,757
Q6NLR2 Q6NLR2_ARATH At1g64650 OS=Arabidopsis thaliana GN=At1g64650 PE=2 SV=1	1	0,033	0,932067932	2164,26	0,757
O48788 Y2267_ARATH Probable inactive receptor kinase At2g26730 OS=Arabidopsis thaliana GN=At2g26730 PE=1 SV=1	1	-0,028	0,931068931	2161,94	0,757
F4I7X1 F4I7X1_ARATH SKU5-similar 6 OS=Arabidopsis thaliana GN=SKU5 PE=4 SV=1	1	0,048	0,933066933	2166,58	0,758
Q0WRW8 B561K_ARATH Cytochrome b561 and DOMON domain-containing protein At3g07570 OS=Arabidopsis thaliana GN=At3g07570 PE=2 SV=1	2	0,025	0,935064935	2171,22	0,758
Q944A2 Q944A2_ARATH Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g20220 PE=1 SV=1	3	0,023	0,935064935	2171,22	0,758
O04308 MPPA2_ARATH Probable mitochondrial-processing peptidase subunit alpha-2, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MPPA2	8	-0,014	0,934065934	2168,9	0,758
P41127 RL131_ARATH 60S ribosomal protein L13-1 OS=Arabidopsis thaliana GN=RPL13B PE=1 SV=1	6	-0,013	0,935064935	2171,22	0,758
Q0WT48 DNJ21_ARATH DnaJ protein ERDJ2A OS=Arabidopsis thaliana GN=ERDJ2A PE=1 SV=1	1	0,031	0,938061938	2178,18	0,759
P46416 GSHB_ARATH Glutathione synthetase, chloroplastic OS=Arabidopsis thaliana GN=GSH2 PE=2 SV=3	5	-0,014	0,938061938	2178,18	0,759
Q8S944 DRP3A_ARATH Dynamin-related protein 3A OS=Arabidopsis thaliana GN=DRP3A PE=1 SV=2	1	0,047	0,94005994	2182,82	0,76
Q9ZUS0 H2B4_ARATH Histone H2B.4 OS=Arabidopsis thaliana GN=At2g37470 PE=1 SV=3	1	0,043	0,938061938	2178,18	0,76
P42643 14331_ARATH 14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	0,039	0,94005994	2182,82	0,76
Q9LNN1 LECT1_ARATH reversed Lectin-like protein At1g53060 OS=Arabidopsis thaliana GN=At1g53060 PE=3 SV=1	1	-0,038	0,938061938	2178,18	0,76
Q9SU08 AUXI1_ARATH Auxilin-related protein 1 OS=Arabidopsis thaliana GN=AUXI1 PE=1 SV=2	1	-0,032	0,941058941	2185,14	0,76
O04316 JAL29_ARATH Nitrile-specifier protein 4 OS=Arabidopsis thaliana GN=NSP4 PE=2 SV=1	2	0,022	0,94005994	2182,82	0,76
Q8VY07 EPN1_ARATH Clathrin interactor EPSIN 1 OS=Arabidopsis thaliana GN=EPSIN1 PE=1 SV=1	1	0,034	0,943056943	2189,78	0,761
Q9FKS0 UKL1_ARATH Uridine kinase-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=UKL1 PE=1 SV=1	3	0,026	0,94005994	2182,82	0,761
Q8GUM2 HSP71_ARATH Heat shock 70 kDa protein 9, mitochondrial OS=Arabidopsis thaliana GN=HSP70-9 PE=1 SV=1	4	0,016	0,943056943	2189,78	0,761
P19456 PMA2_ARATH ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2	3	-0,014	0,942057942	2187,46	0,761
P59224 R5132_ARATH 40S ribosomal protein S13-2 OS=Arabidopsis thaliana GN=RPS13B PE=2 SV=1	1	-0,026	0,944055944	2192,1	0,762
Q9LSV0 GLYR1_ARATH Glyoxylate/succinic semialdehyde reductase 1 OS=Arabidopsis thaliana GN=GLYR1 PE=1 SV=1	5	0,017	0,945054945	2194,42	0,762
O49160 EIF3C_ARATH Eukaryotic translation initiation factor 3 subunit C OS=Arabidopsis thaliana GN=TIF3C1 PE=1 SV=2	5	0,013	0,945054945	2194,42	0,762
Q6RF45 Q6RF45_ARATH TRAF-like family protein OS=Arabidopsis thaliana GN=At2g04170 PE=2 SV=1	1	0,047	0,951048951	2208,34	0,763
P38389 SC61B_ARATH Protein transport protein Sec61 subunit beta OS=Arabidopsis thaliana GN=At2g45070 PE=1 SV=1	1	0,038	0,949050949	2203,7	0,763
Q9SUV8 Q9SUV8_ARATH At4g22610/F7K2_190 OS=Arabidopsis thaliana GN=At4g22610 PE=2 SV=1	1	0,037	0,948051948	2201,38	0,763
Q9FLG1 BXL4_ARATH Beta-D-xylosidase 4 OS=Arabidopsis thaliana GN=BXL4 PE=1 SV=1	1	-0,034	0,948051948	2201,38	0,763
Q8H0V6 AB3F_ARATH ABC transporter F family member 3 OS=Arabidopsis thaliana GN=ABCF3 PE=1 SV=1	1	0,029	0,953046953	2212,98	0,763
Q9CA83 MAOP4_ARATH NADP-dependent malic enzyme 4, chloroplastic OS=Arabidopsis thaliana GN=NADP-ME4 PE=1 SV=1	1	-0,028	0,947052947	2199,06	0,763
O49482 CADH5_ARATH Cinnamyl alcohol dehydrogenase 5 OS=Arabidopsis thaliana GN=CAD5 PE=1 SV=1	1	-0,027	0,95004995	2206,02	0,763
Q9FWA3 G6PD3_ARATH 6-phosphogluconate dehydrogenase, decarboxylating 3 OS=Arabidopsis thaliana GN=At3g02360 PE=2 SV=1	1	0,025	0,947052947	2199,06	0,763
Q9LUR3 FAHD2_ARATH Probable acylpyruvate FAHD2, mitochondrial OS=Arabidopsis thaliana GN=FAHD2 PE=1 SV=1	1	-0,025	0,949050949	2203,7	0,763
Q8W4Q4 Q8W4Q4_ARATH AT4g24800/F6I7_10 OS=Arabidopsis thaliana GN=ECIP1 PE=1 SV=1	1	-0,024	0,947052947	2199,06	0,763
Q84MC2 LOG8_ARATH Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8 OS=Arabidopsis thaliana GN=LOG8 PE=1 SV=1	1	-0,024	0,953046953	2212,98	0,763
Q9FFD8 Q9FFD8_ARATH At5g16470 OS=Arabidopsis thaliana GN=MQK4.20 PE=1 SV=1	1	-0,023	0,952047952	2210,66	0,763
Q9LV28 GPLPC_ARATH Receptor for activated C kinase 1C OS=Arabidopsis thaliana GN=RACK1C PE=1 SV=1	2	0,022	0,95004995	2206,02	0,763
O64806 ACA7_ARATH Putative calcium-transporting ATPase 7, plasma membrane-type OS=Arabidopsis thaliana GN=ACA7 PE=3 SV=2	3	0,021	0,951048951	2208,34	0,763
Q9XIA9 LACS2_ARATH Long chain acyl-CoA synthetase 2 OS=Arabidopsis thaliana GN=LACS2 PE=2 SV=1	1	-0,019	0,95004995	2206,02	0,763
Q9ZV06 NATAL_ARATH Probable acetyltransferase NATA1-like OS=Arabidopsis thaliana GN=At2g39020 PE=2 SV=1	2	0,019	0,953046953	2212,98	0,763
Q945M1 NDUB9_ARATH NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Arabidopsis thaliana GN=CIB22 PE=1 SV=1	2	0,015	0,949050949	2203,7	0,763
P46077 14334_ARATH 14-3-3-like protein GF14 phi OS=Arabidopsis thaliana GN=GRF4 PE=1 SV=2	3	-0,015	0,951048951	2208,34	0,763
Q8L7K9 MAO2_ARATH NAD-dependent malic enzyme 2, mitochondrial OS=Arabidopsis thaliana GN=NAD-ME2 PE=1 SV=1	6	0,012	0,952047952	2210,66	0,763
P93033 FUM1_ARATH Fumarate hydratase 1, mitochondrial OS=Arabidopsis thaliana GN=FUM1 PE=1 SV=2	13	0,011	0,948051948	2201,38	0,763
Q93VT9 RL101_ARATH 60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1	5	-0,011	0,95004995	2206,02	0,763
Q9FJW0 Q9FJW0_ARATH RuvB-like helicase OS=Arabidopsis thaliana GN=At5g67630 PE=2 SV=1	2	-0,022	0,955044955	2217,61	0,764
Q9T029 RS254_ARATH 40S ribosomal protein S25-4 OS=Arabidopsis thaliana GN=RPS25E PE=3 SV=1	1	-0,015	0,956043956	2219,93	0,764
Q9LPV8 ERF1Y_ARATH Eukaryotic peptide chain release factor subunit 1-2 OS=Arabidopsis thaliana GN=ERF1-2 PE=1 SV=1	3	0,014	0,957042957	2222,25	0,764
P29513 TBB5_ARATH Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1	6	0,011	0,956043956	2219,93	0,764
Q9LV48 PERK1_ARATH Proline-rich receptor-like protein kinase PERK1 OS=Arabidopsis thaliana GN=PERK1 PE=2 SV=1	1	-0,035	0,957042957	2222,25	0,765
Q9FIJ4 RD522_ARATH DNA repair RAD52-like protein 2, chloroplastic OS=Arabidopsis thaliana GN=RAD52-2 PE=2 SV=1	1	-0,021	0,958041958	2224,57	0,765

O82514 KAD4_ARATH Adenylate kinase 4 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=2	6	-0,011	0,956043956	2219,93	0,765
Q9CAP8 LACS9_ARATH Long chain acyl-CoA synthetase 9, chloroplastic OS=Arabidopsis thaliana GN=LACS9 PE=1 SV=1	1	-0,02	0,961038961	2231,53	0,766
Q8LB01 DAPB2_ARATH 4-hydroxy-tetrahydronicotinamide reductase 2, chloroplastic OS=Arabidopsis thaliana GN=DAPB2 PE=2 SV=1	3	0,016	0,961038961	2231,53	0,766
Q9M0Y8 NSF_ARATH Vesicle-fusing ATPase OS=Arabidopsis thaliana GN=NSF PE=2 SV=2	3	-0,014	0,959040959	2226,89	0,766
Q9S9N9 CCR1_ARATH Cinnamoyl-CoA reductase 1 OS=Arabidopsis thaliana GN=CCR1 PE=1 SV=1	3	-0,014	0,96003996	2229,21	0,766
O81149 PSA5A_ARATH Proteasome subunit alpha type-5-A OS=Arabidopsis thaliana GN=PAE1 PE=1 SV=1	7	0,01	0,96003996	2229,21	0,766
P42643 14331_ARATH 14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3	1	0,015	0,964035964	2238,49	0,767
P93303 YMF19_ARATH ATP synthase protein YMF19 OS=Arabidopsis thaliana GN=YMF19 PE=1 SV=1	4	-0,012	0,962037962	2233,85	0,767
Q1EBV4 Q1EBV4_ARATH At3g13235 OS=Arabidopsis thaliana GN=DDI1 PE=1 SV=1	3	0,011	0,963036963	2236,17	0,767
P42748 UBC4_ARATH Ubiquitin-conjugating enzyme E2 4 OS=Arabidopsis thaliana GN=UBC4 PE=2 SV=2	1	-0,026	0,965034965	2240,81	0,768
Q39172 AER_ARATH NADPH-dependent oxidoreductase 2-alkenal reductase OS=Arabidopsis thaliana GN=AER PE=1 SV=1	1	-0,023	0,967032967	2245,45	0,768
F4KIB2 TMN8_ARATH Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1	1	-0,022	0,967032967	2245,45	0,768
Q96528 CATA1_ARATH Catalase-1 OS=Arabidopsis thaliana GN=CAT1 PE=1 SV=3	1	-0,019	0,966033966	2243,13	0,768
Q8LCL3 RL272_ARATH 60S ribosomal protein L27-2 OS=Arabidopsis thaliana GN=RPL27B PE=2 SV=2	3	0,014	0,966033966	2243,13	0,768
Q8RXD9 DPE2_ARATH 4-alpha-glucanotransferase DPE2 OS=Arabidopsis thaliana GN=DPE2 PE=1 SV=1	1	-0,014	0,968031968	2247,77	0,768
Q42524 4CL1_ARATH 4-coumarate--CoA ligase 1 OS=Arabidopsis thaliana GN=4CL1 PE=1 SV=1	4	0,012	0,965034965	2240,81	0,768
Q9LT08 PSDE_ARATH 26S proteasome non-ATPase regulatory subunit 14 homolog OS=Arabidopsis thaliana GN=RPN11 PE=1 SV=1	4	-0,011	0,964035964	2238,49	0,768
Q9SIE7 PLAT2_ARATH PLAT domain-containing protein 2 OS=Arabidopsis thaliana GN=PLAT2 PE=2 SV=1	5	-0,011	0,967032967	2245,45	0,768
P42645 14335_ARATH 14-3-3-like protein GF14 epsilon OS=Arabidopsis thaliana GN=GRF5 PE=1 SV=2	2	-0,011	0,968031968	2247,77	0,768
Q9SXC8 UFC1_ARATH Ubiquitin-fold modifier-conjugating enzyme 1 OS=Arabidopsis thaliana GN=At1g27530 PE=2 SV=1	1	-0,021	0,97002997	2252,41	0,769
O49213 FCL1_ARATH GDP-L-fucose synthase 1 OS=Arabidopsis thaliana GN=GER1 PE=1 SV=3	1	0,012	0,97002997	2252,41	0,769
Q8VYF9 SRGT1_ARATH Peptidyl serine alpha-galactosyltransferase OS=Arabidopsis thaliana GN=SERGT1 PE=2 SV=1	1	0,014	0,971028971	2254,73	0,77
Q96327 EBP1_ARATH ERBB-3 BINDING PROTEIN 1 OS=Arabidopsis thaliana GN=EBP1 PE=1 SV=1	10	-0,007	0,97002997	2252,41	0,77
Q9FHY8 HLB1_ARATH Protein HLB1 OS=Arabidopsis thaliana GN=HLB1 PE=1 SV=1	5	-0,009	0,973026973	2259,37	0,771
Q9C7F5 NTF2B_ARATH Nuclear transport factor 2B OS=Arabidopsis thaliana GN=NTF2B PE=1 SV=1	4	-0,008	0,976023976	2266,33	0,771
Q9FKZ4 Q9FKZ4_ARATH Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain-containing protein OS=Arabidopsis thaliana GN=MUD1	1	0,018	0,976023976	2266,33	0,772
Q8GY63 DPNP3_ARATH Probable SAL3 phosphatase OS=Arabidopsis thaliana GN=SAL3 PE=2 SV=1	2	0,013	0,976023976	2266,33	0,772
O65351 SBT17_ARATH Subtilisin-like protease SBT1.7 OS=Arabidopsis thaliana GN=SBT1.7 PE=1 SV=1	1	-0,012	0,975024975	2264,01	0,772
Q93VH5 Q93VH5_ARATH AT5g10730/MAJ23_90 OS=Arabidopsis thaliana GN=MAJ23.90 PE=2 SV=1	2	-0,011	0,976023976	2266,33	0,772
F4HVV6 F4HVV6_ARATH Transcription regulator OS=Arabidopsis thaliana GN=At1g02080 PE=4 SV=1	1	0,011	0,978021978	2270,97	0,772
Q39097 ERF1X_ARATH Eukaryotic peptide chain release factor subunit 1-1 OS=Arabidopsis thaliana GN=ERF1-1 PE=1 SV=2	1	-0,01	0,977022977	2268,65	0,772
Q29Q26 AKR2B_ARATH Ankyrin repeat domain-containing protein 2B OS=Arabidopsis thaliana GN=AKR2B PE=1 SV=1	1	-0,009	0,975024975	2264,01	0,772
Q9M0G0 GAGT3_ARATH Glutathione hydrolase 3 OS=Arabidopsis thaliana GN=GGT3 PE=2 SV=1	2	-0,009	0,976023976	2266,33	0,772
P29515 TBB7_ARATH Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1	1	0,009	0,978021978	2270,97	0,772
P54904 PSCR1_ARATH Pyrroline-5-carboxylate reductase OS=Arabidopsis thaliana GN=PROC1 PE=2 SV=1	3	0,008	0,978021978	2270,97	0,772
Q43725 CYSKM_ARATH Cysteine synthase, mitochondrial OS=Arabidopsis thaliana GN=OASC PE=1 SV=3	9	0,007	0,977022977	2268,65	0,772
Q9FFP6 Q9FFP6_ARATH Pyruvate kinase OS=Arabidopsis thaliana GN=MBK5.16 PE=3 SV=1	2	-0,005	0,979020979	2273,29	0,772
Q8VZH2 APM1_ARATH Aminopeptidase M1 OS=Arabidopsis thaliana GN=APM1 PE=1 SV=1	17	0,004	0,979020979	2273,29	0,772
Q9LMG7 PPA2_ARATH Probable inactive purple acid phosphatase 2 OS=Arabidopsis thaliana GN=PAP2 PE=2 SV=1	1	0,012	0,985014985	2287,2	0,774
P50318 PGKH2_ARATH Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=1 SV=3	2	0,009	0,982017982	2280,25	0,774
Q9LVH6 Q9LVH6_ARATH Aldose 1-epimerase OS=Arabidopsis thaliana GN=At3g17940 PE=3 SV=1	2	0,009	0,984015984	2284,89	0,774
Q8H183 BUP1_ARATH Beta-ureidopropionase OS=Arabidopsis thaliana GN=PYD3 PE=1 SV=1	3	-0,008	0,982017982	2280,25	0,774
Q9LTV9 Q9LTV9_ARATH Defective in cullin neddylation protein OS=Arabidopsis thaliana GN=At3g12760 PE=2 SV=1	1	-0,008	0,983016983	2282,57	0,774
Q9LKA3 MDHM2_ARATH Malate dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=At3g15020 PE=1 SV=1	2	0,008	0,983016983	2282,57	0,774
F4JPD8 F4JPD8_ARATH Nucleoside diphosphate kinase OS=Arabidopsis thaliana GN=At4g23895 PE=3 SV=1	2	0,007	0,985014985	2287,2	0,774
Q42112 RLA02_ARATH 60S acidic ribosomal protein P0-2 OS=Arabidopsis thaliana GN=RPP0B PE=1 SV=2	2	0,005	0,983016983	2282,57	0,774
Q42139 Q42139_ARATH AT4g32260/F10M6_100 OS=Arabidopsis thaliana GN=PDE334 PE=1 SV=2	1	0,012	0,986013986	2289,52	0,775
Q9LML7 U71C3_ARATH UDP-glycosyltransferase 71C3 OS=Arabidopsis thaliana GN=UGT71C3 PE=2 SV=1	1	0,011	0,988011988	2294,16	0,775
P52420 PUR2_ARATH Phosphoribosylamine--glycine ligase, chloroplastic OS=Arabidopsis thaliana GN=PUR2 PE=2 SV=2	1	0,011	0,99000999	2298,8	0,775
Q9LPC5 BIG3_ARATH Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Arabidopsis thaliana GN=BIG3 PE=1 SV=1	1	0,009	0,985014985	2287,2	0,775
Q94JU3 CSN7_ARATH COP9 signalosome complex subunit 7 OS=Arabidopsis thaliana GN=CSN7 PE=1 SV=1	1	-0,007	0,994005994	2308,08	0,775

Q9SIL6 PHB6_ARATH Prohibitin-6, mitochondrial OS=Arabidopsis thaliana GN=PHB6 PE=1 SV=1	1	-0,006	0,993006993	2305,76	0,775
Q9ZUU4 CP29B_ARATH RNA-binding protein CP29B, chloroplastic OS=Arabidopsis thaliana GN=CP29B PE=1 SV=1	1	-0,006	0,996003996	2312,72	0,775
P46032 PTR2_ARATH Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana GN=NPF8.3 PE=1 SV=1	2	-0,005	0,987012987	2291,84	0,775
F4JBU0 F4JBU0_ARATH Phosphoglycerate mutase family protein OS=Arabidopsis thaliana GN=At3g60440 PE=4 SV=1	1	-0,005	0,991008991	2301,12	0,775
Q8RWN9 ODP22_ARATH Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial OS=Arabidopsi	11	0,004	0,985014985	2287,2	0,775
Q9SU63 AL2B4_ARATH Aldehyde dehydrogenase family 2 member B4, mitochondrial OS=Arabidopsis thaliana GN=ALDH2B4 PE=1 SV=1	8	-0,004	0,988011988	2294,16	0,775
P47999 CYSKP_ARATH Cysteine synthase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=OASB PE=1 SV=2	1	-0,004	0,992007992	2303,44	0,775
Q9M8M7 ARGD_ARATH Acetylornithine aminotransferase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=WIN1 PE=1 SV=1	2	0,004	0,992007992	2303,44	0,775
Q94C12 NDBAB_ARATH NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-B OS=Arabidopsis thaliana GN=At3g18410 PE=3 SV=1	1	-0,004	0,994005994	2308,08	0,775
O65570 VILI4_ARATH Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1	2	0,003	0,987012987	2291,84	0,775
Q9LZ99 EXPA9_ARATH Expansin-A9 OS=Arabidopsis thaliana GN=EXPA9 PE=2 SV=1	1	-0,003	0,989010989	2296,48	0,775
P24100 CDKA1_ARATH Cyclin-dependent kinase A-1 OS=Arabidopsis thaliana GN=CDKA-1 PE=1 SV=1	1	0,002	0,994005994	2308,08	0,775
Q9SJU4 ALFP1_ARATH Fructose-bisphosphate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=FBA1 PE=1 SV=2	2	0,002	0,994005994	2308,08	0,775
Q8H1H9 AMO_ARATH Primary amine oxidase OS=Arabidopsis thaliana GN=At1g62810 PE=2 SV=1	2	-0,001	0,997002997	2315,04	0,775
Q84VY3 STAD6_ARATH Stearoyl-[acyl-carrier-protein] 9-desaturase 6, chloroplastic OS=Arabidopsis thaliana GN=S-ACP-DES6 PE=2 SV=2	1	-0,013	0,989010989	2296,48	0,776
Q93XX2 SEOA_ARATH Protein SIEVE ELEMENT OCCLUSION A OS=Arabidopsis thaliana GN=SEOA PE=1 SV=1	3	-0,006	0,992007992	2303,44	0,776
Q9SGE0 AXS2_ARATH UDP-D-apirose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1	3	0,005	0,991008991	2301,12	0,776
Q9XIP8 CDI_ARATH Protein CDI OS=Arabidopsis thaliana GN=CDI PE=2 SV=1	2	-0,005	0,994005994	2308,08	0,776
Q94A84 U72E1_ARATH UDP-glycosyltransferase 72E1 OS=Arabidopsis thaliana GN=UGT72E1 PE=1 SV=1	1	-0,004	0,99000999	2298,8	0,776
B3H7H1 B3H7H1_ARATH AT3G07300 protein OS=Arabidopsis thaliana GN=At3g07300 PE=2 SV=1	1	0,004	0,99000999	2298,8	0,776
Q9FNC4 Q9FNC4_ARATH HAD superfamily, subfamily IIIB acid phosphatase OS=Arabidopsis thaliana GN=MRH10.13 PE=2 SV=1	8	-0,004	0,991008991	2301,12	0,776
Q82597 IPYR5_ARATH Soluble inorganic pyrophosphatase 5 OS=Arabidopsis thaliana GN=PPA5 PE=2 SV=1	1	0,004	0,994005994	2308,08	0,776
Q93ZM7 CH60C_ARATH Chaperonin CPN60-like 2, mitochondrial OS=Arabidopsis thaliana GN=At3g13860 PE=1 SV=2	9	0,003	0,992007992	2303,44	0,776
Q9XEX2 PRX2B_ARATH Peroxiredoxin-2B OS=Arabidopsis thaliana GN=PRXIIB PE=1 SV=1	5	-0,002	0,993006993	2305,76	0,776
O49460 PHB1_ARATH Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1	2	0,002	0,997002997	2315,04	0,776
F4INW4 F4INW4_ARATH P-loop containing nucleoside triphosphate hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g30630 PE=4 SV=1	1	-0,001	0,996003996	2312,72	0,776
Q9ZSP5 AIR3_ARATH Subtilisin-like protease SBT5.3 OS=Arabidopsis thaliana GN=AIR3 PE=2 SV=1	3	0,001	0,996003996	2312,72	0,776
P42645 14335_ARATH 14-3-3-like protein GF14 epsilon OS=Arabidopsis thaliana GN=GRF5 PE=1 SV=2	3	-0,001	0,997002997	2315,04	0,776
P45434 SSRA_ARATH Translocon-associated protein subunit alpha OS=Arabidopsis thaliana GN=At2g21160 PE=2 SV=3	2	0,001	0,998001998	2317,36	0,776
Q8W575 CSN3_ARATH COP9 signalosome complex subunit 3 OS=Arabidopsis thaliana GN=CSN3 PE=1 SV=2	1	-0,001	0,999000999	2319,68	0,776
Q56WN1 GLN11_ARATH Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2	1	-0,001	0,999000999	2319,68	0,776
Q6NPR7 PMT0_ARATH Probable methyltransferase PMT24 OS=Arabidopsis thaliana GN=At1g29470 PE=2 SV=1	2	0,001	1	2322	0,776
F4IWW2 F4IWW2_ARATH 2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=At3g55410 PE=1 SV=1	8	0	0,999000999	2319,68	0,776
Q9SU82 Q9SU82_ARATH Alkaline-phosphatase-like family protein OS=Arabidopsis thaliana GN=At4g29690 PE=4 SV=1	3	0	1	2322	0,776

Table S4: Contents of TCA intermediates in roots of plants cultured in solid MS medium in the absence or presence of adjacent cultures of *P. aurantiogriseum* covered with charcoal filters for 3 days. Values represent the mean $\pm$ SE of determinations in 3 independent experiments. Asterisks indicate significant differences, according to Student's t-test ($P < 0.05$), between VC-treated and non-treated plants.

	-VCs (nmol/g DW)	+VCs (nmol/g DW)
Cis-Aconitate	8.7 $\pm$ 2.0	20.5 $\pm$ 1.6*
Citrate	962 $\pm$ 138	1,409 $\pm$ 130*
Malate	1,011 $\pm$ 125	1,897 $\pm$ 279*
α -ketoglutarate	40.5 $\pm$ 11.7	118.1 $\pm$ 4.8*
Succinate	121.1 $\pm$ 14.7	271.4 $\pm$ 21.5*
Trans-Aconitate	5.1 $\pm$ 2.2	20.0 $\pm$ 1.7*