University of São Paulo
“Luiz de Queiroz” College of Agriculture

Investigating the tomato tolerance to cadmium (Cd) via high throughput
proteomics

Marina de Lima Nogueira

Thesis presented to obtain the degree of Doctor in
Science: Area: Genetics and Plant Breeding

Piracicaba
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Bachelor of Biological Sciences

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versão revisada de acordo com a resolução CoPGr 6018 de 2011

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I. Título

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RESUMO

Investigando a tolerância de tomate ao (Cd) via proteômica de alto rendimento

O problema da toxicidade do cádmio (Cd) agrava-se a cada ano. No entanto, a quantidade de espécies de plantas que apresentam algum grau de tolerância a este metal é baixa. Portanto, é de suma importância entender os mecanismos de tolerância do Cd. Com esse intuito duas cultivares de tomate (TTO e YOSH) exibindo níveis distintos de tolerância ao Cd foram investigadas, expondo-as a 35 μm de CdCl_2 por oito dias. As amostras (raízes, caules e folhas) foram coletadas aos 0, 2, 4, 6 e 8 dias. O comprimento da raiz e área de superfície foram obtidos usando um analisador de imagem WinRhizo PRO 2009c. O método ICP OES foi utilizado para a quantificação de metais nos diferentes tecidos. O índice de translocação (TrI), a absorção de metal e a distribuição de Cd dos nutrientes absorvidos (NA) e eficiência de nutrientes (NUE) foram calculados. O material vegetal usado para indicadores de estresse e análise proteômica foi coletado em nitrogênio líquido. A peroxidação lipídica e o teor de H_2O_2 foram obtidos por espectrometria. Para os dados proteômicos, foi utilizado o método livre de gel. Os indicadores de estresse mostraram a variação nas duas cultivares, evidenciando o estresse causado pelo Cd. A clorose e manchas necróticas foram observadas em plantas expostas ao Cd de maneira menos significativa nos primeiros dias de exposição e mais evidentes no cultivar menos tolerante (TTO) nos últimos dias. A redução do crescimento pode ser observada em ambas as cultivares, mais evidente no TTO. Quanto à distribuição de Cd, as duas cultivares apresentaram comportamento semelhante, com o maior percentual de Cd nas raízes. A absorção de Cd pode interferir nas duas cultivares na absorção, acúmulo e eficiência no uso da maioria dos nutrientes avaliados. Em geral, a interferência do Cd foi mais evidente no TTO do que no YOSH. As maiores porcentagens de TrI também foram observadas na cultivar TTO. Identificação e avaliação da proteína diferencialmente acumulada (DAP) nas raízes das duas cultivares é possível observar que na presença de Cd a cultivar TTO gera uma alteração mais significativa na amplitude do acúmulo e no número de proteínas. Estes resultados sugerem que a cultivar, que apresenta um maior grau de tolerância, tem alguma forma de tornar o Cd indisponível ou um mecanismo que dificulte o transporte de Cd para as folhas.

Palavras-chave: Acúmulo de nutriente; Estresse oxidativo; Gell free; Metais pesados

ABSTRACT

Investigating the tomato tolerance to cadmium (Cd) via high throughput proteomics

The problem of cadmium (Cd) toxicity aggravates every year. However, the amount of plant species presenting some degree of tolerance to this metal is low. Therefore, it is of utmost importance to understand the Cd tolerance mechanisms. Two tomato cultivars exhibiting distinct levels of tolerance to Cd were investigated by exposing them to 35 μM CdCl_2 for eight days. The samples (roots, stems, and leaves) were collected at 0, 2, 4, 6 and 8 days. The root length and surface area were obtained using a WinRhizo PRO 2009c image analyzer. The ICP OES method was used for the quantification of metals in the different tissues. The translocation index (TrI), metal uptake and Cd distribution nutrient absorbed (NA), and nutrient efficiency (NUE) were calculated. The plant material used for stress indicators and proteomics analysis were collected in liquid nitrogen. Lipid peroxidation and H_2O_2 contents were obtained by spectrometry. For the proteomics data the gel-free method was used. The stress indicators showed the variation in both cultivars, evidencing the stress caused by the Cd. Chlorosis and necrotic spots were observed in plants exposed to Cd less significant way in the first days of exposure and more evident in the less tolerant cultivar (TTO) in the last days. The growth reduction can be observed in both cultivars, more evident in TTO. Regarding the Cd distribution, the two cultivars showed similar behavior, with the highest percentage of Cd in the roots. The Cd absorption could interfere with both cultivars in the accumulation absorption and efficiency in the use of most nutrients assessed. In general, the Cd interference was more evident at TTO than at YOSH. Highest percentages of TrI were also observed in TTO cultivar. Identification and evaluation of the differentially accumulated protein (DAP) in the two cultivars roots it is possible to observe that in the presence of Cd the cultivar TTO generates a more significant alteration in the amplitude of the accumulation and the number of proteins. These results suggest that the cultivar, which presents a higher degree of tolerance, has some form to make the Cd unavailable or a mechanism that makes the Cd transportation to the leaves more difficult.

Keywords: Nutrient accumulation; Oxidative stress; Gell free; Heavy metal

1. INTRODUCTION

Agriculture has been changing in the past few decades. Some of these transformations are positive due to the increases in the level of available technology, nevertheless, others are negative mainly due to the establishment of new scenarios regarding environmental issues, which were once imminent and today constitute a reality of the countryside, especially in developing countries. Among the challenges to be solved, those involving climate change and the contamination of soils and water with numerous pollutants can be considered an imperative problem that the society has to overcome over the short- and medium-term.

Climate change has been causing losses in agricultural production in terms of quantity and quality, and the increasing soil contamination due to agriculture, mainly by heavy metals, may impair even more agriculture, not only decreasing plant production but also increasing the contamination of the edible parts of plants with these toxic elements. Unfortunately, there are very few studies approaching the development of management strategies, which can contribute to increase tolerance caused by cadmium (Cd) in plants and decrease the contamination of the edible parts. Thus, soil and water contamination by heavy metals poses a “hidden” and “silent” risk to society, as they may enter the food chain via contamination of the edible parts of agricultural products such as roots, stems, leaves, flowers, and fruits.

The roots are the major gateways for the influx of water, nutrients, and contaminants present in the soil, such as Cd. In this way, it is important to understand the interrelationship between soil and the root system of plants focusing in prevent or decrease the uptake, transport, and accumulation of these toxic elements into the edible parts of plants. Therefore, if the roots of specific genotypes are more efficient in the process of selective ion uptake, these genotypes will probably be more tolerant, developing better, and less likely to contaminate fruits and leaves.

The present thesis aims to study the physiological, biochemical and molecular changes that may be involved to the Cd tolerance process by an integrated analysis of all these processes using different levels of tolerance genotypes of tomato (*Solanum lycopersicum* L.). While response profiles of the system changes in the molecular level of proteins related to

the transport of ions from a nutrient solution to plant tissues were designed based on previous research of our research group.

In analyzes of Cd responses, the exposure time also interferes with the stress level to the plant. The definition of exposure time was done in preliminary studies that were based on visual evaluations of symptoms already known for this type of stress such as chlorosis and reduction of growth (Piotto, 2012; Borges, 2018). Physiological analysis aiming to identify and classify tolerant genotypes can provide advances in genetic improvement findings, these physiological symptoms are consequences of molecular changes that probably begin before the observation of the phenotype.

Tomato has tremendous economic importance due to the increasing consumption and high investments for its cultivation. Due to the economic importance of this crop and its occurrence in cultivated areas with the highest probability of occurrence of soil contaminated with Cd, the tomato is a suitable model for a better understanding of the mechanisms of tolerance, assimilation, and translocation of heavy metals by the roots of plants, and how these mechanisms could contribute to reduce the stress caused by this metal, as well as reduce the contamination of the edible parts.

2. OBJECTIVES AND RESEARCH AIMS

2.1. Main objective

The main aim of this research is to survey the translocation of cadmium, Cd, interference in the uptake of nutrient and perform proteomics of two tomato cultivars under Cd stress conditions in an 8-day experiment.

2.2. Specific Objectives

Survey the translocation of cadmium in the more tolerant tomato cultivar (YOSH) and the less-tolerant tomato cultivar (TTO)

Investigate the Cd interference in the uptake of nutrients and also the nutrient utilization in both tomato cultivar, YOSH, and TTO.

Assess the differentially accumulated proteins in tomato roots under Cd stress in different exposure time.

3. THEORETICAL FRAMEWORK

Heavy metals can occur naturally in the environment. In general, they are present at low concentrations in the soil, although a notable enlargement in such levels can be caused by anthropogenic sources such as mining, fertilizer use, burning of fossil fuels and agroindustry waste final disposal (Gallego *et al.*, 2012). The contamination by heavy metals and some toxic substances can be associated with anthropogenic activities and also due to the low biodegradability of these compounds in the environment, which can cause residual accumulation in soil, water, and air compartments (Lima *et al.*, 2009). Many of these substances are products and by-products of the degradation of agricultural inputs (e.g., herbicides, insecticides, and biocides). In some conditions, the generated products can be even more toxic than the original agrochemicals compounds. This range of substances can pass through the processes of bioaccumulation and biomagnification along the trophic chain and cause changes in the genetic material of several organisms (Lemes *et al.*, 2009; Liman *et al.*, 2010).

The primary form of human and animal exposure to Cd is the ingestion of contaminated plants (Kubo *et al.*, 2016). Plants can have two distinct mechanisms tolerance and resistance to survive upon heavy metals stress. In one mechanism of tolerance, the heavy metal can be avoided by the plant, which means that the plant can survive on contaminated soils and not absorb the pollutant. Regarding the tolerance mechanism, the heavy metal is absorbed by the plant, and it can survive in the presence of the metal in its metabolism, which is a significant way of food contamination by heavy metals (Song *et al.*, 2016).

Due to the high capacity of bioaccumulation and biomagnification along the trophic chain, some compounds and elements can be indicated as a human health issue. Hence, these contaminants must be adequately regulated and their concentration controlled in the environment to reduce the contamination risk to the environmental systems and also to human health.

Regarding the environmental contamination control of water and soil, the Brazilian Council for the Environment (CONAMA) published the Resolution Nº 420/2009, which was later amended by resolution Nº 460, in which concentration values of several compounds in different uses of the soil and groundwater were designed. In the CONAMA Resolution Nº 396/2008, standards for surface water quality can also be checked, inferring maximum values

of potentially toxic substances acceptable in each water use. These resolutions established the maximum values in which each substance can be detected in a specific site without it being considered contaminated according to the performed activities. For Cd this resolution determines as a maximum value: 3 mg.kg⁻¹ for agricultural soil; 8 mg.kg⁻¹ for residential soil; 20 mg.kg⁻¹ for industrial soil

3.1. Cadmium

Because of their high degree of toxicity, arsenic, cadmium, chromium, lead, and mercury rank among the priority metals that are of public health significance (Tchounwou *et al.*, 2014). Cd is a relatively rare chemical element, with atomic number 48, atomic mass 112.4 g mol⁻¹, and ionic radius +2. This metal is naturally present in the environment in small amounts, usually associated with other chemical elements (Ernst *et al.*, 1992; Sebastian *et al.*, 2019). However, as a result of the intensification of human activities, the Cd concentration in the environment has also been increasing (Gallego *et al.*, 2012). The primary sources of this contamination are from industrial and agricultural wastes, incineration of municipal waste, fossil fuels combustion, manufacture of phosphate fertilizers, and zinc mining (O'Neill, 1985; Devesa, Vélez, 2016; Sebastian *et al.*, 2019).

Cd can be used in the manufacture of Ni-Cd batteries, electroplating, plastic stabilizer, pigment, plastic parts finishes, glasses and cleaning pastes, stabilizers. It is also often found in phosphate fertilizers (O'Neill, 1985; Istomim *et al.*, 1999; Kumar *et al.*, 2000; Tolcin, 2015).

3.2. Effects of cadmium on human health

The first case of Cd intoxication was reported around 1900 when workers inhaled Cd-vapors during copper processing. However, until the 1950s, this metal was not considered to be an environmental and food contaminant (Bernard, Lauwerys, 1984; Sherlock, 1984). The toxic potential of Cd was only considered more significant and worrisome after an environmental disaster occurred in Japan in the mid-twentieth century. The Jinzu River was polluted with this metal due to the disposal of tailings from zinc and lead mining, and people were not contaminated through ingestion of contaminated water but the contaminated food

consumption (Valero, 2014). The intoxicated population presented several health symptoms, although the most evident was intense pain in bones and joints.

Several effects have already been observed for Cd contamination in humans, including: hypertension, kidney and liver damages, testicular tissue problems, interference in the male reproductive system and semen quality, bone weakening, intense bone pain, and neurobehavioral problems (Older et al., 1993; Telisman, et al., 2000; Viaene et al., 2000; Leret et al., 2003; Satarug et al., 2003).

3.3. Cadmium as an environmental pollutant

The increase in soil contamination due to the excessive fertilizers use implies a higher concentration of several toxic compounds, including some metals, leading to significant retention of the metal by the plants (Satarug *et al.*, 2003). The half-life of Cd can be considered 15 to 20 years in human (Kirham, 2006). In addition with this extensive half-life period, the Cd also can cause damage on human health, the Cd presence in edible plants has been reported more often and is important to emphasize the main form of human and animal exposure to Cd is the ingestion of contaminated plants (Kubo *et al.*, 2016; Sebastian *et al.*, 2019).

Although it has no biological function in the plant and therefore does not have its uptake system, Cd can be absorbed by plants by cation transporters due to their chemical characteristics and accumulated mainly in the root system (Gratão *et al.*, 2008; Guimarães *et al.*, 2008). Zinc carriers, for example, are known to transport Cd when the Cd concentration is significantly higher than the zinc concentration (Song *et al.*, 2016). The plants readily absorb the Cd²⁺ ions present in the soil solution by the roots, and in some species, are rapidly transported via xylem to the shoot (Lux *et al.*, 2011). The transport via phloem also plays an essential role in the redistribution of the metal in the body of the plants (Mendoza-Cózatl *et al.*, 2011). The transport of Cd between plant structures can occur either through extracellular fluids via the apoplastic as well as simplistic intracellular pathway (Lux *et al.*, 2011; Song *et al.*, 2016).

3.4. Changes in plants caused by cadmium

The plants readily absorb the Cd^{2+} ions present in the soil solution and, in some species, this metal is rapidly transported via xylem to the shoot (Lux *et al.*, 2011). The transport via phloem also provides the redistribution of the metal in the plant body (Mendoza-Cózatl *et al.*, 2011). However, in the majority of the plants described in the literature, the accumulation of this metal occurs in the root system (Vitoria *et al.*, 2001; Pereira *et al.*, 2002). Root uptake involves competition by transporters located in the plasma membrane related to the uptake of other elements, mainly zinc (Clemens, 2006). The mechanisms involved in the processes of Cd uptake and transport in plants are still undefined (Hassan *et al.*, 2005; Redjala *et al.*, 2009). Interactions between Cd and other elements may indicate the presence of common transport mechanisms or the existence of other ways to explain the accumulation of Cd in plants (Redjala *et al.*, 2009).

When a tolerant plant absorbs Cd, the primary response to the stress process is the production of reactive oxygen species (ROS) (Arruda, Azevedo, 2009). The ROS can cause protein oxidation, DNA damage with the lipid peroxidation increase (Gill, Tuteja, 2010). In addition to the alterations caused by the ROS, several other changes are observed when there is contamination by Cd in plants, including decreases in the photosynthetic rate, alterations in plant metabolism, decreases in stomatal aperture, changes in the Calvin cycle, as well as several structural disorders (Gallego *et al.*, 2012; Choppala *et al.*, 2014).

Some authors have already reported that after the entry of Cd in the plant, this metal interferes in the formation of ROS or free radicals (Gallego *et al.*, 2012; Carvalho *et al.*, 2019). ROS are metabolites produced continuously under normal conditions of the aerobic metabolism of plants, but when in excess, they lead the plant to the condition of oxidative stress, where the amount of ROS produced is greater than the amount that the organism is capable of eliminating. Such increases in the amount of ROS are cytotoxic to all organisms (Arruda, Azevedo, 2009) because they cause protein oxidation, DNA damage, and lipid peroxidation. Lipid peroxidation is considered the most drastic effect of heavy metals on plant cells (Quan *et al.*, 2008; Gill, Tuteja, 2010).

The transport of Cd in the roots (Figure 1) can occur either through extracellular fluids via the apoplastic route (red line) or in an intracellular way via the symplast pathway (blue line) (Lux *et al.*, 2011; Song *et al.*, 2016). Once in the root vasculature, it can be transported to aerial organs through the xylem.

Figure 1. Schematic of anatomical sections showing the possible transport pathways of Cd in the plant. Source: Song et al. (2016). Available in: <http://dx.doi.org/10.1080/15226514.2016.1207598>

Chlorosis is also a prevalent symptom in plants contaminated with Cd, resulting from competition between Cd and iron ions by sites of uptake on the plasma membrane. When plants have chlorosis, other symptoms can be detected, such as withering of leaves, yellowish spots, leaf epinasty and inhibition of shoot buds. In the roots, thin structures are formed as well as the elongation of thick roots (Gill, Tuteja, 2010).

The presence of Cd in the plant may also be related to decrease in growth, rate of photosynthesis, enzymatic and metabolic alterations (Dal Corso *et al.*, 2008; Galician *et al.*, 2012). This occurs due to changes caused by this metal in the functions of stomata, electron transport, Calvin cycle, as well as disorders in the structure of thylakoids and the synthesis of chlorophylls (Choppala *et al.*, 2014).

In addition to all the physiological, biochemical and morphological effects observed in plants, we can find in the literature reports of several adverse effects of Cd in animals and humans. The metal is also capable of causing epigenetic variations by exposing the cells. Among the epigenetic variations related to Cd exposure are: changes in DNA methylation

pattern, both global and site-specific, histone modifications and micro RNAs, and these epigenetic changes alter the expression pattern of specific genes, as observed in humans, rats, mice and chickens (Wang *et al.*, 2012).

Epigenetic changes caused by agents such as Cd may have adverse effects on organisms, but in many cases, the alteration of epigenetic indexation may promote the appearance of advantageous characteristics for the adaptation of the organism to stress, for example, the development of tolerance in animals as well as in plants.

3.5. Cd interference in the accumulation and absorption of macro and micronutrients

Some heavy metals like Cd are non-essential to the development of plants, affect the absorption and accumulation of nutrients in different organs, resulting in nutrient deficiency and therefore affecting plant growth. Macronutrients (such as N, Ca, Mg, K, P, and S), and micronutrients (which include Fe, Cu, Mn, Mo, Co, and Zn) are essential for plant growth and play essential roles in modulating the response against toxicity induced by Cd and other heavy metals. (Sebastian *et al.*, 2019).

Metals exert various effects on plants under stress conditions, according to their concentration, plant genotypes and species, for example: potassium is required to maintain anion-cation balance in plant cells and plays an important regulatory role in protein synthesis and enzyme activation; sulfur serves as a constituent of several coenzymes, vitamins, and ferredoxin; calcium is involved in activating the enzymes and plays a role in regulating metabolic activities; phosphorus is one of the major constituents of cell membrane and nucleic acid, and majorly required for phosphorylation reaction; and magnesium is a constituent for chlorophyll biosynthesis (Singh *et al.*, 2016; Sebastian *et al.*, 2019).

Micronutrients, required in less quantity for the biological system (and whose essentiality varies according to the concentration and is based on active micronutrient participation as enzyme cofactors and in the redox reactions), have been reported to play a crucial role in alleviating heavy metal toxicity. Among the effects that nutrients can exert on Cd toxicity, it is relevant to consider the following: reduction of heavy metal solubility in soil; competition for membrane transporters; sequestration of heavy metals in the vacuole; dilution of the concentration of heavy metals by favoring the biomass increase; increasing the efficiency of the antioxidant system; ratio of antagonism or synergism between nutrients, and

heavy metals, according to concentration in soil and tissues, genotype and plant species (Singh *et al.*, 2016). Such information justifies the relevance of studies focused on understanding the relationship between nutrient accumulation in plant tissues and their influence on the modulation of plant response to heavy metals.

3.6. Importance of plant proteomics for the research project

The research group coordinated by Prof. Dr. Ricardo Antunes de Azevedo has been working to evaluate Cd impact on the metabolism of cultivated plants. Issues related to Cd uptake and accumulation in plants have become a primary focus in our group research, and hence, several relevant studies (Borges *et al.*, 2019; Carvalho *et al.*, 2019) have been performed including assessments with tomato, mainly motivated by changes in antioxidant metabolism of cells in stressed plants.

Plants are able to mitigate or even avoid Cd stress by changing the activity of antioxidant enzymes such as superoxide dismutase (SOD, EC 1.15.1.1), catalase (CAT, EC 1.11.1.6), ascorbate peroxidase (APX, EC 1.11.1.11), glutathione peroxidase (GSH-Px, 1.11.1.9) and guaiacol peroxidase (GPX, 1.11.1.7) and the synthesis of non-enzymatic compounds (e.g., ascorbate (AsA) and glutathione (GSH) (Marques *et al.*, 2019).

It is mentioned in our review paper on tolerance mechanisms and antioxidant molecules in response to Cd (Marques *et al.*, 2019) that the detection of the effect of antioxidant enzymes on Cd plant tolerance is also related to the balance between the expression of proteins and their activity, which may be or not enough to avoid the oxidative stress or the decreased tolerance.

Several studies using genomics and gene expression analyses were performed in order to better understand the mechanisms from the phenotypes observed in plants under stress with heavy metal. Although these results are of great importance, they are not always correlated with the quantity and functionality of the proteins, which are responsible for the observed phenotype (Bohnert *et al.*, 2006).

Due to the great importance of knowing the proteins involved in stress responses to different metals, several studies were carried out in this context, most of them using the 2-DE technique as presented in the review written by Hossain and Komatsu (2013).

Proteomics has been used as a valuable tool to identify proteins related to Cd response, uptake and/or translocation, as reported in several recent papers considering differences in the plant genotype and species, age, organ, as well as the length-time of plant exposure (Table 1). However, proteomic studies comparing tomato genotypes with different degrees of tolerance/sensitivity in different Cd exposure time (as a strategy to conclusively determine the contribution of different mechanisms in Cd tolerance) in high impact scientific journals are non-existent.

Based on the information provided before, the use of proteomics is a critical approach to our evaluation on the action of antioxidant molecules and their efficiency in contributing to plant Cd detoxification, and regarding the monitoring of the differential expression of proteins potentially involved in Cd response and tolerance, such as those directly or indirectly related to Cd uptake, translocation and accumulation.

Table 1. Examples of proteomic investigations in order to analyze the plant response to cadmium (Cd) exposure, published in the period 2011–2018.

Plant species	Plant materials (age of the plants when treated with Cd)	Proteomic technologies	[Cd]; exposition time	Growth and treatment conditions	References
<i>Oryza sativa</i>	Leaves (40 days)	2-DE, MALDI-TOF/TOF-MS	10 μM CdSO_4 ; 10 days	Hydroponic	Nwugo and Huerta (2011)
<i>Triticum aestivum</i>	Leaves (7 days)	2-DE, MALDI-TOF-MS	10, 100 and 200 μM CdCl_2 ; 7 days	Hydroponic	Wang <i>et al.</i> (2011)
<i>Brassica juncea</i>	Leaves (2 weeks)	2-DE, nano HPLC, MS/MS ion trap	0, 25, 50 and 100 μM CdCl_2 ; 21 days	Hydroponic	D'Alessandro <i>et al.</i> (2013)
<i>Arabidopsis thaliana</i>	Cultured cells	2-D-DIGE, TOF-MS	50, 100, 200, or 300 μM CdCl_2 ; 24, 48, 72, 96, and 120 hours	Cell culture	Wang <i>et al.</i> (2013)
<i>Populus tremula</i>	Leaves (22–24 leaves stage)	2-D, MALDI-MS/MS	20 μM CdSO_4 ; 56 days	Hydroponic	Sergeant <i>et al.</i> (2014)
<i>Brassica napus</i>	Leaves (five leaf stage)	2-DE, MALDI-TOF-TOF-MS	100 and 500 μM CdCl_2 ; 15 days	Hydroponic	Ali <i>et al.</i> (2015)
<i>Eichhornia crassipes</i>	Leaves (acclimated plants for 15 days)	2-D, MALDI-TOF-TOF-MS	100 mg/L CdCl_2 ; 2, 3, and 5 days	Hydroponic	Li <i>et al.</i> (2015)
<i>Helianthus annuus</i>	Leaves (7 days)	2-D-DIGE, LC–MS/MS	50 or 70 mg of Cd as CdCl_2 ; 45 days	Plastic pots	Lopes Júnior <i>et al.</i> (2015)
<i>Cakile maritima</i> Scop. Sea Rocket	Leaves (2 weeks)	2-DE, nanoHPLC, MS/MS ion trap	25, 50 and 100 μM CdCl_2 ; 21 days	Hydroponic	Taamalli <i>et al.</i> (2015)
<i>Populus yunnanensis</i>	Leaves (18–20 leaves stage)	2-D, MALDI-TOF-TOF-MS	100 μM CdCl_2 ; 4, 8 and 12 days	Hydroponic	Yang <i>et al.</i> (2015)
<i>Sorghum bicolor</i>	Leaves (10 days)	2-DE, MALDI-TOF-TOF-MS	100 and 150 μM CdCl_2 ; 5 days	Hydroponic	Roy <i>et al.</i> (2016)
<i>Triticum polonicum</i>	Roots (two leaf stage)	iTRAQ labeling, LC-MS	40 μM CdSO_4 ; 2 days	Cultured in growth chamber	Wang <i>et al.</i> (2016)
<i>Medicago sativa</i>	Roots (5 days)	iTRAQ labeling, LC-MS/MS	100 μM CdCl_2 ; 12 hours	Hydroponic	Dai <i>et al.</i> (2017)

cont'd

Plant species	Plant materials (age of the plants when treated with Cd)	Proteomic technologies	[Cd]; exposition time	Growth and treatment conditions	References
<i>Cucumis sativus</i>	Leaves (15 days)	iTRAQ labeling, LC-ESI-MS/MS	100 μ M CdCl ₂ ; 10 days	Hydroponic	Gong <i>et al.</i> (2017)
<i>Raphanus sativus</i>	Roots (4 weeks)	iTRAQ labeling, nanoHPLC, TOF-MS/MS	10 and 50 μ M CdCl ₂ ; 12 hours	Hydroponic	Xu <i>et al.</i> (2017)
<i>Sedum alfredii</i>	Leaves (age was not communicated)	iTRAQ labeling, LC-MS/MS	40 and 200 μ M Cd; 15 days	Hydroponic	Zhang <i>et al.</i> (2017)
<i>Oryza sativa</i>	Leaves (first fully expanded leaf stage)	iTRAQ labeling, LC-MS/MS	10 and 100 μ M CdCl ₂ .2.5H ₂ O; 12 days	Hydroponic	Zhong <i>et al.</i> (2017)
<i>Brachypodium distachyon</i>	Roots (three leaf stage)	2-DE, DIGE, MALDI-TOF/TOF-MS	500 μ M CdCl ₂ ; 1, 2, 3 and 4 days	Hydroponic	Chen <i>et al.</i> (2018)
<i>Medicago sativa</i>	Leaves (seeds)	2-D-DIGE, MALDI-TOF/TOF-MS	10 mg per kg soil added as CdSO ₄ ; approximately 4 months	Potting soil	Gutsch <i>et al.</i> (2018a)
<i>Medicago sativa</i>	Stems (seeds)	2-D-DIGE, MALDI-TOF/TOF-MS	10 mg per kg soil added as CdSO ₄ ; approximately 4 months	Potting soil	Gutsch <i>et al.</i> (2018b)

4. METHODOLOGY

4.1. Plant material and growth conditions

For this research, two tomato cultivars with different levels of tolerance were selected: Yoshimatsu with a tolerance index of 0.91 and Tropic-Two Ordens, with an index of 0.07 (Piotto *et al.*, 2018). The classification of the different tomato cultivars according to the tolerance index was described by Piotto *et al.* (2018). Both selected cultivars also presented the highest variation between the tolerance index in the results presented in Carvalho *et al.* (2019), after an evaluation of six different tomato cultivars. In addition, the cultivars did not present large variations concerning the growth and development in non-stress conditions.

The seeds used in this experiment were obtained from plants germinated and maintained in vermiculite watered with a solution prepared based on Hoagland and Arnon (1950), modified for tomato plants accordingly to a protocol established by Piotto (2012). Seeds were extracted from mature fruits and later treated with natural yeast dissolved in distilled water for 24 hours. Next, they were rinsed in distilled water, dried and stored until the beginning of the experiments.

The evaluation was performed in seedlings, mainly because it facilitates the experiment and because of the uniformity of individuals at this stage. After obtaining the seeds of the two cultivars, it was proceeded the chemical chiseling process in 2% HCl solution for 5 minutes under shaking. In the sequence, they were rinsed in water and placed to germinate in styrofoam trays containing vermiculite. After 15 days of germination process, the seedlings were transferred to a hydroponic system with controlled pH ($\text{pH} = 6.0 \pm 0.3$) using 20% strength Hoagland and Arnon (1950), solution modified for tomato plants (Piotto, 2012). After one day of adaptation, the nutrient concentration of the solution rose to 30% and thus reached 50%, when $35 \mu\text{M CdCl}_2$ was added.

Three replicates of roots, stems, and leaves were randomly collected for quantification of Cd, macro, and micronutrients, dry mass, and stress indicators. Also, six biological replicates of roots were collected for analyses of root morphology and proteomic analysis. All samples were collected after 0, 2, 4, 6, and 8 days of exposure to Cd, as described in the following topic.

4.2. Dry mass and metal content

The samples collected on the different days of exposure were separated in paper bags considering stems, roots and leaves, and then all the plant material was dried at 55 °C until the stabilization of the mass. After completing the drying process, the material was weighed to quantify the dry mass. The same samples were grinded until obtaining a powder, and afterward, Cd and nutrients (Ca, Cu, Fe, K, Mg, Mn, Mo, P, and Zn) concentrations were determined by plasma emission spectrometry (ICP-OES, Agilent Technologies, 700 Series, Belgium) after the metal extractions in the heating block (Gielen *et al.*, 2017).

The quantification data obtained by ICP-OES analysis were expressed in milligram of metal per liter of solution, and in order to obtain the total concentration of each of the evaluated nutrients as well as of the Cd in the different plant materials (organs), the Equation 2 was used.

$$C_f = \frac{C_{ICP} \cdot volume}{dm_{part}} \quad \text{Equation 2}$$

In this equation:

C_f is the concentration of the analyzed element in the dry mass of the vegetal material (dm_{part}), i.e., mg_{metal}/g_{part} representing the final concentration regarding the mass of metal present in each unit of the vegetal part dry mass (grams of vegetal organ);

C_{ICP} is the concentration measured after the solution being inject in the ICP-OES equipment;

$Volume$ is the total liquid used to dissolve the dry vegetal mass in the material preparation for the metal quantification.

4.2.1. Metal uptake and Cd distribution

In order to perform the determination of metal uptake, the data of metal concentrations in roots, stems and leaves were used to expand the total metal mass in each part of the plant. Furthermore, for the determination of the Cd uptake of the plants (considering the plant as an evaluation unit) in the experiment, the values of roots, stems,

and leaves were added. The Cd distribution in each organ was calculated using a simple equation (Equation 3).

$$Cd_{\%} = (Cd_{organ} \cdot 100) / Cd_{plant} \quad \text{Equation 3}$$

In this equation:

$Cd_{\%}$ is the percentage of Cd concentration of each organ of the plant comparing to the total mass of the plant, considering the parts like roots, stems, and leaves;

Cd_{organ} is the cadmium accumulation of each organ of the plant;

Finally, Cd_{plant} is the accumulation of cadmium considering the parts proportion for the weighted sum.

4.2.2. Nutrient absorption

The amount of nutrient absorbed (NA) was calculated at the end of the experiment, and for that, in this present research, after eight days of contamination. This index was calculated from Equation 4, and the results are expressed as $mg\ g^{-1}$, as described by Borges *et al.*, 2019.

$$NA = (na_8 - na_0) / (rdm_8 - rdm_0) \quad \text{Equation 4}$$

In this equation:

NA expresses the nutrient absorbed (accumulated) by the plants of the experiment;

$(na_8 - na_0)$ is the the nutrient variation on the first and last day of the experiment;

$(rdm_8 - rdm_0)$ is the difference of dry root masses between the beginning and the end of the assay.

4.2.3. Nutrient efficiency

The measurement of nutrient use efficiency (NUE) was calculated as described by Siddiqi and Glass (1981) and also used by Borges *et al.* (2019), following Equation 5:

$$NUE = dm_8 / na_8 \quad \text{Equation 5}$$

In this equation:

dm_8 is the total dry mass at day 8;

na_8 is the nutrient accumulation at the end of the experiment, eighth day in this research.

4.2.4. Translocation index

With the data obtained by the Cd uptake in in the root, stem and leaf, the Translocation Index (TrI) was calculated. For this the following formula was used.

$$TrI = \left((Cd_{leaf} + Cd_{stem}) / Cd_{plant} \right) \times 100 \quad \text{Equation 6}$$

In this equation:

$(Cd_{leaf} + Cd_{stem})$ is the accumulation of cadmium in the shoots;

Cd_{plant} is the accumulation of cadmium considering the vegetal parts proportion for the weighted sum.

4.3. Stress indicators

The plant material used for analysis of the lipid peroxidation and the determination of the content of hydrogen peroxide (H_2O_2) and MDA was collected in liquid nitrogen for each organ: root, stem, and leaf. Subsequently, the samples were ground into homogeneous powder and stored in a freezer at $-80^\circ C$ until the onset of experiments.

4.3.1. Lipid peroxidation

The lipid peroxidation was estimated by the production of malondialdehyde (MDA), as described by Heath and Packer, (1968). For the leaf samples, 0.2 g was used, and for the

stem and root samples, 0.4 g of the previously macerated material was necessary. This material was homogenized in 2 mL of 1% (w/v) trichloroacetic acid (TCA) containing approximately 20% polyvinylpyrrolidone (PVPP).

The homogenized liquid was centrifuged at 13,000 g for 10 min, in 250 µL of the supernatant was added to 1 ml of 0.5% thiobarbituric acid (TBA). The mixture was heated in a water bath at 95 °C for 30 min, after that period to interrupt the reaction, the tubes were placed in an ice bath for approximately 15 min. The response was obtained at the absorbance ranges of 532 nm and 600 nm, in order to obtain the final result in nmol g⁻¹ of fresh mass, the following equation was applied

$$X = (ABS_{532} - ABS_{600}) / \epsilon 155 \quad \text{Equation 7}$$

$$MDA = (X / 1000) / dm \quad \text{Equation 8}$$

In this equation:

ABS₅₃₂ is the absorbance ranges of 532nm

ABS₆₀₀ is the absorbance ranges of 600nm

dm is the dry mass used to quantify the MDA

4.3.2. H₂O₂ content

The content of H₂O₂ was determined according to Alexieva *et al.* (2001). Pre-macerated samples, as described in the previous item, were homogenized in 2 mL of 0.1% (w/v) TCA, containing approximately 20% of PVPP and centrifuged at 13,000 g for 10 min. Then, 0.2 mL of the supernatant was mixed with 0.2 mL of 100 mM phosphate buffer (pH = 7.5) and 0.8 mL of potassium iodide (1M). The reaction took place during one h in the dark. The absorbance of the reaction was, then, measured at 390 nm in a spectrophotometer. The

H₂O₂ content was determined based on a standard curve using standard concentrations of H₂O₂ and expressed as $\mu\text{mol g}^{-1}$ of fresh weight.

4.3.3. $\Delta\text{H}_2\text{O}_2$ content and ΔLipid peroxidation

In order to better understand the variation of these indicators due to the consequent stress of Cd, both $\Delta\text{H}_2\text{O}_2$ and ΔMDA were made, which consisted in subtracting, from the value obtained in stress condition, the value obtained for control condition at the same analyzed time of the plant.

4.4. Root morphology

The sample was fixed in alcohol 70% for root length and surface area measurements were obtained using a WinRhizo PRO 2009c image analyzer (Regent Instruments Inc., Québec City, QC) coupled with a professional Epson SL 1000 scanner (Japan) equipped with a light transparency unit (TPU), as described by Bouma *et al.* (2000).

4.5. Analyzing Data

For the results of root length, root volume, root, stem, leaf, and plant dry weight, Cd and nutrient accumulation in root stem and leaf, with the use of the software XLSTAT were adjusted linear regression models when is possible and non-linear were adjusted when were necessary.

For the MDA and H₂O₂ were made ANOVA with triple factorial (Time, concentration and cultivar), for Cd% and Trl the ANOVA were double factorial (Time and cultivar) and for NA and NUE as well as done the two way ANOVA, for cultivar and concentration. The means were compared by Tukey's method. These analyses were performed using the R software version 3.4.1.

4.6. Proteomic Analysis

4.6.1. Extraction of proteins

The roots were collected in liquid nitrogen, lyophilized and sent to the Catholic University of Leuven (KU-LEUVEN). The extraction was proceeded using the phenol extraction/ammonia acetate precipitation method as described by Carpentier *et al.* (2005). Extractions were performed from approximately 25 mg of sample, solubilized in a mixture of 8 M urea, 5 mM DTT, and 30 mM tris diluted in milli-q water. Protein quantification was executed using the 2-D Quant Kit®. After quantification, proteins in the total amount of 20 µg were treated with trypsin (Trypsin Protease, MS Grade Thermo Scientific), and the removal of contaminants was by SPE (Solid Phase Extraction) using Pierce C18 Spin Columns (Thermo Scientific).

4.6.2. Identification and analysis of proteins

The root proteins digested (0.5 µg/5 µL) of the different tomato cultivars exposed to Cd, were separated as described in Campos *et al.*, 2016 in an Ultimate 3000 (Thermo Scientific) UPLC system and then in a Q Exactive Orbitrap mass spectrometer (Thermo Scientific). The Q Exactive Orbitrap mass spectrometer (Thermo Scientific, USA) was operated as described in Campos *et al.*, 2018.

Data generated were processed by Progenesis QI (Nonlinear Dynamics) and the protein identification MASCOT version 2.2.06 (Matrix Science) against Tomato Integrated Database. Statistical software (Statistica 7) was used, using uni- and multivariate techniques (PCA) ($p < 0.01$) as well as ANOVA ($p < 0.01$) to identify the proteins that presented variation due to the stress suffered by the presence of Cd. It is important to note that the results of one cultivar were analyzed independently of the results of the other cultivar.

The proteins in which the variation was significant, the differentially accumulated protein (DAP) were grouped according to their molecular function, protein class, cellular component, biological process and pathway using the data of the GO database (<http://geneontology.org/> or more directly <http://pantherdb.org/webservices/go/overrep.jsp>).

Complete clusters were created using the Panda software, based on Euclidean distance. PANDA-view is a free-software designed to provide comprehensive methods for statistical analysis and visualization of data, including the quantitative proteomics data (Chang *et al.*, 2018).

5. RESULTS

5.1. Non-quantified and visual aspects of tomato exposed to cadmium

One of the first symptoms observed in the plants exposed to Cd is the chlorosis. On the second day of exposure, this chlorosis was present in a less significant way than during other days of the experiment. This symptom became more evident during the days of exposure in the two evaluated cultivars, although it was always more evident in the less tolerant cultivar (TTO) than in the more tolerant cultivar (YOSH).

In addition to the chlorosis, in the last days of the experiment it was also possible to observe the appearance of necrotic spots probably in consequence of cell death, and again these spots were also more evident in the cultivar TTO than in YOSH.

These two symptoms are generally observed in hydroponics experiments and usually more evident in cultivars less tolerant Figure 2.

In Figure 2 it is possible to observe the cultivar YOSH in control condition over time (A, B, C and D) and in stress condition in (E, F, G and H). In day two we can see no big change, after four days in stress with Cd is possible to see the chlorosis increase. Moreover, in eighth days it is possible to see necrotic spots.

In the cultivar TTO, it is possible to observe the chlorosis in two days under stress condition (figure 2M), and the necrotic spots begin to appear at day four (figure 2N), but more evident at day six and eighth (figure 2O, P).

Figure 2. Different tomato cultivar subjected to Cd stress in four exposure times. (A) YOSH on day two in the control condition; (B) YOSH on day four in the control condition; (C) YOSH on day six in the control condition; (D) YOSH on eight in control condition; (E) YOSH on day two in stress condition; (F) YOSH on day four in stress condition; (G) YOSH on day six in stress condition; (H) YOSH on eight in stress condition; (I) TTO on day two in control condition; (J) TTO on day four in control condition; (K) TTO on day six in control condition; (L) TTO on eight in control condition; (M) TTO on day two in stress condition; (N) TTO on day four in stress condition; (O) TTO on day six in stress condition; (P) TTO on eight in stress condition

These two symptoms were more evident in TTO cultivar (Figure 3A) with six days submitted to Cd stress and in the eighth day under the Cd stress (Figure 3B). The TTO cultivar is considered less tolerant in the other studies, and with these images, it is possible to see the considerable damage that Cd stress can cause in this cultivar over time.

Figure 3. Magnification of the TTO cultivar subjected to Cd stress in the last days of exposure. (A) TTO on day six in stress condition; (B) TTO on eight in stress condition.

5.2. Effects of Cd on tomato root morphology and tomato biomasses

Regression analysis revealed that in the control condition the cultivar TTO had the highest volume increase (after two days of exposure to the metal) and root length (after four days of exposure). Under Cd-treatment, the average of these morphological parameters was similar among the cultivars, followed by a linear increase until the end of the experiment period. Thus, Cd exposure induced an overall reduction of the averages related to tomato root morphology traits during the time length of the experiment, with more significant declines in the TTO genotype (Figure 4).

The biomasses of the two cultivars were significantly decreased by Cd exposition, with higher declines in the TTO genotype in relation to YOSH for root and leaf dry mass. There was a small trend of increasing dry mass accumulation in the YOSH genotype when compared to TTO in stressed plants, especially between the sixth and eighth days of exposure (Figure 4).

Figure 4. Cd impact on tomato plant growth expressed in dry weight (g) root length (cm) and volume (cm³). The Relationship among tomato cultivars in different Cd (μ M) exposure time in root length (A), root volume (B), root dry mass (C), dry stem mass(D), leaf dry mass (E) and a plant dry mass (F) are represented. Solid black lines represent Tropic Two Orders cultivar (TTO) under control condition, dotted black lines represent TTO cultivar under Cd-stress condition, solid grey lines represent YOSHmatsu (YOSH) in control condition, and dotted grey lines represent YOSH cultivar in Cd-stress condition.

For all growth parameters evaluated the linear regressions were adjusted whenever possible and when the linear regressions had non-significant or negative intercept the non-linear regression was adjusted (Figure 4). The regression for Cd effects on tomato plant growth data can be checked in APPENDIX

5.3. Free hydrogen peroxide and lipid peroxidation levels

The highest H₂O₂ content was verified in leaves, notably in TTO genotype at four and eight days following the Cd-exposure. The MDA accumulation in TTO exposed to Cd was greater compared to YOSH in the second day (leaves) and in the fourth day (stem) after exposure. YOSH presented the highest MDA levels in the stem compared to Cd-stressed TTO after eight days of exposure (Figure 5).

Figure 5. Stress indicators means (n=3) in cultivar tomato (TTO and YOSH) observed in root, stem, and leaf in stress and control conditions at different times. Malondialdehyde (MDA) (A) and H₂O₂ content (B)

Regarding the differences between the means of the treatments with Cd exposition and the control condition, at all times of exposure, the general tendency of increasing the accumulation of Cd-induced stress indicators was observed. It is important to note that the

increase in both MDA and H_2O_2 was higher in TTO than in YOSH plants at most of the times and organs evaluated. The root in YOSH was an exception, in which small variations were observed in the MDA delta, while greater variation for H_2O_2 delta could be detected (Figure 6).

Moreover, despite the reduction induced by this metal presence was also detected in MDA levels (TTO: in Root material at the eighth day of exposition; YOSH: in leaf material at the second day) and H_2O_2 (TTO: Root, after eight days; YOSH: leaf, after two days). Complementary, considering the leaves analysis, the induction of H_2O_2 accumulation by Cd-exposure was detected in TTO at all exposure times (Figure 6).

Figure 6. Difference of stress indicators between stress and control conditions in tomato root stem and leaf in different cultivars (TTO and YOSH) over time. Lipid peroxidation (A) and H₂O₂ content (B)

5.4. Cadmium accumulation and distribution

From the results of Cd distribution and the translocation index, a better understanding of the behavior of Cd after crossing the physical barriers and penetrating the plant by the root is possible. Considering Cd distribution, according to the Tukey's method with 95% of significance, the interaction between exposure time and cultivar was significant ($p = 0.048$) only for leaves. Regarding the stem samples, no significant difference was observed between the cultivars ($p = 0.241$), being different only in relation to the exposure time ($p < 0.001$). Furthermore, the results from the root, the interaction was not significant, but the two parameters presented significant difference individually (cultivar $p = 0.035$, time $p < 0.001$), the same was observed for *Trl* (cultivar $p = 0.035$, time $p < 0.001$), this results can be cheked in figure 7.

The YOSH genotype exhibited lower translocation index at times of six and eight days of exposure compared to TTO. When Cd partitioning in plant tissues is concerned, the percentages of Cd retention in the root of both cultivars were statistically smaller in the two-days analysis compared to the other days of exposure, and higher compared to the percentage of Cd in the other vegetal organs, which was higher on the second day of exposure compared to the others (Figure 7).

Figure 7. Cd distribution in tomato cultivar (TTO and YOSH) over time expressed in Cd % (A) and translocation index (B).

Evaluating the total dry mass of roots, the two tomato genotypes (TTO and YOSH) growing in the presence of $35 \mu\text{M}$ CdCl_2 showed a similar tendency of increase the accumulation of Cd until the second day of exposure, although, after this period, the

accumulation of Cd in YOSH-plants, comparing to TTO ones, was evidenced higher (Figure 8). No significant differences for the concentration of this metal in the roots between the cultivars were noted (Table 2).

Concerning the other nutrients also evaluated in roots samples, the accumulation increase was observed for both cultivars in stress and control conditions, although the tendency of the mass of Ca, Cu and Zn for the cultivars in stress condition was similar between them and presented smaller values than in control condition.

It is also important to observe a small variation between the cultivars while the highest values observed in the cultivar TTO. No conclusion can be summarized from the assessment of Fe mass over time since a considerable variation between the results within each treatment was observed. For all other nutrients (S, P, Mg, Mn, Mo, and K) that the regression models were possible to be adjusted, we can observe a higher amplitude of variation between the equation adjusted for the control in relation to the equation adjusted for the stress condition, and it is more relevant in TTO compared to YOSH (Figure 8).

Figure 8. The relationship among tomato cultivars in different Cd (35 μ M) exposure periods in root nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn). Solid black lines represent Tropic Two Orders cultivar (TTO) under control condition, dotted black lines represent TTO cultivar under Cd-stress condition, solid grey lines represent YOSHmatsu (YOSH) in control condition, and Dotted grey lines represent YOSH cultivar in Cd-stress condition.

Using nutrient accumulation data in roots over growing time of both stress condition and control condition, linear regression models were adjusted when possible and non-linear were adjusted when were necessary (figure 8). The regression for Cd effects on nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn) in tomato root can be checked in APPENDIX B

In the total Cd dry mass of stems, a linear increase over time was similarly observed for both cultivars, contrary to the cadmium mass quantified in the roots, whose greatest increase was noticed in YOSH (Figure 9). Regarding the stems, the TTO plants presented higher concentration of Cd in relation to the YOSH ones at all exposure times, except for the eighth day, when differences among cultivars were not observed (Table 2).

As well as for the data obtained by root analysis, a regression model for the nutrient mass in stem over time. For Mn it was possible to observe that the behavior of if its mass in stem in YOSH cultivar did not vary within stress condition, being that for TTO a decrease in the mass of this nutrient in all the evaluated times was observed for stress condition in relation to control condition. For all other evaluated nutrients (Ca, Cu, S, Fe, P, Mg, Mn, Mo, K, Zn) a drop in nutrient uptake was observed in stress condition in relation to the control condition at all evaluated times. This drop-in stress condition compared to the control condition was higher in YOSH compared to TTO in S.

Figure 9. The relationship among tomato cultivars in different Cd (35 μ M) exposure time in stem nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn). Solid black lines represent Tropic Two Orders cultivar (TTO) under control condition, dotted black lines represent TTO cultivar under Cd-stress condition, solid grey lines represent YOSHmatsu (YOSH) in control condition, and Dotted grey lines represent YOSH cultivar in Cd-stress condition.

With the stem nutrient accumulation under stress and control conditions as well as Cd accumulation data under stress condition, it was possible to adjust linear or non-linear regression models over growing time. (Figure 9). The regression for Cd effects on nutrient

accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn) in tomato stem can be checked in APPENDIX C.

Similar to the stems, in leaves it was observed a trend of linear increase in Cd accumulation as a function of the time length of the experiment as observed for both cultivars (Figure 10). Concerning the leaves measurements, TTO presented the highest concentration of Cd at the time of two, six and eight days of exposure, while YOSH presented the highest concentration of the metal on the fourth day of exposure (Table 2).

An increase of the nutrient accumulation in leaves was observed over time for both cultivars and different treatments (control and stress condition). Note that, in stress condition, it could be detected a reduction in the accumulation in the control condition of all evaluated nutrients, even though it occurs in a lower intensity for Mn. It is also possible to observe a more pronounced reduction in the accumulation of S, P, Mo, K, and Zn in stress condition concerning the control condition in the TTO cultivar comparing to the YOSH.

Figure 10. The relationship among tomato cultivars in different Cd (35µM) exposure time in leaf nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn). Solid black lines represent Tropic Two Orders cultivar (TTO) under control condition, dotted black lines represent TTO cultivar under Cd-stress condition, solid grey lines represent YOSHmatsu (YOSH) in control condition, and Dotted grey lines represent YOSH cultivar in Cd-stress condition.

The data of nutrient accumulation and Cd accumulation in leaves also were adjusted linear regression models whenever possible and in cases where linear regressions were not possible was adjusted model of non-linear regression. This adjustment was taken for the data obtained over growing time for the two cultivars studied in control condition and stress condition (Figure 10). The regression for Cd effects on nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn) in tomato leaf can be checked in APPENDIX D.

5.5. Nutritional status of tomato cultivars

Overall, nutrient levels accumulated in dry mass of each plant organ in the tomato cultivars were disturbed by Cd treatment, except the accumulation of some nutrients in roots (*e.g.*, Fe, K), stem (*e.g.*, Mn) and leaf (*e.g.*, Mn) of YOSH-plants (Table 2). Regarding the total dry mass, the key decreases of nutrient accumulation induced by Cd concentration over time in TTO compared to YOSH genotype (both comparing to their control conditions) were observed considering the other elements, mainly Ca (in roots and leaves), S (in roots and leaves), Cu (in roots and leaves), Fe (in roots, stems, and leaves), P (in roots and leaves), Mg (in roots and leaves), Mn (in roots, stems, and leaves), Mo (in roots and leaves), K (in roots, stems, and leaves), and Zn (in roots and leaves).

Under Cd treatment, the contrast of nutritional accumulation by total dry mass of each organ over time showing higher means in YOSH genotype comparing to TTO was observed for Ca (in stems), S (in roots, stems, and leaves), Fe (in roots), P (in roots and leaves), Mg (in roots and leaves), Mn (in roots, stems, and leaves), Mo (in roots, stems, and leaves), K (in roots, stems, and leaves), and Zn in leaves (Table 2). Despite that, higher accumulation average values in TTO plants compared to YOSH for Mg and Zn in the stem (Table 2) were also detected.

Considering the nutrient concentrations per gram of root dry mass under treatment submitted to the Cd presence, the YOSH plants presented of higher accumulation average

concerning TTO for Ca (in plants of two days exposed to the metal), Fe (four days of assays), Mn (two days of assays). On the contrary, higher accumulation averages in TTO root dry mass comparing to YOSH were measured for Mg (in the second-day plants), P (also in the second day), Cu (in the second and eighth days), Mo (in the eighth day) and finally, Zn (in the fourth and eighth days) (Table 2).

In nutrient concentration in stem the highest concentrations of Ca (in second, fourth, and sixth days), Mg (in second, sixth, and eighth days), Mn (in second, sixth, and eighth days), P (in second, fourth, and sixth days), Cu (in all the analyzed times) and Zn (in second, sixth, and eighth days) were observed in TTO plants; and S (in second, fourth, and eighth days) and Mo (in second, sixth, and eighth days) for YOSH (Table 2).

In the dry leaf mass and considering the treatment with Cd, the TTO presented higher concentration means for Ca (in all the analyzed times), Mg (in the eighth day), Mn (in fourth and eighth days), P (in second and eighth days), S (in the second day of assay), Cu (in second, sixth, and eighth days), Mo (in second, fourth and sixth days), Zn (in the eighth days), while in this organ YOSH presented higher concentration averages only for sulfur (S) in four days of experiment (Table 2).

Table 2. Cadmium (Cd) and nutrients' concentrations in the roots, stems, and leaves of different cultivar tomato (TTO and YOSH) in control and stress conditions represented with their respective sample standard deviation.

[] metal	Time (d)	0			2		4		6		8	
	[] Cd (mg/g)	0	0	35	0	35	0	35	0	35		
	Root											
Ca (mg/g)	TTO	5.06±0.14	5.06±0.24	4.68±0.12	5.27±0.34	5.28±0.12	5.96±0.06	6.32±0.58	5.95±0.56	6.37±0.27		
	YOSH	5.52±0.23	5.02±0.11	5.37±0.14	5.89±0.43	5.35±0.09	7.21±1.04	6.62±0.69	5.58±0.39	5.92±0.19		
Cd (mg/g)	TTO	-	-	1.51±0.09	-	2.14±0.16	-	2.63±0.15	-	2.65±0.05		
	YOSH	-	-	1.38±0.2	-	2.48±0.26	-	2.79±0.37	-	2.6±0.33		
Fe (mg/g)	TTO	2.99±0.26	2.34±0.45	2.79±0.11	2.23±0.09	2.41±0.08	2.94±0.46	3.06±0.35	1.57±0.04	2.62±0.27		
	YOSH	3.69±0.43	3.03±0.39	2.71±0.48	2.87±0.17	2.87±0.17	2.61±0.46	2.88±0.30	1.85±0.37	2.29±0.06		
K (mg/g)	TTO	17.98±1.7	19.04±0.46	16.79±1.48	16.87±1.57	16±1.40	14.87±1.58	15.38±0.40	12.48±0.61	15.6±1.38		
	YOSH	19.02±0.71	18.43±0.51	18.37±0.64	16.45±0.82	16.93±1.65	14.3±1.59	15.96±0.67	11.47±0.67	15.95±0.48		
Mg (mg/g)	TTO	5.41±0.41	5.52±0.37	5.99±0.1	5.49±0.35	6.13±0.21	6.48±0.91	6.64±0.59	6.45±0.2	6.16±0.55		
	YOSH	6.49±0.4	6.01±0.46	5.87±0.7	5.07±0.38	5.86±0.45	6.22±0.18	5.85±0.35	5.99±0.45	5.79±0.24		
Mn (mg/g)	TTO	0.47±0.06	1.17±0.12	0.26±0.02	1.46±0.08	0.20±0.01	1.35±0.09	0.24±0.03	0.87±0.08	0.27±0.01		
	YOSH	0.69±0.09	1.26±0.09	0.34±0.03	1.46±0.24	0.23±0.02	1.38±0.27	0.27±0.04	0.81±0.10	0.34±0.06		
P (mg/g)	TTO	10.00±0.59	10.46±0.4	9.41±0.69	10.53±0.22	9.11±0.38	10.8±1.09	9.14±0.37	8.11±0.51	7.7±0.26		
	YOSH	9.24±0.64	8.71±0.37	8.10±0.53	9.25±0.64	8.97±0.43	9.75±0.57	8.98±0.76	6.59±0.49	7.57±0.38		
S (mg/g)	TTO	5.08±0.45	5.37±0.24	5.01±0.5	5.18±0.14	5.07±0.35	5.67±0.27	5.52±0.23	6.20±0.36	5.24±0.19		
	YOSH	4.85±0.28	4.27±0.23	4.56±0.38	4.48±0.56	5.78±0.42	4.55±0.06	5.47±0.41	6.09±0.08	5.41±0.33		
Cu (µg/g)	TTO	68±8	115±13	72±5	108±3	63±6	88±4	63±1	54±4	57±3		
	YOSH	54±9	82±6	48±7	95±19	64±6	82±9	52±7	50±5	45±3		
Mo (µg/g)	TTO	16±2	14±1	12±1	12±0	12±0	13±1	13±1	16±2	13±0		
	YOSH	14±1	10±0	12±1	10±1	13±1	11±0	13±1	15±0	12±0		

Zn (µg/g)	TTO	106±12	91±5	64±6	112±16	57±2	73±4	51±4	57±5	49±4
	YOSH	95±13	81±5	64±1	81±8	48±3	86±11	49±5	56±3	38±3
Stem										
Ca (mg/g)	TTO	8.83±0.45	10.14±0.27	10.51±0.06	11.00±0.47	9.76±0.25	11.54±1.44	10.8±0.22	10.75±0.53	9.28±0.22
	YOSH	8.27±0.25	9.88±0.26	9.45±0.89	11.19±0.64	9.16±0.55	9.86±1.64	9.57±0.12	10.44±0.39	9.12±0.16
Cd (mg/g)	TTO	-	-	0.36±0.00	-	0.28±0.03	-	0.28±0.01	-	0.27±0.05
	YOSH	-	-	0.31±0.02	-	0.14±0.10	-	0.19±0.00	-	0.29±0.01
Fe (mg/g)	TTO	0.09±0.03	0.05±0.00	0.06±0.02	0.07±0.01	0.06±0.00	0.08±0.02	0.05±0.01	0.08±0.04	0.05±0.01
	YOSH	0.07±0.01	0.08±0.03	0.04±0.00	0.05±0.01	0.09±0.03	0.05±0.011	0.04±0.00	0.09±0.04	0.04±0.01
K (mg/g)	TTO	21.28±0.96	19.5±1.12	18.5±0.79	17.95±0.97	20.49±1.21	16.66±0.44	18.34±1.46	20.06±2.25	17.02±0.6
	YOSH	20.8±1.45	19.86±1.21	20.14±1.97	20.26±1.65	20.5±1.56	15.84±1.22	18.01±1.86	19.34±0.96	19.81±2.27
Mg (mg/g)	TTO	4.96±0.37	4.44±0.23	4.68±0.09	3.88±0.17	4.89±0.14	3.71±0.08	4.79±0.1	4.23±0.2	4.32±0.2
	YOSH	4.23±0.45	3.85±0.07	3.92±0.33	3.75±0.3	3.61±0.73	3.12±0.04	2.85±0.08	3.59±0.11	3.61±0.14
Mn (mg/g)	TTO	0.08±0.01	0.07±0.00	0.06±0.00	0.04±0.00	0.05±0.00	0.03±0.00	0.05±0.00	0.05±0.00	0.05±0.00
	YOSH	0.06±0.01	0.06±0.00	0.05±0.00	0.02±0.00	0.04±0.01	0.02±0.00	0.04±0.00	0.04±0.00	0.04±0.00
P (mg/g)	TTO	6.8±0.47	7.31±0.3	7.47±0.31	6.43±0.28	7.13±0.21	5.26±0.33	7.89±0.38	6.75±0.1	6.99±0.65
	YOSH	6.69±0.16	6.4±0.14	6.05±0.53	6.13±0.19	6.61±0.23	4.88±0.32	5.88±0.11	5.68±0.27	6.96±0.19
S (mg/g)	TTO	1.71±0.18	1.86±0.03	1.78±0.08	1.53±0.08	1.96±0.06	1.59±0.06	2.14±0.13	1.62±0.03	1.84±0.20
	YOSH	2.36±0.11	2.58±0.08	2.05±0.18	2.43±0.11	2.27±0.16	2.34±0.08	2.00±0.04	2.39±0.06	2.21±0.07
Cu (µg/g)	TTO	0.46±0.03	0.53±0.01	0.51±0.02	0.47±0.02	0.43±0.03	0.4±0.01	0.42±0.02	0.51±0.01	0.42±0.03
	YOSH	0.38±0.05	0.46±0.00	0.35±0.04	0.4±0.02	0.33±0.05	0.34±0.01	0.28±0.01	0.43±0.01	0.32±0.01
Mo (µg/g)	TTO	0.36±0.03	0.42±0.02	0.34±0.00	0.31±0.02	0.42±0.01	0.39±0.03	0.48±0.02	0.35±0.00	0.33±0.02
	YOSH	0.5±0.04	0.53±0.01	0.46±0.04	0.41±0.02	0.54±0.04	0.4±0.02	0.55±0.01	0.46±0.01	0.5±0.01
Zn (µg/g)	TTO	7±0.3	6±0.3	6±0.4	5±0.1	4±0.1	5±0.1	4±0.1	5±0.1	4±0.3
	YOSH	5±1.5	5±0.2	4±0.7	4±0.1	3±1.9	3±0.0	2±0.0	4±0.1	3±0.1
Leave										
Ca (mg/g)	TTO	22.94±1.26	23±0.76	22.91±0.73	24.25±0.77	22.05±0.39	23.97±0.68	23.34±1.65	22.58±1.26	25.85±0.66
	YOSH	20.54±0.51	22.41±0.19	19.87±0.5	24.53±1.08	20.21±0.51	23.44±0.96	20.37±0.28	22.69±0.18	20.84±0.99

Cd (mg/g)	TTO	-	-	0.37±0.00	-	0.33±0.01	-	0.46±0.04	-	0.54±0.03
	YOSH	-	-	0.32±0.01	-	0.4±0.00	-	0.37±0.01	-	0.37±0.02
Fe (mg/g)	TTO	0.18±0.02	0.19±0.08	0.15±0.01	0.25±0.14	0.14±0.02	0.18±0.04	0.13±0.04	0.17±0.01	0.16±0.03
	YOSH	0.20±0.02	0.17±0.01	0.21±0.089	0.16±0.02	0.13±0	0.16±0.01	0.12±0.01	0.16±0.01	0.16±0.05
K (mg/g)	TTO	13.57±1.41	15.79±0.75	13.17±0.87	13.92±0.64	12.55±0.42	13.23±1.09	13.79±0.73	12.34±1.08	14.04±0.67
	YOSH	13.44±1.20	15.19±0.33	13.97±1.35	14.86±0.79	12.87±0.82	12.52±1.03	14.54±0.67	11.51±0.75	14±0.98
Mg (mg/g)	TTO	5.21±0.35	5.27±0.18	5.01±0.29	4.64±0.12	4.7±0.08	4.3±0.24	4.84±0.23	4.27±0.03	5.19±0.18
	YOSH	5.19±0.29	5.33±0.09	5.13±0.24	4.93±0.26	4.77±0.25	4.46±0.30	5.04±0.19	4.45±0.16	4.73±0.20
Mn (mg/g)	TTO	0.17±0.01	0.16±0	0.16±0.01	0.14±0.00	0.18±0.00	0.11±0.00	0.18±0.02	0.09±0.01	0.22±0.00
	YOSH	0.16±0.01	0.15±0.00	0.15±0.01	0.13±0.01	0.15±0.00	0.11±0.00	0.16±0.00	0.1±0.01	0.18±0.01
P (mg/g)	TTO	7.93±0.4	7.58±0.21	7.54±0.19	7.29±0.16	6.48±0.12	6.68±0.2	7.87±0.44	6.12±0.08	7.81±0.35
	YOSH	7.8±0.27	7.71±0.13	7.3±0.01	7.17±0.29	6.89±0.32	7.02±0.30	7.09±0.14	5.74±0.23	7.04±0.36
S (mg/g)	TTO	5.92±0.22	5.92±0.19	6.23±0.15	5.97±0.07	5.68±0.33	5.43±0.16	6.47±0.46	7.15±0.51	7.77±0.02
	YOSH	5.76±0.21	5.71±0.06	5.46±0.16	5.87±0.24	6.18±0.14	5.75±0.27	6.97±0.24	6.28±0.07	7.81±0.38
Cu (µg/g)	TTO	11±1.2	12±0.5	11±0.8	12±0.4	8±0.1	9±0.6	8±0.9	8±0.5	8±0.2
	YOSH	11±0.4	12±0.3	9.00±0.6	11±0.7	8±0.3	10±0.4	6±0.4	8±0.5	6±0.3
Mo (µg/g)	TTO	14±1.1	13±1.3	13±0.6	12±0.0	13±0.5	10±0.4	15±1.0	12±0.9	17±0.4
	YOSH	12±0.3	10±0.1	10±0.7	11±0.3	11±0.7	10±0.5	13±0.7	10±0.5	15±1.2
Zn (µg/g)	TTO	35±1.8	31±2.1	28±1.4	24±0.9	25±0.4	21±0.5	24±2.4	18±0.6	25±0.4
	YOSH	39±1.6	33±2.0	29±1.8	26±0.5	26±0.9	23±1.7	23±0.5	19±1.9	23±1.0

5.6. Nutrient absorption and use efficiency

The data obtained by the previously described equation for nutrient absorption (Equation 4) were submitted to ANOVA, and afterward, the means were evaluated using the Tukey's test. In this analysis, it was possible to conclude that a significant difference was not observed even for different cultivar or stress condition for Ca and K measurements. The interaction between evaluated and stress condition was significant for Cu p-value = 0.046, Mg p-value = 0.00413, P p-value = 0.025 and S-value = 0.001. There was no significant difference between cultivars for Fe p-value = 0.99 and Mn p-value = 0.21, with difference between treatments (p-value = 0.007 and p-value <0.001). In spite of the significant interaction, a significant difference was observed between cultivars and between treatments for Mo (p-value = 0.036 and p-value = 0.00409 respectively) and Zn (p-value <0.001)

Both genotypes (YOSH and TTO) exhibited similar NA for nutrients evaluated when grown without Cd-stress, except for S and Zn, for which YOSH and TTO, respectively, presented the highest mean values of NA in the control condition (Figure 11).

Figure 11. Means of nutrient absorption (NA) in tomato genotypes TTO and YOSH in eight days after Cd addition, in control and stress condition.

In plants grown with Cd in the nutrient solution, TTO genotype presented higher NA for Mg, P and Zn compared to YOSH. The Cd presence induced the decreasing of NA in YOSH plants for the nutrients Cu, Fe, Mg, S, and Zn, while in TTO it induced the reduction of NA for Fe and Zn. In addition, the Cd led an increasing trend for Mg, Mn, P, and S in TTO, and Mn and Mo in YOSH.

The NUE data also were submitted to the mean test. The results observed for iron concentration did not present a significant difference, probably due to the high coefficient of variation (71.01%). For the results of K, Ca and Mo only a significant difference between the concentrations was observed (p-value <0.001; p-value = 0.003 and p-value <0.001,

respectively). A significant interaction between cultivar and treatment for Mg, P, S and Zn (p-value = 0.021, p-value = 0.031, p-value = 0.00014 and p-value = 0.00044, respectively) was observed. Although the interaction was not significant, a significant difference was observed between cultivars and treatments for Mn (p-value <0.001 and p-value = 0.011, respectively) and Cu (p-value <0.001).

In the control condition, YOSH and TTO presented the highest NUE averages for Zn and S, respectively, and similar means for the other nutrients. Under Cd stress condition, YOSH presented a higher mean of NUE for Ca, Cu, Mg, Mn, P, and S compared to TTO (Figure12). Additionally, for the other nutrients, statistical differences were not detected among the cultivars. Cd treatment induced a decrease in NUE for nutrients, except for Fe (in both cultivars) and Zn (YOSH).

Figure 12. Means of nutrient use efficiency (NUE) in tomato genotypes TTO and YOSH in eight days after Cd addition, in control and stress condition.

5.7. Root proteomics identification and quantification

A total of, 2,443 proteins were identified in TTO and 2,431 in YOSH with minimum one identified peptide. Besides, we quantified 1,909 proteins in TTO and 1,897 in YOSH with at least one peptide was used for quantification. From this 246 in TTO and 69 in YOSH, were influenced by the stress treatment and differentially accumulated protein (DAP) with $p < 0.001$ (APPENDIX E and F).

Before performing the analyses of variance (ANOVA) for the identification of the DAPs, the abundance results of quantified proteins were used for PCA. In the PCA plots, it is possible to observe the grouping made for the stress in all evaluation times was well all the control conditions for PC2 in TTO (Figure 13 A) and PC1 in YOSH (Figure 13 B). The grouping made by the PCA was used to filter the data facilitating the execution of the ANOVA.

Figure 13. Principal Component Analysis (PCA) the 1,909 proteins in TTO (A) and the 1,897 proteins in YOSH (B) under stress at different times.

The differentially accumulated protein (DAP) Set enrichment analysis was performed (SEA) for these proteins influenced by stress in both cultivars. For molecular

function, category 169 and 45 proteins were significant GO terms for TTO and YOSH respectively (Figure 14). In this category, in addition to the molecular functions clusters contemplated by proteins significant in YOSH, there were also others clusters with expressive proteins in TTO like transnational regulator activity, molecular transducer activity, molecular function regulator and transporter activity. The percentage of proteins significant in these clusters was less than 20%, and most proteins were influenced by stress in TTO with the same functions as proteins influenced by stress in YOSH. It is important to note that the number of proteins influenced by stress in TTO higher than in YOSH. It is important to observe that the cluster with the more significant amounts of proteins was catalytic activity. The percentage of DAPs in this cluster in YOSH is higher than in TTO, but it is important to emphasize that the cultivar TTO present the most substantial amount of DAPs and as well the substantial amount of cluster.

Figure 14. Molecular function of 169 and 45 DAP in TTO (A) and YOSH (B) tomato roots under Cd stress after two, four, six and eight days.

Only for TTO there were DAPs with transporter activity, being this cluster composed of eight proteins. This function is important because it can help to understand the absorption and translocation of the Cd and the other substances that can change in the stress condition. The presence of DAPs with this activity only in TTO cultivar can be related to the most considerable variations in TTO for the uptake nutrients than in YOSH.

Table 3. Proteins classified as transporter activity differentially accumulated proteins in tomato cultivar TTO

Accession	description	Family
K4CDC2	Uncharacterized protein	ATP SYNTHASE, H ⁺ -TRANSPORTING, MITOCHONDRIAL FO COMPLEX, SUBUNIT G
K4DAV2	ATP synthase subunit d, mitochondrial	ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL
K4BGT9	Uncharacterized protein	MITOCHONDRIAL OUTER MEMBRANE PROTEIN PORIN 1
K4AXB5	Uncharacterized protein	V-TYPE PROTON ATPASE SUBUNIT D
K4ATR9	Uncharacterized protein	MITOCHONDRIAL OUTER MEMBRANE PROTEIN PORIN-LIKE-RELATED
K4B8B1	Uncharacterized protein	ABC TRANSPORTER B FAMILY MEMBER 7-RELATED
K4C3F2	Uncharacterized protein	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 HOMOLOG 1-RELATED
K4B778	Uncharacterized protein	SUBFAMILY NOT NAMED

The second category evaluated was "protein class" in which 147 significant DAPs were detected for TTO and 40 for YOSH, under GO terms (Figure 15). In addition to the clusters of DAPs in YOSH cultivar, in the TTO cultivar, it can also be observed transporter proteins, chaperone, ligase, cytoskeletal, signaling molecule, enzyme modulator, carrier protein, receptor, and storage protein. In both cultivars, the cluster that has the highest percentage of DAPs was oxydoreductase 25% in YOSH and 20% in TTO. Another cluster with high representativeness in this analysis is hydrolase with 20% in YOSH and 28% in TTO.

Figure 15. Protein class of 147 and 40 DAP in TTO (A) and YOSH (B) tomato roots under Cd stress after two, four, six and eight days.

The proteins were also classified in the Biological process category. In these category 177 differentially accumulated proteins for TTO and 53 differentially accumulated proteins for YOSH were significant Go terms (Figure 16). Even with the considerable variation in the number of significant proteins in TTO in YOSH the biological processes in which they are involved are practicing the same, except for the developmental process, which only appeared in TTO, and represented with only 3% of TTO proteins. Concerning the biological process, it is important to emphasize that in the two cultivars most of the proteins that varied with the stress caused by the Cd are proteins of the metabolic process. Another cluster that also stands out due to the similarity in the two cultivars is the response to stimulus proteins with 11% for both cultivars.

Figure 16. Biological process of 177 and 53 DAP in TTO (A) and YOSH (B) tomato roots under Cd stress after two, four, six and eight days.

An important cluster for a better understanding of the tomato behavior under Cd stress is the response to a stimulus. It is not surprised being present in both cultivars since it is the group of proteins often responsible for any level of stress tolerance. It is possible to observe 20 DAPs in TTO and 6 in YOSH (Table 4), YOSH may possible not present the same stress of TTO. Probably the TTO enters a stress state with a lower concentration of Cd, and in this concentration, the stress is more sense in TTO than in YOSH.

Table 4. Proteins classified as a response to stimulus differentially accumulated proteins in tomato cultivar (TTO and YOSH)

Accession	Description	Family
TTO		
K4BKB2	Uncharacterized protein	SUBFAMILY NOT NAMED
Q7XAV2	Superoxide dismutase [Cu-Zn]	SUPEROXIDE DISMUTASE [CU-ZN]
K4CMV0	Peroxidase	SUBFAMILY NOT NAMED
K4D0Y5	Uncharacterized protein	LEUCINE-RICH REPEAT (LRR) FAMILY PROTEIN
K4D1H1	Uncharacterized protein	SUBFAMILY NOT NAMED
K4AX22	Superoxide dismutase [Cu-Zn]	SUPEROXIDE DISMUTASE [CU-ZN]
K4CWC5	PR10 protein	SUBFAMILY NOT NAMED
K4AVE6	Pyruvate kinase	PYRUVATE KINASE-RELATED
K4BI68	Uncharacterized protein	ENDOPLASMIC RETICULUM CHAPERONE BIP
K4C0T4	Peroxidase	SUBFAMILY NOT NAMED
K4C6L0	Protein disulfide-isomerase	PROTEIN DISULFIDE ISOMERASE-LIKE 1-2
K4B277	Peroxidase	PEROXIDASE 71
K4CVS3	Pyruvate kinase	PLASTIDIAL PYRUVATE KINASE 1, CHLOROPLASTIC
K4D1H0	Uncharacterized protein	SUBFAMILY NOT NAMED
K4B413	Uncharacterized protein	L-ASCORBATE PEROXIDASE 3
K4BSR4	Annexin	ANNEXIN D2
K4CN78	Pyruvate kinase	PLASTIDIAL PYRUVATE KINASE 3, CHLOROPLASTIC
K4CN56	Uncharacterized protein	ABSCISIC ACID RECEPTOR PYL1
K4DBB7	Peroxidase	SUBFAMILY NOT NAMED
K4CUU6	Peroxidase	SUBFAMILY NOT NAMED
YOSH		
Q5NE21	Carbonic anhydrase	BETA CARBONIC ANHYDRASE 4
Q3I5C4	Cytosolic ascorbate peroxidase 1	L-ASCORBATE PEROXIDASE 1, CYTOSOLIC
K4D1H0	Uncharacterized protein	SUBFAMILY NOT NAMED
K4D1H1	Uncharacterized protein	SUBFAMILY NOT NAMED
K4BTH6	Peroxidase	SUBFAMILY NOT NAMED
K4CC70	Uncharacterized protein	SUBFAMILY NOT NAMED

As well in the other categories evaluated for Cellular component the cultivar TTO also presented the higher number of differentially accumulated proteins significant GO

terms. In total, 135 for TTO and 35 for YOSH (Figure 17). However, the difference between the clusters numbers of cellular components category represented in the two cultivars was lower than for the other categories evaluated. In this category TTO only presented two clusters more than YOSH, proteins supramolecular complex and extracellular region with only 3% of total proteins significant.

Figure 17. Cellular component of 135 and 35 DAP in TTO (A) and YOSH (B) tomato roots under Cd stress after two, four, six and eight day

In the pathway, category 51 DAPs in TTO cultivar were significant in GO terms, and only 13 DAPs were significant for YOSH (Table 5). In consonance with the other categories evaluated, TTO cultivar presented a more significant number of clusters than YOSH, which was expected since the number of DAPs in the TTO is more extensive than in YOSH. Some clusters that help us to understand the characteristics observed in the tomato in stress caused by the Cd, although present in both cultivars, present a higher number of proteins in the TTO than in the YOSH, which is the case of apoptosis signaling proteins.

Table 5. Pathway classification of differentially accumulated proteins in tomato cultivar (TTO and YOSH) during Cd treatment.

YOSHmatsu cultivar		
Pathway Accession	Uniprot Accession	Term Description
P00026	K4B978	Heterotrimeric G-protein signaling pathway-Gi alpha, and Gs alpha-mediated pathway
P00024	K4D3E4	Glycolysis
P00006	K4BJ06	Apoptosis signaling pathway
P02744	K4D3E4	Fructose galactose metabolism
P00027	K4B978	Heterotrimeric G-protein signaling pathway-Gq alpha, and Go alpha-mediated pathway
P02762	K4C1C9	Pentose phosphate pathway
P02783	K4CJ67	Tryptophan biosynthesis
P02737	K4CYL4 K4CJ67	Cysteine biosynthesis
P00029	K4B978	Huntington disease
P00060	K4D6E8	Ubiquitin proteasome pathway
P00013	K4D6E8	Cell cycle
P00051	K4CW40	TCA cycle
Tropic Two Orders cultivar		
Pathway Accession	Uniprot Accession	Term Description
P00024	K4CN78 K4CVS3	Glycolysis
P00032	D9J1Y9,	Insulin/IGF pathway-mitogen activated protein kinase

	K4AZN6	kinase/MAP kinase cascade
P00019	D9J1Y9, K4AZN6	Endothelin signaling pathway
P02773	P43282	S adenosyl methionine biosynthesis
P00034	K4ASZ8	Integrin signalling pathway
P00031	D9J1Y9 K4AZN6	Inflammation mediated by chemokine, and cytokine signaling pathway
P00060	K4BAN9	Ubiquitin proteasome pathway
P02749	K4BDZ7	Leucine biosynthesis
P02775	K4AYN8	Salvage pyrimidine ribonucleotides
P02766	K4CVH1	Phenylethylamine degradation
P02738	K4AYN8	De novo purine biosynthesis
P02762	K4BNC2	Pentose phosphate pathway
P02737	K4CYL4, K4CJ67	Cysteine biosynthesis
P00036	D9J1Y9	Interleukin signaling pathway
P02787	K4BAF3	Vitamin B6 metabolism
P00047	D9J1Y9	PDGF signaling pathway
P02759	K4BAF3	PLP biosynthesis
P00013	K4BAN9	Cell cycle
P00018	D9J1Y9 K4AZN6	EGF receptor signaling pathway
P00049	D9J1Y9 K4BI68, K4AZN6	Parkinson disease
P02772	K4AXC0	Pyruvate metabolism
P00051	K4AXC0	TCA cycle
P04372	K4DBP0	5-Hydroxytryptamine degradation
P00035	D9J1Y9, K4AZN6	Interferon-gamma signaling pathway
P00006	D9J1Y9 K4BI68, K4AZN6	Apoptosis signaling pathway
P02740	K4AYN8	De novo pyrimidine ribonucleotides biosynthesis
P02730	K4CK47	Asparagine and aspartate biosynthesis

P02747	K4B8G4	Histidine biosynthesis
P06959	D9J1Y9	CCKR signaling map
P00029	K4ASZ8	Huntington disease
P02776	K4BAF3	Serine-glycine biosynthesis
P02745	K4AXS2	Glutamine glutamate conversion
P00021	D9J1Y9	FGF signaling pathway
	K4C891, K4AZN6	
P00003	D9J1Y9 K4AZN6	Alzheimer disease-amyloid secretase pathway
P00052	D9J1Y9 K4AZN6	TGF-beta signaling pathway
P02783	K4CJ67	Tryptophan biosynthesis

In this category, it is important to emphasize the apoptosis signaling proteins, because the apoptosis is one characteristic usually observed in plants under toxic metal stress. In this cluster, there is only one DAP in YOSH and three DAPs in TTO. This DAP observed in YOSH is one protein upregulated (Figure 18 D) in the eighth day without variation in the other days. About the three DAPs in TTO is possible to observe two upregulated (Figure 18 B, C) and one downregulated (Figure 18 A).

The activity of apoptosis signaling proteins in stress condition can be observed morphologically by the presence of the smallest necrotic spots more evident in the cultivar TTO than in Cultivar YOSH, becoming more evident in the last days of exposure, as well as apoptosis signaling proteins.

Figure 18. Variability plots of apoptosis signaling proteins in Cd stress and control condition in TTO (A, B, and C) and YOSH(D).

The TTO considering the sensitive genotype under stress condition showed exclusive clusters in all categories evaluated, as well as higher proteins amounts in all the shared clusters. In the heatmaps is easily observed this amount of DAPs variability between TTO and YOSH independent of the exposure time (Figure 19). Both heatmaps also showed a significant amount of proteins with small changes under stress condition. It is possible to observe different protein behavior in both cultivars. One of this protein's behavior is with significant variation only in one exposure time or more than one time but not in all. Another behavior observed is proteins with the same variation behavior over time (behavior more evident in TTO). In YOSH heatmap is possible to see the greater similarity between two and four days of stress evidencing a higher percentage of immediate response proteins.

Figure 19. Hierarchical clustering and heatmap analysis of differentially accumulated proteins observed in tomato roots of TTO (A) and YOSH (B)

6. DISCUSSION

In the present research, it was performed a temporal dynamics evaluation of the growth and accumulation of Cd and nutrients in tomato cultivars, aiming to highlight contrasting patterns of response related to the modulation of translocation and biomass production among cultivars.

The reduction of root growth induced by Cd is known to be one of the earliest and distinct symptoms of Cd toxicity (Rodríguez-Serrano *et al.*, 2006; Lux *et al.*, 2011). Other authors, in turn, have pointed out that Cd concentrations in organs, which indicate the status of uptake and distribution, are important criteria for clarifying the toxicity in plants (Gao *et al.* 2010; Xu *et al.* 2009; Wang *et al.*, 2015).

It was verified that in both cultivars the Cd-induced the decrease of the means of the root morphological parameters evaluated. According to authors verified that Cd excess can affect the range of processes that result in modifications of the root architecture, probably through hormonal signals (Alves *et al.*, 2017; Pompeu *et al.*, 2017; Souza *et al.*, 2017), generating damages of reduction in the length and volume of the root. These parameters vary according to plant species (Lu *et al.*, 2013; Wang *et al.*, 2015; Xia *et al.*, 2016; Borges *et al.*, 2019). This reduction may also be directly involved in water and nutrients absorption by plants (Pinto, Ferreira, 2015; Zhao *et al.*, 2017).

Although the cultivar TTO showed the highest decay induced by Cd for the morphological parameters, only the parameters of dry mass differed in the treatment with the metal. The YOSH cultivar presented advantage in terms of the production of dry mass for all the organs, under Cd stress condition.

In both cultivars, there was a more considerable Cd accumulation in the roots, although the accumulation of this element in the tomato tissues occurred in all organs within the first 24 hours of exposure and continued over time, which is in agreement with temporal studies of the accumulation of Cd contamination, such as for maize (Anjum *et al.*, 2015), soybean (Perez-Chaca *et al.*, 2014) and tomato (Borges *et al.*, 2018).

The accumulation of Cd predominantly in the root has been described as the main mechanism to limit metal transport and accumulation in leaves to protect shoots and the photosynthetic apparatus against Cd dangerous effects (Bashri, Prasad, 2015; Branco-Neves *et al.*, 2017). The highest Cd allocation in the roots was detected in the YOSH cultivar, related

to its lower translocation index and lower concentration of Cd in stem and leaf in most exposure times.

In this present experiment, the lipid peroxidation induced by Cd toxicity was also determined by evaluating the accumulation of MDA, an aldehyde that represents one of the main stress indicators in cells when membrane lipids are affected by reactive oxygen species (ROS).

Heavy metals cause molecular oxygen reduction (O_2), culminating in the production of unstable intermediates, that is, potentially increasing the production of ROS, such as hydrogen peroxide (H_2O_2). Besides, those are also generated at low concentrations in plant cells as signaling molecules and during normal processes of aerobic metabolism, such as chloroplast photosynthesis, photorespiration in peroxisomes, as well as the electron transport chain in the mitochondria (Syta *et al.*, 2013), and has a role in cellular expansion facilitating the expanding abilities of the cell wall (Nogueirol *et al.*, 2015).

The excessive production of ROS and substantial oxidative damage generates the so-called oxidative stress (Syta *et al.*, 2013). If not effectively and rapidly removed, excessive levels of ROS are responsible for various damages to macromolecules and cellular structures, which includes RNA, DNA damage, enzyme inhibition, protein oxidation, peroxidation (oxidative degradation) of membrane lipids, loss of membrane selectivity and cell death (Reis *et al.*, 2016).

The increase in Cd-induced MDA and H_2O_2 levels has been reported in several plant species, such as Arabidopsis (Cho, Sohn, 2004), rice (Tripathi *et al.*, 2013), cotton (Khan *et al.*, 2013), tomato (Borges *et al.*, 2018). According to the results obtained in the present thesis, it was possible to note the general pattern of increased levels of stress indicators caused by the metal of both genotypes and tissues analyzed at each exposure time analyzed, although the increase did not follow a linear pattern, and the decreased levels of MDA and H_2O_2 caused by Cd was also observed, which ratifies the relevance of the present study for the verification of the general pattern of the accumulation of stress and response indicators at each time.

In this context, it is necessary to consider that the increase of levels of lipid peroxidation is not only related to the levels of accumulation of Cd in each organ, but also to the balance of the synthesis and activity of antioxidant molecules, the levels of different ROS and the interaction between root and shoot at each exposure time.

Lipid peroxidation is one oxidative stress result influenced by the disequilibrium between ROS production and ROS scavenge. The interference of Cd in this balance, corroborated by the findings of this present research, results in an accumulation of ROS and MDA, which can cause programmed cell death (Jiang *et al.*, 2019).

The induction of apoptosis through ROS in animals is elucidated as described in Wang *et al.* (2019), that using a model of mouse Leydig cells it could be observed an increase in the apoptosis and the cell viability reduction, caused due to the concentration of Cd or the exposure time of the experiment. This increase was correlated to oxidative stress since a concentration-dependent increase in ROS was also observed (Wang *et al.*, 2019a).

Recent research with plant cells (Jiang *et al.*, 2019) correlated programmed cell death (PCD) with stress caused by Cd: besides increased PCD in tobacco cells, Cd also caused an increase in MDA levels. The same correlation was observed in studies evaluating cell: Kumbhakar *et al.*, (2019) evaluated the toxicity of the cadmium sulfide (CdS) in *Nigella sativa* L. and detected an increase of dead cells and an increment in the amount of MDA after the exposure to nanomaterials.

Based on data obtained in this thesis, it was also possible to observe a particular connection between cells death, MDA and H₂O₂ content. Even though it was not performed the quantification of apoptotic cells and the necrotic points observed in both cultivars, it was observed variation in one apoptotic signal protein in YOSH at exposure time and three proteins in TTO. Hence, the variation in apoptotic signal proteins, MDA and H₂O₂ was higher in the less tolerant cultivar (TTO) than in the most tolerant cultivar (YOSH).

The analysis over time revealed that the highest induction of H₂O₂ by Cd-exposure in TTO leaves was the contrast detected between cultivars that was maintained at all exposure times. The H₂O₂ induction by Cd-exposure may be related to both the highest translocation and the lowest efficiency of antioxidant system molecules (such as peroxidases) of TTO compared to YOSH. The cultivar YOSH presented the highest leaf biomass and total biomass in the treatment with Cd. Regarding the differences detected concerning the MDA delta, on the second day of exposure to Cd. YOSH presented the lowest values of delta MDA for root and leaf, suggesting an efficient early response of this cultivar in the different organs, which may constitute a mechanism before the symptoms caused by Cd are evident. In our study, were detected proteins involved in the protect mechanisms to scavenge of ROS in both cultivar. In TTO cultivar were identified peroxidase, superoxido

dismutases, and ascorbate peroxidases. And in YOSH cultivar were identified cytosolic ascorbate peroxidase. Studies have shown that peroxidase abundance and activity of peroxidase increased significantly in tomato roots under Cd stress (Borges, 2018). Research with wheat were observer variation in peroxidases and other proteins involved in the scavenging mechanisms in response to drug stress in as well (Wang *et al.*, 2019b).

For the nutritional analyzes in general, the absorption pattern of the macro and micronutrients followed that of the Cd-induced plant growth (i.e., higher root and leaf dry mass decrease for TTO, and dry mass for the stem, with YOSH the highest mass mean for this organ under treatment with Cd). It is an exception for the accumulation of Fe and K (roots), Mn (stem and leaf) in YOSH. All these results confirm the effect of Cd on nutritional imbalance. The increase of the dry mass of the cultivars over time, besides promoting the increase of the nutrient absorption. Probably can exert a dilution effect of the concentration of each nutrient per gram of dry mass and modulate the level of accumulation in each organ.

When significant differences were detected for the concentration of S, the highest averages were detected for YOSH in comparison to Cd-treated TTO, confirming the more significant accumulation of S in this condition and, therefore, it is possible that other mechanisms are related to the more accumulation of S in YOSH besides the smaller biomass of this cultivar.

Sulfur (S) is an essential element absorbed by the plants in their oxidized state, being later reduced to H₂S (which acts as a secondary messenger for the regulation of levels of transcription factors responsive to heavy metals) and in the first instance cysteine is incorporated before it is used in metabolic processes. The cycle involving cysteine and H₂S is related to the maintenance of levels of bioactive molecules, such as GSH and phytochelatins (PCs), potentially related to Cd-induced stress tolerance (Jia *et al.*, 2016).

The incorporation of S into thiol compounds, such as PCs (which act on Cd sequestration in the vacuole), is known to be crucial for the defense of plants against induced oxidative stress and regulation of the activity of antioxidant molecules (Adhikari *et al.*, 2018; Marques *et al.*, 2019). Besides the relation of such incorporation with the synthesis of phytohormones related to the vegetal tolerance, with the synthesis of chlorophyll and with the photosynthetic apparatus Cd (Gill, Tuteja, 2011; Bashir *et al.*, 2015). By means of such information, it is possible to infer that the greater accumulation of S by YOSH compared to TTO observed in the present study may be a mechanism of tolerance, although further

studies are required to verify the relationship between the accumulation of S and its metabolization for the synthesis of molecules involved in tolerance to Cd.

In addition, the increase of Cd allocation in YOSH roots could be related to the modulation of PC levels (which in turn are associated with the metabolism of S). That sequester Cd from the roots, thus reducing its translocation to the aerial part. In addition to other mechanisms that favor the greater retention of Cd in the root, such as those present in tolerant plants develop extracellular barriers and can store Cd chelates in the vacuoles (Luz *et al.*, 2011). The induction of a high proportion of Cd in the soluble fraction as well as in its chemical form that could limit root-to-shoot translocation (Su *et al.*, 2014). In turn, Uraguchi *et al.* (2009), verified that root-to-shoot Cd translocation via the xylem is the primary and common physiological process determining the Cd accumulation level in shoots and grains of rice plants, although Cd accumulation varies considerably among plant species and also among cultivars within species (Gratão *et al.* 2008).

For the other macronutrients (Ca, Mg, K, and P) and micronutrients (Cu, Fe, Mn, Mo, Zn) considering all the concentrations obtained at all exposure times under the treatment with Cd, with the exception of Ca on leaf (for which higher TTO levels were detected at all exposure times, according to the lower dry mass observed in this organ). The pattern of accumulation in the total dry mass of the cultivars in terms of concentration did not follow the dilution pattern generated by the growth of the plants, confirming that. In general, the cultivar YOSH presented greater accumulation of all nutrients under Cd stress condition.

Analyzing the latter exposure to the metal, although Cd also induced differential absorption patterns (NA) The general pattern of reduction of absorption and nutrient accumulation and plant growth was followed by the reduction of NUE (defined the amount of biomass produced per unit of nutrient absorbed) induced by Cd for most of the nutrients on the last day of exposure. The NUE is based on a) uptake efficiency, b) incorporation efficiency and c) utilization efficiency (Baligar *et al.*, 2001). When an improved NUE was observed in YOSH compared to TTO for most nutrients. The information obtained on the highest biomass and NUE means in YOSH are in consonance with the results obtained by Borges *et al.* (2019). The biomass value inferred that higher values of NUE could be correlated with higher biomass allocation to the maintenance of root viability in plant tomatoes during Cd exposure. Such information is essential for future studies focused on the

expression pattern of transporters present in roots, the synergistic relationship between the different nutrients and the modulation of Cd tolerance.

In addition, plant nutritional balance is directly related to the antioxidant response of plants to heavy metals. In this context, several studies analyzing the effect of supplementation or deficiency of macro- and micronutrients under Cd stress have highlighted the contribution of these nutrients to the modulation of the antioxidant response to this metal. These nutrients can be involved in antioxidant metabolism (e.g., sulfur related to the GSH metabolism) and enzymatic activation (e.g., iron, zinc, and copper, related to the activation of SODs) (Marques *et al.*, 2019). Sebastian and Prasad (2015), antioxidant enzymes and non-enzymatic antioxidant metabolites were found to play important roles in the alleviation of Cd stress under Fe or Mn supplement and concluded that the presence of excess Fe and Mn protects rice plants from Cd stress, in a way different from those that reported the negative relation of micronutrients such as Fe (Morrissey, Guerinot, 2009) and Mg (Hermans *et al.*, 2011), with increased tolerance to Cd. However, it must be considered that differences in the plant genotype, age, organ, and tissue (intrinsic factors), as well as the length-time of plant exposure, Cd concentration in the growing media, growth media properties, presence of plant-associated microorganism (extrinsic factors) may affect the plant sensitivity/tolerance to Cd toxicity and modulation of the antioxidant system (Marques *et al.*, 2019).

According to our results, nutrient accumulation of the YOSH genotype may help to cope with the Cd-induced stress, reflected on the rate growth rate compared to the TTO sensitive genotype.

Differences in levels of translocation and tolerance can be explained not only by the modulation of Cd accumulation but also by the modulation of nutritional levels and the understanding of proteins differentially expressed by the root system, which is the first tissue of contact with the metal it enters the plant system.

Regarding the proteomic analyses, we found that in both cultivars, in the molecular function category, catalytic activity and binding represented the first and second highest percentage, respectively, of the proteins differentially expressed in response to Cd over time. These results are in agreement with those obtained by Xu *et al.* (2017), which verified that catalytic activity, binding, and transporter activity were the largest categories in the molecular function category in their study focused on dissecting radish root proteome

changes in response to Cd. These results also contribute to the understanding of future studies focused on the balance between the synthesis of enzymes (such as those related to antioxidant response) and their catalytic activity, aiming to discriminate the temporal response between the cultivars analyzed.

TTO presented groups of proteins not present in YOSH, such as transcription regulator activity, transporter activity (category of molecular function) and chaperone (category protein class).

In stress conditions, the induced synthesis of HSPs (Heat shock proteins, having molecular weights ranging from 10 to 200 KD) plays a significant role functions as molecular chaperones in maintaining the cellular homeostasis by assisting accurate folding of nascent and stress accumulated misfolded proteins, preventing protein aggregation or by promoting selective degradation of misfolded or denatured proteins (Hassan *et al.*, 2017). Cd-induced differential expression of chaperones/HSPs is also evident in response to various heavy metals including Cd. Furthermore, increased the abundance of defense proteins for effective ROS scavenging and molecular chaperones for re-establishing normal protein conformation help HM-stressed plants to maintain redox homeostasis (Hossain, Komatsu, 2013).

Several families of plasma membrane transporters responsible for the uptake of metals are known, such as HMAs (heavy metal ATPases), NRAMP (natural resistance-associated macrophages), CTR (copper transporters), CDF (cations diffusion facilitator) and ZIP (zinc and iron conveyors). However, features such as biological function, subcellular localization and metal specificity of most of these transporters are still unknown in plants (Gupta *et al.*, 2014).

Due to the chemical similarity, many transporters for divalent ions such as Zn^{2+} , as well as Ca^{2+} channels, facilitate the absorption of Cd^{2+} by the roots and subsequent distribution in the plants. Competition for binding sites may reduce the absorption of essential ions (such as Cu, Fe, Mg, Mn, Zn) in the roots and cause nutritional deficiency (Küpper, Andresen, 2016). In this context, future analyses are necessary to verify the relationship between the differential expression of transporters in TTO roots with their response to Cd.

The direct transcriptional regulation of abiotic stress-responsive genes is performed by transcription factors (TFs), which are regulated by signaling molecules. Cd-responsive TFs can share the same signal transduction pathway carried by other stresses (DalCorso *et al.*,

2010). Several TFs are key downstream effectors of Cd stress transcriptional pathways and trigger the expression of Cd detoxification genes, converging Cd stress signals (Chmielowska-Bąk *et al.*, 2014; DalCorso *et al.*, 2010).

Concerning the protein class, only the cultivar YOSH presented defense proteins. According to Dalcorso *et al.* (2013), heavy metals exert toxicities in plants through four proposed mechanisms: (i) similarities with the nutrient cations, which result into a competition for absorption at root surface; (ii) direct interaction of heavy metals with sulfhydryl (-SH) of functional proteins, which disrupts their structure and function, and thus, renders them inactive; (iii) displacement of essential cations from specific binding sites that lead to a collapse of function; and (iv) generation of reactive oxygen species (ROS).

Plants utilize strategies that prevent or reduce uptake by restricting metal ions to the apoplast through binding them to the cell wall or cellular exudates, or by inhibiting long-distance transport. In contrast, when present at elevated concentrations, cells activate a complex network of storage and detoxification strategies, such as chelation of heavy metal ions with phytochelatins and metallothioneins in the cytosol, trafficking, and sequestration into the vacuole by vacuolar transporters (Singh *et al.*, 2016).

According to Hossain, Komatsu (2013), proteomic analyses strongly indicate that accumulation of defense proteins chiefly enzymatic components of ascorbate-GSH cycle, POD, CAT, GSH, GSTs, Gly I, Prx, Trx help cells to mitigate heavy metal-induced oxidative stress by scavenging ROS, although other defense proteins such as Pathogenesis related proteins also show increased Cd-induced expression. In this context, the differentially expressed defense proteins in YOSH could allow them to cope with the negative consequences of Cd toxicity better than TTO.

YOSH also showed isomerase and calcium-binding protein as differentially accumulated protein classes, which was not detected in TTO, while lyase was detected in both cultivars.

Hossain *et al.* (2011), D'Alessandro *et al.* (2013) and Li *et al.* (2015) verified that triosephosphate isomerase (a key enzyme in glycolysis which plays an important role in efficient energy production) showed increased abundance in studies of exposure to Cd.

Wang *et al.* (2016) found that Cd induced the increase of the relative abundance of glucose-6-phosphate isomerase and lactoglobulinase lyase and inferred that sulfate availability for the synthesis of metal chelation such as GSH. The cytosolic O-acetylserine

(thiol)lyase gene was regulated by heavy metals and can function in Cd tolerance (Dominguez-Solís *et al.*, 2001).

Ca concentration in cells greatly increases during Cd stress and it stimulates calcium-binding proteins (e.g., calmodulin-like) that interact with Ca ions. Ca-binding changes calmodulin conformation and so it regulates a variety of mechanisms, including ion transport, gene regulation, metabolism, and stress tolerance that coordinate, at least in part, the plant response to Cd (DalCorso *et al.*, 2010).

Overall, the results indicated that both cultivars had an active response to Cd stress (which is in agreement with the tolerance to the Cd presented by both cultivars), having TTO presented more considerable number of differentially expressed proteins and having YOSH cultivar advantage in terms of expression of defense proteins.

7. FINAL CONSIDERATIONS

In this research, it was observed a general pattern of growth, nutrient accumulation, stress levels and protein set of two tomato cultivars under stress condition (with 35 μm CdCl_2 and Hoagland and Arnon solution) and control condition (only Hoagland and Arnon solution).

The cultivars used in this experiment were identified with different tolerance indices in previous studies of the research group. The present investigation was performed using different exposure times, and it was possible to note that in the first days of exposure to the metal, a variation was observed between the two cultivars. The previous Works just could classify the TTO as less tolerant than YOSH because they evaluated the tolerance index in the exposure time similar to the last exposure time in the present research.

The growth reduction caused by Cd stress can be observed in both cultivars, being more evident in the cultivar considered less tolerant (TTO). It is important to emphasize that in the first days evaluated this reduction was practically the same. In addition to the more significant reduction, the TTO cultivar (considered less tolerant) also presented higher morphological stress symptoms in shorter exposure time. The variety YOSH also presented several morphological symptoms, but more evident in the last evaluated time. Among these morphological symptoms are the necrotic spots that are the consequence of the cells that have started the apoptosis. This symptom is interesting since it presents an interesting correlation with the variation of apoptotic signal proteins present in the two cultivars. Unfortunately as in this work was not quantified the necrotic points we can not guarantee the correlation, becoming interesting the quantification of this parameter in future research.

The higher accumulation of Cd in the root was observed in both cultivars. This accumulation has already been described as a form of protection so that it does not arrive in significant concentrations in the shoots. Moreover, in this present Thesis, the cultivar that accumulated more Cd in the root was the cultivar considered more tolerant in the previous works (YOSH). It is important to emphasize that in the first time of evaluated exposure no difference between the two cultivars was observed. This result helps us to understand the variation in the tolerance index observed in previous studies with longer exposure time.

The absorption of the Cd could interfere both cultivars in the accumulation, absorption, and efficiency in the use of most nutrients assessed. In general, Cd varies the

nutrient use efficiency at TTO more than at YOSH. This reduction in the efficiency in the use of some nutrients may be the cause of the more significant loss of biomass. Not only the efficiency in use but also the absorption was affected more in the TTO than in the YOSH. With this, in addition to being less efficient, the available quantity is also lower. The result of these two parameters together is evidenced in the greater reduction of the biomass gain in the cultivar TTO in relation to YOSH.

Concerning the stress indicators evaluated, we can conclude that the two cultivars present a variation in the stress level of the plants in stress condition about the plants in control condition already in the first evaluated time. In general, TTO presents more variation in stress indicators than YOSH.

In the identification and evaluation of the DAPs in the two cultivars roots, it is possible to observe that in the presence of Cd the cultivar TTO generates a more significant alteration in the amplitude of the accumulation and in the number of proteins that vary the accumulation in the presence of the Cd. Because of the higher number of proteins that differ in the presence of Cd, there are more clusters represented for the DAPs in TTO than in YOSH in most of the categories evaluated. In both cultivars it was possible to observe proteins related to response to the stimulus, being several proteins in this group related to the defense to oxidative stress. Also in this protein cluster, the highest number of DAPs is in TTO than in YOSH. With this, we can observe that the reaction to the stress caused by this Cd concentration in the TTO is more evident and more accentuated.

Considering all the results exposed, we conclude that the presence of Cd interferes more significantly in the TTO cultivar than the YOSH cultivar, possibly the TTO cultivar felt more the presence of the Cd concentration used than the YOSH. With all the variation observed in the protein set of the two cultivars over time, possibly more biochemical, morphological and anatomical analyzes over time would be interesting. Thus, it would be possible to correlate these characteristics more efficiently with the observed protein modifications. Gene expression analysis would also be interesting to understand better if the proteins that have a lower abundance in the presence of Cd is a consequence of not producing this protein or an increase in its degradability that can be caused by the presence of Cd. It is important to understand a little bit more about the activity of some important proteins related to the stress response. If the increase of the protein abundance is correlated with the activity increase.

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APPENDICES

APPENDIX A. Regression for Cd effects on tomato plant growth expressed in root length; root volume; root dry weight; stem dry weight; leaf dry weight and plant dry weight.

	TTO control condition	TTO stress conditon	YOSH control condition	YOSH stress condition
Length	Y= 446,426+159,292*T R2=0,80; p<0,001	Y= 408,622+75,922*T R2=0,71; p<0,001	Y=484,388+105,71*T R2=0,62; p<0,001	Y= 433,952+63,707*T R2=0,52; p<0,001
Volume	Y= 0,509+0,163*T R2=0,67; p<0,001	Y= 0,578+0,163*T R2=0,70; p<0,001	Y=0,534+0,135*T R2=0,68; p<0,001	Y= 0,553+0,084*T R2=0,62, p<0,001
Root dry weight	Y= 0,018+0,020*T R2=0,85, p<0,001	Y=0,041+0,009*T R2=0,083; p<0,001	Y=0,0188+0,0180*T R2=0,80; p<0,001	Y= 0,028+0,014*T R2=0,90; p<0,001
Stem dry weight	Y= 0,0376*Exp(0,3008*T) R2= 0,97, p<0,001	Y=0,023+0,018*T R2=0,91; p<0,001	Y=0,04055*Exp(0,3098*T) R2= 0,97; p<0,001	Y =0,007+0,028*T R2=0,93; p<0,001
Leaf dry weight	Y= 0,1299*Exp(0,2316*T) R2=0,94, p<0,001	Y=0,025+0,0172*T R2=0,87; p<0,001	Y=0,1317*Exp(0,218*T) R2=0,94; p<0,001	Y=0,0359+0,0152*T R2=0,88; p<0,001
Plant dry weight	Y= 0,2034*Exp(0,2245*T) R2= 0,95, p<0,001	Y=0,179+0,053*T R2=0,93; p<0,001	Y=0,2007*Exp(0,244*T) R2= 0,96, p<0,001	Y=0,137+0,081*T R2=0,94 , p<0,001

APPENDIX B Regression for Cd effects on nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn) in tomato root

	TTO control condition	TTO stress conditon	YOSH control condition	YOSH stress condition
Cd		Cd=0,0117+0,0364*T R2=0,92; p<0,001		Cd=0,001+0,0469*T R2=0,93; p<0,001
Ca	Ca=0,092+0,121*T R2=0,86; p<0,001	Ca=0,159+0,067*T R2=0,83; p<0,001	Ca=0,102+0,11*T R2=0,80; p<0,001	Ca=0,134+0,087*T R2=0,94; p<0,001
Cu	Cu=0,00098+0,000664*T R2=0,94; p<0,001	Cu=0,00286+0,000439*T R2=0,67; p<0,001	Cu=0,002639+0,000866*T R2=0,61; p<0,001	Cu=0,00176+0,00062*T R2=0,85; p<0,001
S	S=0,598*Exp(0,2828*T) R2=0,94; p<0,001	S=0,187+0,04177*T R2=0,81; p<0,001	S=0,710*Exp(0,235*T R2=0,94; p<0,001	S=0,123+0,0792*T R2=0,91; p<0,001
Fe	Fe=0,098+0,0286*T R2=0,76; p<0,001	Fe=0,111+0,0237*Y R2=0,69; p<0,001	Fe=0,1106+0,0264*T R2=0,74; p<0,001	Fe=0,108+0,0288*T R2=0,88; p<0,001
p	P=0,338+0,162*Y R2=0,76; p<0,001	P=0,407+0,0625*T R2=0,70; p<0,001	P=0,274+0,119*T R2=0,77; p<0,001	P=0,272+0,105*T R2=0,89; p<0,001
Mg	Mg=0,0903+0,134*T R2=0,78; p<0,001	Mg=0,219+0,060*T R2=0,86; p<0,001	Mg=0,108+0,106*T R2=0,81; p<0,001	Mg=0,177+0,0775*T R2=0,88; p<0,001
Mn	Mn=0,0303+0,0203*T R2=0,78; p<0,001	Mn=0,0128*Exp(0,0969) R2=0,56; p<0,001	Mn=0,0363+0,0164*T R2=0,60; p<0,001	Mn=0,0127*Exp(0,1574*T R2=0,65; p<0,001
Mo	Mo=0,00047*Exp(0,224*T R2=0,84; p<0,001	Mo=0,00051+0,00011*T R2=0,71; p<0,001	Mo=0,000286*Exp(0,266*T) R2=0,86; p<0,001	Mo=0,000337+0,000174*T R2=0,89; p<0,001
K	K=0,655+0,221*T R2=0,71; p<0,001	K=0,694+0,125*T R2=0,82; p<0,001	K=0,598+0,176*T R2=0,79; p<0,001	K=0,569+0,204*T R2=0,86; p<0,001
Zn	Zn=0,00411+0,00094*T R2=0,70; p<0,001	Zn=0,00324+0,00029*T R2=0,75; p<0,001	Zn=0,028+0,00097*T R2=0,68; p<0,001	Zn=0,0028+0,00033*T R2=0,69 p<0,001

APPENDIX C. Regression for Cd effects on nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn) in tomato stem

	TTO control condition	TTO stress conditon	YOSH control condition	YOSH stress condition
Cd		$Cd=0,00385+0,0055*T$ $R^2=0,89; p<0,001$		$Cd=0,00403+0,00547*T$ $R^2=0,92; p<0,001$
Ca	$Ca=0,363*Exp(0,323*T)$ $R^2=0,94, p<0,001$	$Ca=0,3736*Exp(0,2011*T)$ $R^2=0,92; p<0,001$	$Ca=0,461*Exp(0,294*T)$ $R^2=0,92; p<0,001$	$Ca=0,335*Exp(0,246*T)$ $R^2=0,96; p<0,001$
Cu	$Cu=0,00022*Exp(0,2512*T)$ $R^2=0,96; p<0,001$	$Cu=0,000196*Exp(0,166*T)$ $R^2=0,86; p<0,001$	$Cu=0,0002*Exp(0,2596*T)$ $R^2=0,95; p<0,001$	$Cu=0,0001516*Exp(0,193*T)$ $R^2=0,91; p<0,001$
S	$S=0,0585+0,0612*T$ $R^2=0,91; p<0,001$	$S=0,03417+0,03875*T$ $R^2=0,89; p<0,001$	$S=0,1024*Exp(0,3004*T)$ $R^2=0,97; p<0,001$	$S=0,0378+0,0547*T$ $R^2=0,93; p<0,001$
Fe	$Fe=0,00266*Exp(0,310*T)$ $R^2=0,81; p<0,001$	$Fe=0,002+0,00077*T$ $R^2=0,78; p<0,001$	$Fe=0,00294*Exp(0,2751*t)$ $R^2=0,71; p<0,001$	$Fe=0,00121+0,00113*T$ $R^2=0,69; p<0,001$
p	$P=0,327*Exp(0,24*T)$ $R^2=0,93; p<0,001$	$P=0,166+0,137*T$ $R^2=0,88; p<0,001$	$P=0,3016*Exp(0,26*T)$ $R^2=0,94; p<0,001$	$P=0,113+0,161*T$ $R^2=0,95; p<0,001$
Mg	$Mg=0,183*Exp(0,266*T)$ $R^2=0,95; p<0,001$	$Mg=0,123+0,0836*T$ $R^2=0,88; p<0,001$	$Mg=0,178*Exp(0,269*T)$ $R^2=0,95; p<0,001$	$Mg=0,10631+0,07508*T$ $R^2=0,88; p<0,001$
Mn	$Mn=0,00213+0,001158*T$ $R^2=0,83; p<0,001$	$Mn=0,002033+0,0007726*T$ $R^2=0,75; p<0,001$	$Mn=0,001547+0,001027*T$ $R^2=0,83; p<0,001$	$Mn=0,00077+0,001113*T$ $R^2=0,83; p<0,001$
Mo	$Mo=0,000192*Exp(0,255*T)$ $R^2=0,93; p<0,001$	$Mo=0,000152*Exp(0,207*T)$ $R^2=0,93; p<0,001$	$Mo=0,00024*Exp(0,2559*T)$ $R^2=0,97; p<0,001$	$Mo=0,0002247*Exp(0,224*T)$ $R^2=0,96; p<0,001$
K	$K=0,8463*Exp(0,2633*T)$ $R^2=0,95; p<0,001$	$K=0,804*Exp(0,177*T)$ $R^2=0,85; p<0,001$	$K=0,9933*Exp(0,259*T)$ $R^2=0,94; p<0,001$	$K=0,8458*Exp(0,212*T)$ $R^2=0,91; p<0,001$
Zn	$Zn=0,00259*Exp(0,2529*T)$ $R^2=0,9; p<0,001$	$Zn=0,002317+0,000446*T$ $R^2=0,76; p<0,001$	$Zn=0,00175*Exp(0,279*T)$ $R^2=0,92; p<0,001$	$Zn=0,00176+0,000244*T$ $R^2=0,72; p<0,001$

APPENDIX D. Regression for Cd effects on nutrient accumulation (Cd, Ca, Cu, S, Fe, P, Mg, Mn, Mo, K e Zn) in tomato leaf

	TTO control condition	TTO stress conditon	YOSH control condition	YOSH stress condition
Cd		Cd=0,01+0,01997*T R2=0,92; p<0,001		Cd=0,015+0,0183*T R2=0,92; p<0,001
Ca	Ca=1,1279+20,478*T R2=0,90; p<0,001	Ca=2,53+0,70163*T R2=,91; p<0,001	Ca=1,2291+1,848*T R2=0,92; p<0,001	Ca=2,041+0,821*T R2=0,94; p<0,001
Cu	Cu=0,00103+0,000697*T R2=0,86; p<0,001	Cu=0,00132+0,000156*T R2=0,65; p<0,001	Cu=0,0011+0,0006369*T R2=0,87; p<0,001	Cu=0,001255+0,0001696*T R2=0,77; p<0,001
S	S=0,0516+0,6163*T R2=0,83; p<0,001	S=0,61+0,21887*T R2=0,90; p<0,001	S=0,24789+0,499*T R2=0,90; p<0,001	S=0,438+0,332*T R2=0,94; p<0,001
Fe	Fe=0,012+0,01433*T R2=0,84; p<0,001	Fe=0,01676+0,00440*T R2=0,68; p<0,001	Fe=0,0132+0,012*T R2=0,89; p<0,001	Fe=0,0169+0,0055*T R2=,61; p<0,001
p	P=0,55+0,529*T R2=0,93; p<0,001	P=0,8727+0,205*T R2=0,91; p<0,001	P=0,6953+0,451*T R2=0,90; p<0,001	P=0,799+0,2649*T R2=0,92; p<0,001
Mg	Mg=0,3368+0,36289*T R2=0,91; p<0,001	Mg=0,597+0,1314*T R2=0,90; p<0,001	Mg=0,3999+0,339*T R2=0,89; p<0,001	Mg=0,55469+0,1819*T R2=0,89; p<0,001
Mn	Mn=0,01679+0,00736*T R2=0,83; p<0,001	Mn=0,0172+0,0063*T R2=0,92; p<0,001	Mn=0,0159+0,00684*T R2=0,82; p<0,001	Mn=0,01485+0,00697*T R2=0,92; p<0,001
Mo	Mo=0,000755+0,0009688*T R2=0,84; p<0,001	Mo=0,001436+0,000472*T R2=0,90; p<0,001	Mo=0,0007164+0,000789*T R2=0,89; p<0,001	Mo=0,000849+0,000616*T R2=0,92; p<0,001
K	K=0,9495+10,798*T R2=0,92; p<0,001	K=1,5717+0,3694*T R2=0,93; p<0,001	K=1,2926+0,8871*T R2=0,88; p<0,001	K=1,3724+0,56237*T R2=0,90; p<0,001
Zn	Zn=0,00319+0,001414*T R2=0,89; p<0,001	Zn=0,00389+0,0000511*T R2=0,81; p<0,001	Zn=0,003876+0,001282*T R2=0,82; p<0,001	Zn=0,004+0,00067*T R2=0,87; p<0,001

APPENDIX E Proteins detected in more tolerant genotype YOSH in different Cd exposure periods in roots.

Accession	Peptide count	Peptides used for quantitation	Confidence score	DAP	Description
Q9LWA3	16	10	640.28		Subtilisin-like protease
K4B1L5	5	5	200.12		Uncharacterized protein
K4B2X0	8	7	315.67		Uncharacterized protein
K4D3M6	14	12	837.32		Uncharacterized protein
K4BUC5	25	15	1019.58	Yes	Uncharacterized protein
K4AR66	15	8	560.33		Peroxidase
K4AT60	7	6	250.56		Uncharacterized protein
K4CGI0	5	1	90.03		Uncharacterized protein
K4BM69	10	10	275	Yes	Uncharacterized protein
O80432	5	5	275.6		Mitochondrial small heat shock protein
K4CNZ3	21	13	1363.47		Uncharacterized protein
K4C145	1	1	58.81		Uncharacterized protein
K4CNZ0	19	5	894	Yes	Uncharacterized protein
K4CVR2	7	1	190.66	Yes	Uncharacterized protein
K4BEL1	24	1	1382.78		Uncharacterized protein
Q38JE1	7	5	150.86		Temperature-induced lipocalin
K4B553	19	17	703.72	Yes	Uncharacterized protein
Q6A1K7	10	10	447.68		1-aminocyclopropane-1-carboxylate oxidase
K4CVH1	5	2	60.31		Amine oxidase
K4BV08	3	1	60.7		Patatin
K4CC21	5	1	194.79		Uncharacterized protein
X4Y6L7	11	3	60.44	Yes	Dicer-like protein 3
ADH2	37	28	2724.93		Alcohol dehydrogenase 2
K4CWC5	14	10	993.22		PR10 protein
K4CNZ7	7	5	166.5		Uncharacterized protein
K4CQN4	3	1	102.16	Yes	Uncharacterized protein
K4BIC0	31	21	1049.44	Yes	Uncharacterized protein
K4B030	4	2	196.57		Uncharacterized protein
Q9FT17	6	1	105.81		Lipoxygenase
K4B7W2	2	2	79.16	Yes	Uncharacterized protein
K4ASM4	4	2	43.65		Uncharacterized protein
K4BRF6	3	3	109.75		Uncharacterized protein
K4BAE6	16	11	558.54		Catalase
Q0H8U4	7	3	500.06		Pathogenesis-related protein
K4CRH8	7	5	180.9		Uncharacterized protein
K4B1Y6	12	12	511.23	Yes	Uncharacterized protein
K4DBP0	9	7	328.2		Uncharacterized protein
LOXA	26	16	1067.67	Yes	Linoleate 9S-lipoxygenase A
K4D203	11	7	385.37		Lysine--tRNA ligase
K4CMV0	7	4	249.92		Peroxidase
K4BKK9	4	1	125.1		Uncharacterized protein
K4CC17	3	2	80.91		Uncharacterized protein
K4CUU6	14	9	674.33		Uncharacterized protein
K4B9B4	3	1	35	Yes	Uncharacterized protein
RSI1	2	2	60.62		Protein RSI-1
K4DFH8	4	3	198.38		Uncharacterized protein
K4C4Z6	29	3	1756.75		Uncharacterized protein
K4BEU1	3	3	179.87		Uncharacterized protein
Q4W8D2	6	5	129.97		2-oxoglutarate-dependent dioxygenase
NP24	8	6	821.05	Yes	Protein NP24

K4D1H1	12	6	967.59	Yes	Uncharacterized protein
K4D4Y1	4	4	391.04		Uncharacterized protein
O64439	4	2	291.43		Germin-like protein
K4BNT2	6	5	537.92	Yes	Uncharacterized protein
K4CVE4	8	7	199.95		Uncharacterized protein
Q5NE21	12	11	545.03	Yes	Carbonic anhydrase
K4BK44	4	1	32.44	Yes	Protein-L-isoaspartate O-methyltransferase
Q9S898	1	1	76.06		23 kDa heat-induced protein (Fragment)
K4BBL4	7	4	129.9	Yes	Uncharacterized protein
K4CUC1	8	6	305.62		Uncharacterized protein
Q9FT22	12	4	346.5		Putative glutathione S-transferase T2
CHIC	13	7	1151.21		Basic 30 kDa endochitinase
O48625	4	4	139.89		Lemir
K4B031	4	2	233.64		Uncharacterized protein
K4BTH6	24	16	1820.34	Yes	Peroxidase
K4CAY2	7	5	313.11		Uncharacterized protein
K4BRL8	3	2	60.58	Yes	Uncharacterized protein
K4CF67	15	12	384.13		Uncharacterized protein
K4CRI5	6	6	178.95		Uncharacterized protein
K4C7W1	5	5	88.16		Uncharacterized protein
K4CNF0	7	7	529.03	Yes	Uncharacterized protein
K4C9I5	8	2	395.71		Uncharacterized protein
K4CC45	2	2	97.97	Yes	Uncharacterized protein
K4CDL3	23	14	931.84		Aspartate aminotransferase
K4CRI1	3	1	53.36		Uncharacterized protein
K4B6U4	2	2	68.61	Yes	Patatin
K4CYL4	5	5	149.62	Yes	Cysteine synthase
K4CU14	6	3	248.63		Uncharacterized protein
K4C1Q9	8	6	378.72	Yes	Peroxidase
K4DC18	36	12	1700.88		Uncharacterized protein
L7Q568	6	3	217.84		Glycine rich RNA binding protein 1a
K4C9W3	38	2	2490.09		Uncharacterized protein
Q5NE18	23	21	1245.37		Formate dehydrogenase
K4CW30	1	1	54.57		Uncharacterized protein
K4D1H0	17	8	1744.04	Yes	Uncharacterized protein
K4BJ06	7	5	211.95	Yes	Uncharacterized protein
K4C7V4	5	5	140.7		Uncharacterized protein
K4AX22	6	5	328.41		Superoxide dismutase [Cu-Zn]
K4C310	6	5	274.38		Uncharacterized protein
K4BNY7	5	1	132.2	Yes	Uncharacterized protein
K4DBB7	5	1	155.57		Uncharacterized protein
K4CIH8	4	1	141.07		Uncharacterized protein
K4CRI2	2	1	61.49		Uncharacterized protein
K4CWR9	5	4	185.62	Yes	Uncharacterized protein
K4BW14	19	7	752.27		Uncharacterized protein
K4CIU0	10	1	539.06		Uncharacterized protein
K4B978	5	4	164.94	Yes	Uncharacterized protein
K4CRA2	4	1	277.1		Uncharacterized protein
K4DFI3	5	4	113.5		Uncharacterized protein
K4D467	7	1	266.17	Yes	Uncharacterized protein
K4DGL5	6	5	327.81		Uncharacterized protein
K4CVI4	21	15	1271.65		Cysteine synthase
K4BQ85	21	17	745.38		Uncharacterized protein
K4B277	14	11	1318.78		Peroxidase
K4D0P3	16	8	801.21		Uncharacterized protein
K4D0H2	11	3	581.66	Yes	Uncharacterized protein

K4D4F5	10	7	253.77		Uncharacterized protein
K4CL66	2	2	49.77	Yes	Uncharacterized protein
K4BW77	4	1	98.88		Uncharacterized protein
K4DHD5	6	5	230.37		Uncharacterized protein
Q84KJ2	5	5	361.42		Copper chaperone
K4CEV0	4	2	65.79		Uncharacterized protein
K4CFF2	8	1	434.98		Peroxidase
Q7Y1Y6	8	6	98.39		Mitogen-activated protein kinase
K4D3E4	24	9	1471.16	Yes	Fructose-bisphosphate aldolase
G8XSL1	7	5	85.88		GSH1
K4CNR6	7	4	204.31	Yes	Uncharacterized protein
SCRK2	27	22	1917.87		Fructokinase-2
K4AS65	20	14	1299.26	Yes	Uncharacterized protein
K4CWL0	14	11	635.83		Uncharacterized protein
K4BKZ7	4	2	69.83		Uncharacterized protein
K4CX40	9	8	353.3		Uncharacterized protein
K4CFM5	22	13	1285.12		Ketol-acid reductoisomerase
K4CM55	3	3	62.82	Yes	Uncharacterized protein
K4CXY9	6	4	195.82		Uncharacterized protein
K4C6X6	3	2	132.4		Uncharacterized protein
K4BQ64	1	1	23.04		Uncharacterized protein
K4B055	5	5	139.55	Yes	Uncharacterized protein
K4C792	5	1	38.73		Uncharacterized protein
K4CIH4	7	6	343.71		Patatin
K4ASR4	3	2	50.24		Uncharacterized protein
Q672Q3	5	5	251.53		Uncharacterized protein
K4C8R3	6	4	233.87		Uncharacterized protein
K4BHZ4	15	15	739.16	Yes	Uncharacterized protein
K4CVQ4	13	12	388.86		Uncharacterized protein
K4BAX2	2	2	78.81		Uncharacterized protein
Q7XAV2	2	2	78.08		Superoxide dismutase [Cu-Zn]
Q9AWA9	15	13	852.35		Non-symbiotic hemoglobin class 1
K4CUR8	5	1	219.66		Uncharacterized protein
K4D297	22	13	1242.77		Glutamate dehydrogenase
K4DAD5	24	13	1066.33	Yes	Uncharacterized protein
K4CP64	8	4	690.44		Uncharacterized protein
K4DBI4	9	3	305.74		Gamma aminobutyrate transaminase 2
K4D451	9	1	424.66		Phenylalanine ammonia-lyase
K4D3Y9	24	5	1752.46		Uncharacterized protein
K4B3Y5	2	2	145.72		Uncharacterized protein
K4B7M2	15	14	520.19		Uncharacterized protein
Q9M726	5	2	62.68	Yes	SNF1
K4CEJ1	35	24	1119.26		Uncharacterized protein
Q3I5C4	16	1	1130.4	Yes	Cytosolic ascorbate peroxidase 1
K4C977	15	14	544.46		Uncharacterized protein
K4C144	36	22	2296.57		Malic enzyme
K4BJ73	9	7	845.19	Yes	Uncharacterized protein
B6RQ70	2	2	76.12		Asr2
K4CDW6	2	2	39.74		Uncharacterized protein
K4CWC6	9	8	417.56		Uncharacterized protein
K4BCQ9	9	9	174.97		Uncharacterized protein
B1N678	1	1	87.62		Defensin protein
Q9XEX8	5	4	67.49		Remorin 1
K4DH53	4	1	41.48		Uncharacterized protein
K4CSN4	4	2	41.29		Uncharacterized protein
K4C376	22	18	1148.24		Protein disulfide-isomerase

K4BUL5	2	1	40.87		Uncharacterized protein
K4CC70	1	1	207.17	Yes	Uncharacterized protein
K4CRQ5	4	3	191.57		Uncharacterized protein
K4B3C2	8	1	61.52		Uncharacterized protein
K4C868	8	6	125.84		Uncharacterized protein
K4D4V2	3	2	175.42		Uncharacterized protein
K4BDZ7	9	7	243.42		Uncharacterized protein
K4AYN8	3	3	49.78		UMP-CMP kinase
METK3	29	11	1556.11		S-adenosylmethionine synthase 3
K4B962	2	2	53.76	Yes	Uncharacterized protein
K4B118	1	1	26.94		Uncharacterized protein
K4D5T8	16	10	700.79		Uncharacterized protein
K4BH22	4	4	241.88		Uncharacterized protein
K4B1F9	12	8	303.76		Uncharacterized protein
K4BJD6	8	4	138.27		Uncharacterized protein
K4CMI7	10	7	322.46		Uncharacterized protein
K4B1G7	5	4	233.76		Uncharacterized protein
K4DG39	9	4	192.12	Yes	Uncharacterized protein
K4BJ74	9	8	696.16		Uncharacterized protein
K4B9E5	3	2	40.72	Yes	Uncharacterized protein
K4B2I9	26	9	1387.38		Uncharacterized protein
K4CC42	7	7	500.82		Uncharacterized protein
K4CX21	8	8	516.55	Yes	Uncharacterized protein
K4CW40	20	15	1596.36	Yes	Malate dehydrogenase
K4B5D3	4	2	46.33		Uncharacterized protein
K4DGU7	3	1	90.8		Uncharacterized protein
K4DC81	5	4	140.62		Uncharacterized protein
K4BYW1	11	7	191.04		Glucose-6-phosphate 1-dehydrogenase
K4BDB9	9	1	527.3		Uncharacterized protein
K4BKR7	16	10	783		Uncharacterized protein
K4ASJ4	17	15	602.28		Uncharacterized protein
K4CH96	10	1	629.49		Uncharacterized protein
K4B6X9	4	3	146.21		Uncharacterized protein
K4C3H8	5	2	158.18		Uncharacterized protein
K4AXS2	12	7	457.65		Glutamine synthetase
E13B	20	17	1827.22	Yes	Glucan endo-1,3-beta-glucosidase B
K4CEY6	10	8	408.19		Uncharacterized protein
K4D1W6	19	12	738.23		Peroxidase
K4CRJ3	8	4	277.95		Uncharacterized protein
K4CJW3	21	7	635.59		Lipoxygenase
K4BPV5	21	12	1502.09		Glutamine synthetase
K4CQF3	2	2	41.46		Carboxypeptidase
K4B267	13	13	484.47		Uncharacterized protein
K4B1S4	14	11	374.68		Uncharacterized protein
K4CFF0	24	18	1820.88		Peroxidase
K4BPK4	16	12	1589.11		Triosephosphate isomerase
K4D5S3	2	2	43.71		Uncharacterized protein
K4C869	2	2	72.12		Uncharacterized protein
K4B170	7	5	327.33		Uncharacterized protein
K4BLA1	13	9	730.74	Yes	Uncharacterized protein
K4C242	4	2	100.58		Uncharacterized protein
K4BAW0	6	2	110.85		Fructose-bisphosphate aldolase
14332	19	5	1343.16		14-3-3 protein 2
K4DHE9	9	6	371.54		Uncharacterized protein
K4B8E6	6	6	186.7		Uncharacterized protein
K4AY19	5	4	139.15		Uncharacterized protein

K4C2K4	2	1	79.28		Uncharacterized protein
OPR3	8	7	245.56		12-oxophytodienoate reductase 3
K4B2L1	7	3	121.31		Uncharacterized protein
K4AYE5	2	1	33.02	Yes	Uncharacterized protein
K4DF56	6	2	388.44	Yes	40S ribosomal protein S12
K4AYV3	2	2	170.39		Uncharacterized protein
K4BJA2	1	1	52.07		Uncharacterized protein
Q9LEG3	10	9	923.08		Putative alcohol dehydrogenase
K4C3V1	7	1	266.36		Ribosomal protein L19
K4D1X7	5	3	105.98		Uncharacterized protein
K4BBF4	10	6	190.46		Uncharacterized protein
K4BWS2	6	2	83.76		Uncharacterized protein
K4BN60	17	12	714.75		Uncharacterized protein
K4BVZ8	3	2	90.79		Uncharacterized protein
K4C2F8	8	1	335.12		Uncharacterized protein
O65820	6	4	94.69	Yes	Histone H1
K4AXR6	4	4	157.74		Uncharacterized protein
K4B8V1	14	9	792.68		Uncharacterized protein
K4C3H1	1	1	27.39		Uncharacterized protein
K4DFU3	22	13	1301.86	Yes	6-phosphogluconate dehydrogenase, decarboxylating
K4DB11	11	3	337.45		Uncharacterized protein
K4DB46	11	3	339.94		Uncharacterized protein
K4CHG7	5	3	281.84	Yes	Small ubiquitin-related modifier
K4CR90	47	9	3190.39		Uncharacterized protein
K4D9S4	7	3	213.63		Uncharacterized protein
K4DCV3	8	2	369.23		Malate dehydrogenase
K4C1P5	3	1	147.63		Uncharacterized protein
K4BL65	2	2	68.83		Uncharacterized protein
K4CWC4	16	9	1271.97		PR10 protein
K4CV78	8	7	315.66		Uncharacterized protein
K4BPX5	9	1	231.71		Uncharacterized protein
K4B7P2	5	4	230.14		Uncharacterized protein
K4D7N0	1	1	75.68		Uncharacterized protein
K4CAH4	15	9	488.49		Uncharacterized protein
K4C7U7	7	1	156.19		Uncharacterized protein
Q40131	14	12	522.3		Uncharacterized protein
Q7Y0S1	3	2	74.72		Chitinase
PLAS	1	1	37.13		Plastocyanin, chloroplastic
K4DHM3	21	1	1378.88		Adenosylhomocysteinase
METK2	14	3	799.3		S-adenosylmethionine synthase 2
K4C8C6	1	1	24.59		Uncharacterized protein
K4CP14	11	5	424.04		Uncharacterized protein
K4C5T5	4	2	79.82		Uncharacterized protein
K4BLW8	9	4	240.12		Uncharacterized protein
K4B249	28	1	1711.37		Uncharacterized protein
K4BTQ4	3	1	61.85		Uncharacterized protein
K4CJG6	3	1	38.94		Uncharacterized protein
K4BV28	5	1	113.3		Uncharacterized protein
K4CX56	2	2	44.39		Uncharacterized protein
K4CRN4	6	3	54.37		Uncharacterized protein
K4DB71	9	1	407.5		Uncharacterized protein
K4C1V8	2	2	51.49		Uncharacterized protein
Q53J23	2	2	31.52		EDS1-like protein, putative
K4B2Z4	4	2	88.02		Uncharacterized protein
K4BE93	19	13	920.07		Peroxidase
A8W7B5	6	1	123.87		Heat shock protein 70

K4DFR1	46	24	2972.54		Uncharacterized protein
K4C7I1	10	9	366.29		Uncharacterized protein
K4CN78	4	3	69.33		Pyruvate kinase
K4CUX6	14	11	581.24		Elongation factor Tu
K4BBT1	1	1	28.44		Uncharacterized protein
K4B7E5	6	4	144.38		Uncharacterized protein
CYSP3	5	5	252.52		Cysteine proteinase 3
K4BAV2	4	4	78.34		Uncharacterized protein
K4D331	12	12	281.74		NADH-cytochrome b5 reductase
K4D9N5	5	5	135.93		Xyloglucan endotransglucosylase/hydrolase
K4CEK7	7	6	179.79		Uncharacterized protein
K4DF99	33	8	1213.05		Uncharacterized protein
K4CGT6	23	1	499.55		Uncharacterized protein
K4CBF0	21	14	656.37		Acetyltransferase component of pyruvate dehydrogenase complex
SPDE	4	4	88.47		Spermidine synthase
K4B171	6	5	253.66		Uncharacterized protein
K4CVU7	1	1	61.66	Yes	Uncharacterized protein
K4D1Z3	14	12	911.11		Uncharacterized protein
K4D489	4	2	51.06		Uncharacterized protein
K4D1V6	1	1	35.03		Uncharacterized protein
K4BP30	27	20	1167.74		Pyruvate kinase
K4BTY9	24	5	1722.74		14-3-3 protein 3
RBL	12	3	484.14		Ribulose biphosphate carboxylase large chain
K4CP65	8	3	880.99		Uncharacterized protein
E0XN34	9	5	243.27		Alpha-mannosidase
K4DAC6	23	1	1524.58		Elongation factor 1-alpha
K4CNU7	2	2	110.42		Uncharacterized protein
K4C3R0	8	3	66.11		Uncharacterized protein
K4CWT9	4	1	136.62		Uncharacterized protein
K4D5K8	19	8	987.87		Uncharacterized protein
K4C3F2	1	1	21.35		Uncharacterized protein
K4D6E8	6	4	279.41	Yes	Eukaryotic translation initiation factor 3 subunit F
K4BVU7	16	13	811.92		Uncharacterized protein
K4D9S9	10	4	488.1		Uncharacterized protein
K4DI03	4	2	38.36		Signal recognition particle 9 kDa protein
K4BQ24	6	3	87.86		Uncharacterized protein
K4BX57	2	1	33.86		Uncharacterized protein
K4BFI7	4	2	168.15		Uncharacterized protein
K4C9A8	3	3	121.32		Uncharacterized protein
K4CQ30	4	4	128.51		Uncharacterized protein
K4BNT3	10	7	674.7		Uncharacterized protein
K4D5I0	8	3	330.25		Uncharacterized protein
K4D2B1	6	6	267.75		Uncharacterized protein
K4BN62	21	12	1154.99		Uncharacterized protein
K4BRG8	23	19	1054.36		Uncharacterized protein
K4CWW8	5	1	110.07		Uncharacterized protein
K4BLU5	3	3	64.62		Uncharacterized protein
K4BTE8	2	2	33.73		Uncharacterized protein
K4ATB4	23	4	1220.04		Uncharacterized protein
K4BCC3	9	9	204.41		Uncharacterized protein
K4CHM9	7	4	112.39		Uncharacterized protein
K4B891	3	3	110.63		Uncharacterized protein
K4B2Z8	5	2	123.08		Uncharacterized protein
B1Q3F1	22	16	851.92		Glutamate decarboxylase
K4CJ91	8	5	351.63		Uncharacterized protein

K4C635	7	4	174.66		Acyl-[acyl-carrier-protein] desaturase
K4CVB0	2	1	24.75		Pectinesterase
K4D4T0	5	3	265.03		Uncharacterized protein
K4B2X5	19	16	713.1		Uncharacterized protein
K4CGY4	3	2	48.46		Uncharacterized protein
K4C7K0	4	1	69.57		Uncharacterized protein
K4B876	7	1	335.7		Uncharacterized protein
K4D2Z0	6	6	524.92		Uncharacterized protein
Q93YH0	1	1	76.58		ATP-dependent Clp protease proteolytic subunit
K4CP63	7	3	626.82		Uncharacterized protein
K4D444	5	4	354.95		Uncharacterized protein
K4B808	8	1	53.43	Yes	Uncharacterized protein
K4B1M0	11	5	231.56		Uncharacterized protein
K4B8U9	3	2	102.5		Uncharacterized protein
K4C8F8	4	1	88.09		Uncharacterized protein
O49877	11	9	903.38		CYP1
K4CNT4	8	7	273.85		Uncharacterized protein
K4C4L0	7	1	89.91		Glutamate dehydrogenase
K4C2E1	21	7	843.58		Uncharacterized protein
K4CBP6	3	3	135.78		Uncharacterized protein
K4CR48	1	1	48.6		CASP-like protein
K4CJ67	10	7	414.65	Yes	Uncharacterized protein
K4D8S6	18	16	924.34		Uncharacterized protein
K4D4Q9	6	3	225.76		Uncharacterized protein
K4B381	5	3	166.7	Yes	N-acetyl-gamma-glutamyl-phosphate reductase
PMM	6	1	109.05		Phosphomannomutase
K4BLR2	3	1	87.44		Uncharacterized protein
K4AVB7	24	19	1082.51		Uncharacterized protein
K4CEB3	51	32	2272.14		Uncharacterized protein
K4BFY7	6	1	68.2		Uncharacterized protein
K4BJE4	7	5	143.24		Uncharacterized protein
K4CJ99	11	6	363.09		Uncharacterized protein
K4B1V0	2	2	151.47		Uncharacterized protein
K4CXS7	24	10	779.76		Uncharacterized protein
K4CSD7	10	9	476.44		Uncharacterized protein
K4C1C9	33	28	1796.49	Yes	Uncharacterized protein
K4C0T4	16	6	929.77		Peroxidase
K4CIK9	5	3	110.22		Uncharacterized protein
K4B0B4	6	4	360.91		Uncharacterized protein
K4BSR4	26	23	1476.61		Annexin
K4B1G1	5	4	152.84		Uncharacterized protein
K4CQJ3	10	4	540.69		Uncharacterized protein
E0Z1D0	57	24	3352.53		Sucrose synthase isoform 3
K4B3J8	13	8	595.29		Uncharacterized protein
RAN1	12	10	628.79		GTP-binding nuclear protein Ran1
ATPA	7	5	255.36		ATP synthase subunit alpha, chloroplastic
K4ATC7	1	1	22.91		Uncharacterized protein
K4B1G9	10	5	274.05		Uncharacterized protein
Q9XGY1	2	2	72.13		Small zinc finger-like protein
K4BU44	4	3	49.68		Uncharacterized protein
K4BCP0	2	2	33.92		Uncharacterized protein
K4D4V8	9	6	170.41		Uncharacterized protein
K4BF54	4	2	52.64		Uncharacterized protein
K4BFG9	3	1	42.48		Uncharacterized protein
K4B2M8	6	5	508.39		Uncharacterized protein
K4APU2	16	13	1069.85		Uncharacterized protein

K4DAA0	9	5	539.41		Uncharacterized protein
K4CF87	15	12	709.99		Uncharacterized protein
K4DC13	5	4	119.1		Uncharacterized protein
K4DFA0	32	6	1111.85		Uncharacterized protein
14337	17	6	859.7		14-3-3 protein 7
K4CA24	36	3	2220.64		Uncharacterized protein
K4ASU4	10	2	262.57		ATP synthase subunit beta, chloroplastic
K4B9Y9	5	3	217.59		1-aminocyclopropane-1-carboxylate oxidase 4
K4BMF9	2	1	28.15		Uncharacterized protein
K4CBD9	2	1	64.79		Uncharacterized protein
IMA	11	5	323.99		Importin subunit alpha
K4CW86	14	12	496.55		Uncharacterized protein
K4AVE9	5	5	92.69		Uncharacterized protein
K4D955	5	5	125.83		Uncharacterized protein
K4CA69	7	2	94.55		Uncharacterized protein
K4BD54	17	14	1039.48		Peroxidase
K4D5Z5	3	2	22.64		Uncharacterized protein
CATA1	33	19	2112.64		Catalase isozyme 1
K4CHE0	4	1	76.26		Uncharacterized protein
K4D126	3	2	76.24		Uncharacterized protein
K4DAT6	2	1	37.17		Uncharacterized protein
K4CX43	6	4	313.55		Uncharacterized protein
K4BVN6	29	16	1322.03		Uncharacterized protein
Q9M5A8	5	3	201.7		Chaperonin 21
K4AQ32	15	11	524.73		Uncharacterized protein
K4BBG0	3	1	69.78		Uncharacterized protein
K4CPC2	21	17	669.86		Uncharacterized protein
K4C8P4	3	2	114.5		Uncharacterized protein
K4D557	2	2	87.23		Uncharacterized protein
K4BSK2	3	3	139.73	Yes	Uncharacterized protein
K4CVW4	5	2	170.56		Uncharacterized protein
K4BM58	7	6	153.92		Uncharacterized protein
K4CCK4	2	1	27.22		Uncharacterized protein
K4C8H8	5	1	154.97		Uncharacterized protein
K4C0T5	14	2	789.32		Peroxidase
K4CWE4	32	11	1202.82		Uncharacterized protein
K4CQT3	2	1	51.66		Uncharacterized protein
K4BU57	5	3	300.16		Uncharacterized protein
K4BMF0	11	8	313.93		Uncharacterized protein
Q9FT20	4	3	63.19		Putative glutathione S-transferase T4
K4CHY3	29	19	1760.31		Phosphoglycerate kinase
K4BVD4	7	7	173.87		Uncharacterized protein
K4B1J4	10	9	309.12		Uncharacterized protein
K4CDS1	1	1	21.52		Translation machinery-associated protein 22
K4BXC7	10	5	254.94		Uncharacterized protein
O65004	7	6	226.59		Farnesyl pyrophosphate synthase
O82575	4	2	251.49		Fruit-ripening protein
K4C227	33	16	1631.06		Uncharacterized protein
K4CVC0	7	1	263.28		Ribosomal protein L19
K4BKM5	3	2	65.95		Uncharacterized protein
K4BP03	2	1	63.52		Uncharacterized protein
K4C288	3	2	152.02		Uncharacterized protein
Q94K24	7	5	529.16		Ran binding protein-1
K4BTJ0	5	3	72.57		Uncharacterized protein
K4C3S6	5	1	35.48		Uncharacterized protein
K4AZZ3	3	1	52.35		Uncharacterized protein

K4CSH4	6	2	252.59		Uncharacterized protein
K4D9L5	45	7	2979.92		Uncharacterized protein
K4CAN7	9	3	321.17		Uncharacterized protein
K4CI69	15	15	1032.88		Uncharacterized protein
K4BMV8	9	6	141.21		Protein ROOT HAIR DEFECTIVE 3 homolog
K4C234	10	2	168.31		Uncharacterized protein
K4BPB5	1	1	33.04		Uncharacterized protein
K4DAS6	17	10	1128.81		Uncharacterized protein
K4C8B3	4	4	118.78		Uncharacterized protein
K4CAM3	1	1	53.23		Uncharacterized protein
K4B4U4	6	2	62.88		Glyceraldehyde-3-phosphate dehydrogenase
K4C6L0	16	15	455.5		Protein disulfide-isomerase
K4CFP5	4	1	143.18		Uncharacterized protein
K4B7K6	5	5	231.29		Uncharacterized protein
K4CD72	3	1	36.9		Uncharacterized protein
Q6R8F6	4	4	99.79		Cystathionine gamma synthase
K4CHJ0	6	6	252.12		Uncharacterized protein
K4D713	4	3	61.16		Uncharacterized protein
K4CLE4	4	3	128.81		Uncharacterized protein
K4BPJ4	18	7	809.15		Uncharacterized protein
K4D2S2	13	7	237.87		Adenylosuccinate synthetase, chloroplastic
K4CES3	4	1	51.84	Yes	Uncharacterized protein
K4B166	18	12	625.98		Uncharacterized protein
K4CL75	45	36	3000.55		Uncharacterized protein
PER1	4	3	259.13		Suberization-associated anionic peroxidase 1
K4DAS7	8	6	238.07	Yes	Uncharacterized protein
K4CEG6	5	1	64.4		Uncharacterized protein
K4C261	30	10	1702.46		Serine hydroxymethyltransferase
K4BBN1	8	4	213.01		Uncharacterized protein
K4CMQ3	5	1	48.86		Uncharacterized protein
K4CFD4	47	20	2513.16		Aconitate hydratase
K4BJ62	1	1	52.31		Uncharacterized protein
K4CVS3	2	2	45.17		Pyruvate kinase
K4CEU2	8	4	233.52		Uncharacterized protein
Q4W5U7	17	13	840.59		Calnexin-like protein
K4B4Z2	13	9	334.37		Uncharacterized protein
K4CE62	4	3	80.53		Uncharacterized protein
K4B9G0	3	2	48.56		Uncharacterized protein
K4BDL5	3	3	219.74		Uncharacterized protein
K4B3Z2	9	8	666.11		Uncharacterized protein
K4CNZ8	3	2	35.2		Uncharacterized protein
K4BJD2	3	3	93.1		Inositol-tetrakisphosphate 1-kinase
K4CCD2	13	7	713.58		Uncharacterized protein
K4BX77	7	4	174.8		3-isopropylmalate dehydrogenase
K4CA36	9	5	194.6		Uncharacterized protein
K4AXN3	6	4	340.34		Uncharacterized protein
K4D7U2	12	6	251.39		Uncharacterized protein
K4BVH5	3	3	99.42		Uncharacterized protein
K4BV31	4	3	93.05		Uncharacterized protein
K4B110	17	8	585.44		26S protease regulatory subunit 6A homolog
K4BYC0	9	5	236.33		Uncharacterized protein
K4DA99	9	7	1106.01		Uncharacterized protein
K4DC84	13	7	157.76		Uncharacterized protein
K4D184	6	2	341.58		Peptidyl-prolyl cis-trans isomerase
K4D389	6	3	166.89		Uncharacterized protein
K4DH69	6	5	242.41		Uncharacterized protein

K4C2V5	15	10	414.02		T-complex protein 1 subunit gamma
K4AWA0	6	5	346.34		Uncharacterized protein
K4B1V5	6	2	381.68		40S ribosomal protein S12
K4B7E7	3	3	211.24		Uncharacterized protein
K4D3X7	2	1	34.38		Uncharacterized protein
Q9SMD3	14	1	972.71		Ascorbate peroxidase
K4C6W9	13	9	727.89		Uncharacterized protein
K4BLG1	2	2	62.25		Uncharacterized protein
K4DCI6	8	4	164.8		Citrate synthase
K4B318	4	1	51.16		Uncharacterized protein
K4BYA0	8	1	42.75		Uncharacterized protein
K4CNL0	3	1	45.54		Uncharacterized protein
K4BK46	3	1	48.87		Uncharacterized protein
K4DGY9	2	2	23.12		Sugar-porter family protein 6
K4DBU7	3	3	209.08		Profilin
K4BCR8	3	3	82.97		Uncharacterized protein
K4CQW8	28	23	1740.97		Uncharacterized protein
K4D637	1	1	49.92		Uncharacterized protein
K4C9G1	5	3	300.84		Uncharacterized protein
K4CNT3	2	2	57.71		Uncharacterized protein
K4CKX4	19	4	1003.43		Uncharacterized protein
K4CQ01	2	1	151.01		Uncharacterized protein
RBS1	3	1	133.77		Ribulose biphosphate carboxylase small chain 1, chloroplastic
K4D340	12	9	390.7		Uncharacterized protein
K4C9P9	6	3	81.18		Uncharacterized protein
K4B137	2	2	130.51		Uncharacterized protein
K4BUT9	12	8	485.1		Uncharacterized protein
K4CPL7	1	1	26.69		Uncharacterized protein
K4BI68	29	6	1638.61		Uncharacterized protein
K4CPM4	12	7	280.94		Uncharacterized protein
K4D3M1	15	1	793.19		Uncharacterized protein
K4CN56	4	2	105.99		Uncharacterized protein
K4CDV2	15	1	1005.95	Yes	Uncharacterized protein
K4CQY0	3	3	73.77		Uncharacterized protein
K4C4X4	5	3	130.58		60S ribosomal protein L36
K4AX34	10	7	366.46		Peroxidase
Q2QJT5	4	4	75.15		ASR4
K4D0T6	9	4	125.1		Adenylyl cyclase-associated protein
K4CMJ7	6	5	194.09		Eukaryotic translation initiation factor 3 subunit G
K4D601	24	16	1378		Uncharacterized protein
K4BPS9	2	1	52.13		Uncharacterized protein
K4CX83	21	14	1107.76		Glyceraldehyde-3-phosphate dehydrogenase
K4CWZ4	7	3	44.29		Uncharacterized protein
ENO	32	13	2653.83		Enolase
K4BLN8	5	1	41.33		Uncharacterized protein
K4BNC2	18	7	837.8		6-phosphogluconate dehydrogenase, decarboxylating
K4BDF9	7	4	137.89		Uncharacterized protein
14338	11	6	428.89		14-3-3 protein 8
K4DA65	4	3	151.42		Uncharacterized protein
K4BTY6	23	13	929.63		Uncharacterized protein
K4BK43	9	7	154.66		Uncharacterized protein
B5M9E5	7	3	141		Beta-glucosidase 08
K4C4W6	36	4	2205.2		Uncharacterized protein
K4BT79	5	2	142.55		Uncharacterized protein
K4D371	3	3	24.11		Uncharacterized protein

K4BFW3	4	3	76.77		Uncharacterized protein
K4BHY1	7	3	255.74		Uncharacterized protein
D2KQI9	9	7	276.41		Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial
K4BW98	4	1	132.15		Uncharacterized protein
K4BNB4	10	2	282.7		Pyruvate dehydrogenase E1 component subunit alpha
K4B7P7	4	1	53.46		Uncharacterized protein
K4CNF2	13	1	871.19		Isocitrate dehydrogenase [NAD] subunit, mitochondrial
K4D1W3	20	2	838.23		Peroxidase
K4ASJ6	3	2	151.45		Peroxidase
K4D473	39	2	2791.3		Uncharacterized protein
K4CHA8	3	2	46.61		Uncharacterized protein
K4BNP7	4	4	226.2		Uncharacterized protein
K4D5H1	6	3	138.88		Uncharacterized protein
K4C2D7	12	2	464.14		Uncharacterized protein
K4BV32	2	1	28.07		Uncharacterized protein
K4C8H3	13	11	469.3		Uncharacterized protein
K4D3J8	6	2	342.48		Plasmamembrane intrinsic protein 25
Q4PS96	6	6	91.94		Plastidic hexokinase
K4BFL6	5	1	255.39		Uncharacterized protein
O04678	10	1	295.01	Yes	P69B protein
K4BTH5	2	1	78.41		Uncharacterized protein
K4BEB0	1	1	28.58		Uncharacterized protein
K4AZZ5	10	5	221.91		Uncharacterized protein
K4CDC2	4	4	97.8		Uncharacterized protein
14336	23	3	1886.65		14-3-3 protein 6
Q1PCD2	3	1	50.12		Glucose-6-phosphate isomerase
14339	17	6	936.9		14-3-3 protein 9
K4CR67	5	1	308.85		Histone H2A
K4AT78	2	1	47.41		Uncharacterized protein
K4CHH2	2	2	37.9		GrpE protein homolog
K4CMU5	4	2	89.22		Uncharacterized protein
K4B9P2	32	7	2406.3		Pectinesterase
K4AY17	2	1	38.83		Uncharacterized protein
K4D9V2	1	1	36.91		Uncharacterized protein
K4C0Y7	5	2	46.95		Uncharacterized protein
O81536	25	22	1529.94		Annexin
K4C9H1	2	1	49.35		Uncharacterized protein
PSBA	2	2	148.3		Photosystem II protein D1
K4BAN9	5	2	275.48		Uncharacterized protein
K4B8D2	8	8	311.99		Uncharacterized protein
K4CHA5	1	1	44.92		Uncharacterized protein
PPOD	16	1	720		Polyphenol oxidase D, chloroplastic
K4BM57	10	6	252.89		Uncharacterized protein
K4CXD9	8	1	489.01		40S ribosomal protein S8
K4C6Y1	3	2	30.69		Uncharacterized protein
K4DEV8	4	1	84.16		Uncharacterized protein
K4CWV7	2	2	67.14		Uncharacterized protein
K4AQC2	4	4	154.42		Uncharacterized protein
K4CVT4	13	11	291.97		Uncharacterized protein
K4B3G5	7	5	208.53		Uncharacterized protein
K4BF68	2	2	106.79		Uncharacterized protein
K4D0E5	12	3	288.6		Uncharacterized protein
K4CHA0	8	2	85.9		Pectinesterase
K4CBN7	10	8	216.68		Uncharacterized protein
K4DHP7	4	3	98.31		Uncharacterized protein

K4BPR4	25	4	2093.38	Uncharacterized protein
K4DBW0	4	3	110.2	Uncharacterized protein
PSBO	3	3	53.32	Oxygen-evolving enhancer protein 1, chloroplastic
K4CJ21	14	11	437.37	Malic enzyme
K4B740	18	9	1089.12	UDP-glucose 6-dehydrogenase
K4CRJ2	6	3	150.11	Uncharacterized protein
K4B894	2	2	61.39	Uncharacterized protein
K4BG52	2	1	45.72	Acetolactate synthase
K4BEI9	4	4	123.83	SGT1-1
K4BM40	18	10	577.17	T-complex protein 1 subunit delta
K4B813	6	2	273.04	Uncharacterized protein
K4CQB7	5	2	374.1	Uncharacterized protein
K4BQD6	7	6	323.26	Uncharacterized protein
K4C7U1	5	1	116.81	Ribosomal protein L37
K4AV63	20	13	1024.58	Uncharacterized protein
Q645M9	5	1	92.6	Glyoxisomal malate dehydrogenase
K4AZQ9	2	1	56.1	Reticulon-like protein
K4C726	13	13	504.68	Uncharacterized protein
K4DGN7	9	1	372.94	Uncharacterized protein
K4CH57	1	1	47.63	Uncharacterized protein
K4C6V9	3	2	54.39	Uncharacterized protein
K4CRI4	5	1	130.32	Uncharacterized protein
Q8VWR0	6	2	239.25	Profilin
K4DHW5	10	5	232.76	Uncharacterized protein
K4CU16	5	1	151.94	Uncharacterized protein
K4C7C4	12	9	485.06	Uncharacterized protein
K4B489	4	2	89.58	Aminoacylase-1
K4BK27	2	2	50.76	Uncharacterized protein
Q672Q6	6	3	103.14	Photosystem II oxygen-evolving complex protein 3
Q0PY39	3	3	118.94	Auxin repressed/dormancy associated protein
Q4A1N1	4	3	134.41	Non-specific lipid-transfer protein
K4D677	2	1	20.92	Uncharacterized protein
K4DAV2	12	6	288.64	Uncharacterized protein
K4CP13	5	5	183	Phospholipase D
K4B169	8	2	307.95	Uncharacterized protein
K4CPS8	32	7	1746.06	Uncharacterized protein
K4DHX8	2	2	36.22	Uncharacterized protein
IF5A4	9	3	422.99	Eukaryotic translation initiation factor 5A-4
K4CAN4	22	17	986.88	Succinyl-CoA ligase subunit beta
K4CP92	5	5	119.55	Glutathione peroxidase
K4AT31	10	6	311.98	Uncharacterized protein
Q2PQI9	6	4	207.42	Nascent polypeptide-associated complex subunit beta
K4CTZ5	5	1	79.12	Uncharacterized protein
K4AZ16	10	7	423.35	T-complex protein 1 subunit alpha
K4BBM6	6	4	182.27	Peroxidase
K4C2U0	6	4	145.35	Proteasome subunit beta type
K4AW95	19	6	949.81	Uncharacterized protein
K4BSP6	6	5	230.59	Uncharacterized protein
K4BB19	6	2	53.05	Uncharacterized protein
K4CWR4	38	1	2694.31	Adenosylhomocysteinase
K4CHF9	8	5	354.97	Uncharacterized protein
K4C1G0	1	1	47.99	Uncharacterized protein
K4CNR8	4	4	185.08	Uncharacterized protein
K4C8R4	20	7	1221.44	Glyceraldehyde-3-phosphate dehydrogenase
K4D9Y0	3	2	31.14	Uncharacterized protein
K4DBU5	5	2	65.7	Uncharacterized protein

K4D5U3	19	13	1359.13	Glutamine synthetase
AGUB	2	2	41.13	N-carbamoylputrescine amidase
K4BTH7	12	6	510.75	Peroxidase
K4CPP4	4	1	40.56	Uncharacterized protein
K4B2X1	8	7	200.73	Uncharacterized protein
Q9S875	4	1	171.25	TOM P14A protein (Fragment)
K4D3I3	25	7	1292.41	S-adenosylmethionine synthase
K4C5M1	7	4	405.99	Uncharacterized protein
Q53U35	4	1	104.14	Similar to pathogenesis-related protein STH-2
K4BJC4	12	7	295.26	Uncharacterized protein
K4CBT5	4	3	56.91	Uncharacterized protein
K4CQ62	14	9	383.09	Uncharacterized protein
K4CRE8	4	1	107.32	Uncharacterized protein
K4B375	6	3	72.19	Uncharacterized protein
K4BEW2	2	1	64.92	Serine/threonine-protein phosphatase
PSBC	1	1	69.6	Photosystem II CP43 reaction center protein
K4CA55	12	8	421.81	Peptidyl-prolyl cis-trans isomerase
K4BK61	15	8	489.7	Uncharacterized protein
K4BBN7	8	6	236.58	Uncharacterized protein
K4BIH2	5	5	285.81	Uncharacterized protein
K4C131	3	3	138.54	Uncharacterized protein
K4BJW4	16	4	703.37	Glyceraldehyde-3-phosphate dehydrogenase
K4B0I7	9	3	405.39	Uncharacterized protein
K4CGP6	12	2	419.68	Uncharacterized protein
K4CMM7	15	3	639.05	Uncharacterized protein
K4C2X8	5	4	217.28	Uncharacterized protein
Q8H0Q1	5	5	104.28	Proliferating cell nuclear antigen
K4C2W4	9	4	273.34	Protein disulfide-isomerase
K4D443	2	1	157.41	Uncharacterized protein
OLP1	10	9	574.65	Osmotin-like protein
K4CGT2	5	2	136.11	Uncharacterized protein
K4C6Q9	3	3	100.05	Uncharacterized protein
K4AYE4	8	7	458.21	Uncharacterized protein
K4C2D6	14	11	1117.52	Uncharacterized protein
EF1A	28	2	1944.15	Elongation factor 1-alpha
K4CAX7	1	1	31.52	Uncharacterized protein
K4CAM4	2	1	22.27	Uncharacterized protein
K4BG30	10	5	417.56	Peroxidase
K4BVG4	5	3	305.48	Thioredoxin
14334	20	6	1540.44	14-3-3 protein 4
K4C956	14	4	724.67	Uncharacterized protein
K4BHX1	1	1	65.77	Uncharacterized protein
K4CLT6	6	5	153.83	Uncharacterized protein
K4C753	3	2	100.29	Uncharacterized protein
K4D482	5	3	123.84	Uncharacterized protein
H6V7A0	6	1	406.89	MIP (Fragment)
A9LRT7	13	5	363.5	Isopentenyl diphosphate isomerase
K4ASX2	6	3	182.98	Uncharacterized protein
IER1	1	1	94.05	Ethylene-responsive proteinase inhibitor 1
K4D5V2	22	16	765.27	Uncharacterized protein
K4CNG6	7	4	219.47	Uncharacterized protein
K4BUB7	16	11	641.55	Serine hydroxymethyltransferase
K4DHE3	11	1	670.45	Uncharacterized protein
K4BCV6	13	8	224.85	Uncharacterized protein
K4D5G8	9	1	281.33	Uncharacterized protein
K4CG60	12	9	273.76	Aspartate aminotransferase

K4CW98	3	1	126.76	Uncharacterized protein
Q6SKP4	19	3	807.03	Ribosomal protein L3
K4D6L1	9	8	223.94	Eukaryotic translation initiation factor 3 subunit I
E5LBC4	10	7	369.24	Prephenate aminotransferase
K4BV11	4	2	40.86	Uncharacterized protein
K4CND0	4	4	156.22	Uncharacterized protein
K4C502	4	1	114.49	Uncharacterized protein
K4B0S5	11	4	476.88	Uncharacterized protein
K4CGI1	3	1	50.61	Uncharacterized protein
K4B3X5	12	7	552.48	Triosephosphate isomerase
K4D6I5	6	4	103.2	Nitrate reductase
K4BEV0	10	2	721.18	40S ribosomal protein AS
K4CBV4	4	3	80.94	Uncharacterized protein
K4D9G1	7	5	130.9	Uncharacterized protein
K4C2Q2	4	1	50.49	Uncharacterized protein
K4BH21	4	1	226.79	Peroxidase
K4C2B1	2	2	41.99	Uncharacterized protein
K4D338	59	35	5245.83	Uncharacterized protein
K4B2Z1	3	1	55.11	Uncharacterized protein
K4DC87	2	1	22.15	Uncharacterized protein
K4B3A1	7	6	142.19	Uncharacterized protein
K4BVG7	4	2	179.18	Uncharacterized protein
Q38MV0	37	3	2288.88	Beta-tubulin
K4C8X8	12	7	583.64	Uncharacterized protein
K4BP76	5	5	58.43	Uncharacterized protein
K4BPX0	1	1	38.07	Uncharacterized protein
K4AWF0	15	10	626.97	Importin subunit alpha
K4CW69	4	3	217.26	Cyanate hydratase
K4DCV6	3	1	111.18	Uncharacterized protein
K4CBX5	18	3	622.96	Purple acid phosphatase
K4AS92	6	4	130.43	Uncharacterized protein
K4CH51	5	2	209.57	Uncharacterized protein
K4AR83	5	1	91.57	Uncharacterized protein
K4AY52	3	1	86.42	Non-specific lipid-transfer protein
Q53Z32	50	10	3422.46	Molecular chaperone Hsp90-2
K4C768	2	2	39.27	Uncharacterized protein
B1Q3F2	4	1	244.03	Glutamate decarboxylase
K4CJJ4	5	1	123.94	Uncharacterized protein
K4BNY4	4	3	129.78	4-hydroxy-4-methyl-2-oxoglutarate aldolase
K4CPG9	4	2	120.62	Reticulon-like protein
K4ASQ6	6	5	269.37	Uncharacterized protein
A0A097PKA6	4	4	154.17	Homoserine kinase (Fragment)
K4CBD6	4	3	105.82	Xylose isomerase
Q7Y240	8	7	488.69	Thioredoxin peroxidase 1
K4D1R1	7	5	178.25	Uncharacterized protein
K4AYA3	11	9	560.15	Uncharacterized protein
K4CQV5	25	9	1892.33	Fructose-bisphosphate aldolase
K4DHJ5	10	2	360.83	Uncharacterized protein
Q9SDZ6	22	19	671.44	Phospholipase D alpha (Fragment)
K4DG42	4	2	73.96	Uncharacterized protein
K4D2B6	6	4	123.99	Uncharacterized protein
K4DDC7	1	1	24.57	Uncharacterized protein
K4BN73	3	1	45.91	Uncharacterized protein
K4D3F2	3	1	48.96	Uncharacterized protein
K4BRS2	15	10	568.34	Protein disulfide-isomerase
K4CWE3	3	2	74.84	Uncharacterized protein

K4C2U7	4	3	156.79	Uncharacterized protein
K4CGJ8	3	1	31.26	Uncharacterized protein
K4BVM3	14	11	381.57	Uncharacterized protein
B2LW68	9	5	687.01	PR1 protein
K4CEK6	9	5	307.56	Uncharacterized protein
K4CND8	1	1	51	Uncharacterized protein
O82777	13	3	397.65	Subtilisin-like protease
K4D465	6	3	176.68	Uncharacterized protein
K4BTQ3	5	1	114.26	Uncharacterized protein
K4B215	3	3	126.34	Uncharacterized protein
K4CAL7	11	7	372.3	Uncharacterized protein
K4CAH3	11	5	469.86	40S ribosomal protein S8
A6N6K8	9	7	433.05	Phenylacetaldehyde reductase
K4AT27	4	3	49.78	Dihydroorotate dehydrogenase (quinone), mitochondrial
K4C2E8	6	5	188.37	Beta-hexosaminidase
K4CQR9	13	2	528.56	Pyruvate kinase
K4BY90	2	1	32.92	Uncharacterized protein
K4CGW4	1	1	31.45	Uncharacterized protein
K4CK47	13	5	419.09	Aspartate aminotransferase
K4D433	3	1	138.59	Uncharacterized protein
K4BX93	4	2	86.44	Uncharacterized protein
K4AX99	10	1	448.1	Uncharacterized protein
K4ASG5	4	3	49.87	Uncharacterized protein
K4C5Z4	1	1	52.97	Uncharacterized protein
XTH1	9	7	305.95	Probable xyloglucan endotransglucosylase/hydrolase 1
Q8GZD8	22	18	1207.71	Leucine aminopeptidase 2, chloroplastic
K4BGK0	11	5	307.58	Uncharacterized protein
K4B112	6	1	347.17	Uncharacterized protein
K4BDY4	5	1	72.88	Uncharacterized protein
K4AZP5	5	3	229.88	Uncharacterized protein
K4D5K6	3	1	72.81	Uncharacterized protein
K4BEU4	6	5	115.08	Uncharacterized protein
Q6UJX4	50	10	2984.54	Molecular chaperone Hsp90-1
K4AVE6	5	3	75.36	Pyruvate kinase
K4CTJ3	3	2	50.33	Uncharacterized protein
Q49B52	23	20	1217.37	Monodehydroascorbate reductase
K4B0G3	12	1	514.88	Uncharacterized protein
K4C034	5	2	118.73	Uncharacterized protein
K4AT98	3	1	160.15	Uncharacterized protein
K4AX86	3	3	55.51	Uncharacterized protein
K4DBQ4	12	8	199.16	Uncharacterized protein
K4BCJ1	1	1	41.76	Uncharacterized protein
E5KBY0	2	2	77.26	Snakin-2
K4D9A5	3	1	45.39	Uncharacterized protein
K4B033	14	7	655.72	Uncharacterized protein
K4CPB3	9	7	145.65	Uncharacterized protein
K4DGM3	2	2	42.39	Uncharacterized protein
K4BJY6	4	1	234.65	Uncharacterized protein
K4D3F8	18	6	876.5	Pyruvate kinase
Q40164	9	1	544.95	Ubiquitin
K4C2U1	13	2	375.35	Phenylalanine ammonia-lyase
K4ATR8	10	10	359.25	Uncharacterized protein
K4B937	6	4	139.36	Eukaryotic translation initiation factor 3 subunit D
K4BML6	3	1	38.91	Uncharacterized protein
K4BXV0	10	8	349.78	Uncharacterized protein

K4C5K3	3	1	125.12	Uncharacterized protein
K4D533	6	4	158.35	Uncharacterized protein
K4D5T9	5	1	93.98	Uncharacterized protein
K4DFV6	9	7	500.53	Uncharacterized protein
K4B778	9	4	440.77	Uncharacterized protein
K4ASC8	11	9	530.84	Uncharacterized protein
C6K2K9	15	3	593.5	GDP-mannose 3',5'-epimerase
K4AXX8	3	1	52.41	Uncharacterized protein
K4BXD4	16	7	639.28	Uncharacterized protein
K4CAI5	6	5	219.87	Uncharacterized protein
K4C8Q9	7	2	329.54	Uncharacterized protein
K4B1Z2	8	6	566.03	Uncharacterized protein
K4AXJ9	8	2	311.91	Uncharacterized protein
K4CXI1	2	1	23.59	Uncharacterized protein
K4C9J1	4	1	50.78	Protein argonaute
K4ASC2	22	9	1941.59	Isocitrate dehydrogenase [NADP]
K4CEN4	2	1	21.42	Uncharacterized protein
K4CK49	13	6	570.47	Importin subunit alpha
K4ASV3	3	2	111.34	Photosystem II CP47 reaction center protein
K4B8S7	7	4	159.59	Uncharacterized protein
K4CET6	4	1	39.13	Uncharacterized protein
K4C275	6	6	248.2	Uncharacterized protein
Q52QQ4	14	5	849.85	Ascorbate peroxidase
K4CQ64	3	2	86.58	Uncharacterized protein
K4BIL3	6	4	245.81	Uncharacterized protein
K4CEE4	3	1	76.86	Uncharacterized protein
K4B7I5	3	2	73.17	Uncharacterized protein
K4ASG1	7	2	144.3	Serine/threonine-protein phosphatase
Q9SMD1	3	1	54.75	Small ubiquitin-related modifier
K4C5S4	43	4	1961.62	Clathrin heavy chain
K4D2Y4	8	5	227.45	Uncharacterized protein
K4DA57	18	13	640.05	Uncharacterized protein
K4B546	14	11	336.67	Obg-like ATPase 1
K4BN29	3	2	60.08	Uncharacterized protein
K4AZ93	1	1	27.34	Uncharacterized protein
K4DA30	3	2	54.99	Uncharacterized protein
K4C2Y2	5	2	79.34	Uncharacterized protein
K4B929	3	2	94.46	Uncharacterized protein
K4DHX7	5	3	75.4	Uncharacterized protein
K4D2J1	5	4	96.07	Inosine-5'-monophosphate dehydrogenase
K4CX88	9	1	518.09	Uncharacterized protein
Q5D8D3	9	7	190.58	Acyl-coenzyme A oxidase
K4DH72	30	1	1780.19	Uncharacterized protein
K4B0W1	2	1	68.84	Uncharacterized protein
K4CF48	12	10	475.41	Uncharacterized protein
K4AQV9	2	1	21.3	Uncharacterized protein
K4D1E2	3	1	27.51	Uncharacterized protein
K4D1N1	3	1	115.49	Uncharacterized protein
K4BVZ4	3	3	88.8	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
K4DC06	1	1	42.21	Uncharacterized protein
K4CE22	6	3	107.65	Uncharacterized protein
K4AXV8	6	2	59.82	Uncharacterized protein
K4D5Z8	9	1	532.46	Isocitrate dehydrogenase [NADP]
K4CID1	9	6	162.44	Uncharacterized protein
Q6QLU0	2	1	38.74	Protein phosphatase 2C

K4D027	2	2	155.48	Uncharacterized protein
K4B6J6	13	1	540.06	Uncharacterized protein
K4BB47	14	10	566.85	Uncharacterized protein
K4CIH7	30	1	2309.01	Uncharacterized protein
K4CV90	4	4	91.41	Uncharacterized protein
K4BLS9	4	1	74.06	Uncharacterized protein
Q94KH6	4	1	73	Calcium-dependent protein kinase CDPK1
A0A097PM10	6	4	129.43	LOS4 (Fragment)
K4CEF1	5	1	38.07	Uncharacterized protein
K4BA58	1	1	36.81	Uncharacterized protein
K4BUN4	8	4	399.85	Uncharacterized protein
K4D7V9	14	8	363.32	Uncharacterized protein
K4BAZ3	18	3	1153.93	Peroxidase
K4BM30	1	1	49.08	Uncharacterized protein
K4AYP1	4	2	180.38	Uncharacterized protein
K4AWT6	4	3	104.65	Uncharacterized protein
K4D0G7	2	2	55.03	Uncharacterized protein
K4AX35	4	1	62.14	Peroxidase
K4BU58	3	3	94.41	Uncharacterized protein
K4CR73	11	5	273.23	Eukaryotic translation initiation factor 3 subunit A
K4BU29	4	2	206.84	40S ribosomal protein S21
K4AXB5	7	6	199.77	Uncharacterized protein
K4CGU8	19	13	1850.92	Malate dehydrogenase
K4BDV8	2	1	27.02	Uncharacterized protein
K4D9W7	5	4	515.28	Uncharacterized protein
K4DA40	10	9	322.55	Uncharacterized protein
K4CQE3	15	8	187.24	Uncharacterized protein
K4B212	1	1	94.14	Uncharacterized protein
K4BF00	8	7	387.5	Uncharacterized protein
A9QNE7	2	1	22.68	ABA 8'-hydroxylase
K4B303	13	11	593.11	Uncharacterized protein
K4C263	4	1	167.49	Uncharacterized protein
K4BHA1	10	7	122.37	Uncharacterized protein
K4B1M7	13	8	209.72	Uncharacterized protein
K4CLR4	3	3	100.13	Uncharacterized protein
RS25	9	1	319.8	40S ribosomal protein S25
K4CET1	5	5	111.94	Uncharacterized protein
D2Y3F4	12	8	399.52	Alcohol dehydrogenase class III
K4BDN9	3	3	118.64	Translocon-associated protein subunit beta
K4BKV2	17	12	641.29	Uncharacterized protein
K4CU87	1	1	41.39	Uncharacterized protein
K4ATR9	5	2	163.46	Uncharacterized protein
K4C3Y2	5	1	42.27	Uncharacterized protein
K4BC24	10	2	633.04	UDP-glucose 6-dehydrogenase
K4BKH5	6	2	178.22	Uncharacterized protein
K4DFF9	9	6	212.86	Ubiquitin carboxyl-terminal hydrolase
K4B256	4	2	72.37	Uncharacterized protein
K4BTL1	11	10	459.81	Uncharacterized protein
K4DAM1	11	4	202.84	Uncharacterized protein
K4D1W4	19	1	877.41	Peroxidase
K4D4D5	1	1	52.99	Uncharacterized protein
K4DBI3	4	2	44.05	Uncharacterized protein
K4C762	3	2	54.29	Uncharacterized protein
K4DCK2	6	3	100.42	Uncharacterized protein
K4B445	3	2	37.59	Uncharacterized protein
K4CZX7	3	1	42.22	Uncharacterized protein

K4BAP8	3	2	31.55	Uncharacterized protein
K4CQZ3	2	1	105.63	Uncharacterized protein
K4B438	24	4	1594.31	Uncharacterized protein
Q8H6B5	7	5	148.07	Putative dehydrogenase
K4BL13	17	15	907.3	Uncharacterized protein
K4CNI4	3	3	64.21	Uncharacterized protein
K4CWD6	1	1	21.24	Uncharacterized protein
H1	5	3	93.65	Histone H1
K4CPI7	11	2	388.05	Uncharacterized protein
K4AXU8	2	2	116.47	Uncharacterized protein
K4C8H9	3	3	55.74	Uncharacterized protein
K4BDH9	18	14	677.22	Glucose-6-phosphate 1-dehydrogenase
Q9XEX7	14	1	691.74	Heat shock protein 90 (Fragment)
K4CKC6	2	1	58.43	Uncharacterized protein
K4BL38	12	4	558.08	Uncharacterized protein
K4CQB5	32	16	1547.95	Uncharacterized protein
K4BNL3	13	8	417.78	Uncharacterized protein
K4BEK3	4	2	82.94	Pyruvate kinase
B7U4A4	2	1	94.46	Ubiquitin conjugating enzyme
K4DA71	5	4	233.63	Proteasome subunit beta type
K4D4F0	2	1	55.94	Uncharacterized protein
K4BSK3	12	5	121.54	Uncharacterized protein
K4B6E8	7	5	163.39	Uncharacterized protein
K4BKE0	1	1	23.44	Uncharacterized protein
K4DBV1	20	17	1445.57	Uncharacterized protein
K4C241	12	3	421.86	Uncharacterized protein
K4BQ70	4	4	144.81	Uncharacterized protein
Q6EAL9	3	2	136.35	Arachidonic acid-induced DEA1
K4BEV1	2	2	22.74	Alpha-galactosidase
K4B989	15	11	634.34	Uncharacterized protein
K4BY59	5	3	59.14	Uncharacterized protein
K4CM58	3	2	123.82	Eukaryotic translation initiation factor 3 subunit L
K4BVE0	4	2	62.99	Uncharacterized protein
K4BN81	10	7	349.8	Uncharacterized protein
K4CVG4	5	2	96.45	Lipoxygenase
K4CRG8	4	3	305.43	Uncharacterized protein
K4D5B3	6	1	46.62	Uncharacterized protein
K4C952	7	3	180.91	Lysine--tRNA ligase
K4CNQ1	2	1	169.46	Uncharacterized protein
K4BR30	7	1	61.1	Uncharacterized protein
K4AZG1	11	10	454.83	Malic enzyme
K4CPY2	2	1	54.77	Uncharacterized protein
K4CEJ5	5	1	232.59	60S ribosomal protein L27
K4CME9	7	2	167.09	Uncharacterized protein
K4CJR2	1	1	26.66	Uncharacterized protein
K4CXX8	8	5	310.48	Proteasome subunit alpha type
K4BMH6	9	1	281.91	Uncharacterized protein
K4B6Q6	5	1	49.03	Uncharacterized protein
K4BAF3	10	9	333.31	Phosphoserine aminotransferase
K4B111	8	3	447.49	Translationally-controlled tumor protein homolog
K4CAN6	2	1	48.11	Uncharacterized protein
B1Q3F8	8	7	303.83	Succinic semialdehyde dehydrogenase
B1PLH3	1	1	30.12	Cycloartenol synthase
K4BGN7	2	2	52.95	Uncharacterized protein
A8WBX7	6	4	161.13	Mevalonate diphosphate decarboxylase
K4C5F4	4	4	232.19	Superoxide dismutase

Q8GT30	17	6	737.9	Dihydrolipoyl dehydrogenase
Q949K3	2	2	28.28	Suppressor-like protein
K4CNS8	3	1	61.47	Uncharacterized protein
IF5A2	7	4	254.13	Eukaryotic translation initiation factor 5A-2
K4D1P2	14	8	439.71	Uncharacterized protein
K4BPH8	8	2	338.16	Uncharacterized protein
O22549	2	2	71.14	Inorganic phosphate transporter
K4BU61	1	1	31.52	Uncharacterized protein
K4BP29	1	1	46.48	Alpha-galactosidase
K4B9Q0	2	1	34.56	Uncharacterized protein
K4DAL9	11	3	340.52	Uncharacterized protein
K4BJI5	8	2	359.09	Uncharacterized protein
K4BS97	6	3	146.63	Uncharacterized protein
K4B2K0	7	5	158.92	Uncharacterized protein
K4CB65	12	8	561.27	Uncharacterized protein
K4C891	12	6	422.62	Uncharacterized protein
K4B2V0	3	1	35.45	Uncharacterized protein
K4CLQ6	5	3	88.51	Phospholipase D
K4BHG4	9	6	230.88	Alpha-1,4 glucan phosphorylase
K4CP66	5	4	219.75	Uncharacterized protein
Q38JD4	4	2	63.28	Temperature-induced lipocalin
K4ASQ2	3	1	35.37	Uncharacterized protein
K4C950	11	2	750.86	Uncharacterized protein
K4DFV3	10	2	596.79	Plasmamembrane intrinsic protein 13
K4CVC2	9	7	130.35	Uncharacterized protein
K4BDV0	5	1	132.86	Uncharacterized protein
K4D8F9	2	1	27.27	Uncharacterized protein
K4C1P6	2	1	86.99	Uncharacterized protein
K4DA09	6	4	245.89	Uncharacterized protein
K4D7A1	1	1	37.86	Uncharacterized protein
K4CR71	3	2	97.54	Uncharacterized protein
K4CFU2	3	1	89.73	Uncharacterized protein
K4D5N7	3	1	65.86	Uncharacterized protein
K4B440	10	6	237.64	Uncharacterized protein
K4ATN9	3	2	52.16	Uncharacterized protein
K4AXP6	9	7	458.05	Uncharacterized protein
K4BGT9	6	2	156.85	Uncharacterized protein
K4D4E6	37	1	2486.58	Uncharacterized protein
Q53U42	4	4	250.43	Similar to aquaporin
K4CBV3	6	1	88.53	Uncharacterized protein
K4DHW9	4	1	68.78	Uncharacterized protein
K4BGC0	2	2	65.01	Uncharacterized protein
K4ASE8	3	2	74.69	Uncharacterized protein
K4CFP9	4	4	241.33	Uncharacterized protein
K4BF11	1	1	28.62	Peroxidase
K4BX34	17	11	1120.35	Fructose-bisphosphate aldolase
K4CLS8	6	4	248.86	Cytochrome b-c1 complex subunit 7
K4BIG6	3	2	25.23	Uncharacterized protein
K4CG47	4	2	141.01	Proteasome subunit alpha type
K4BT19	12	11	926.43	Uncharacterized protein
K4D992	2	1	34.38	Uncharacterized protein
K4B414	2	1	26.12	Uncharacterized protein
D0EXD9	3	3	159.26	Hexose transporter 1
K4B3F4	6	4	215.68	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit
K4DBV8	2	2	76.69	Uncharacterized protein

K4AWT4	4	4	398.55		40S ribosomal protein S21
K4DH49	21	7	954.29		Uncharacterized protein
K4BIL6	3	2	31.9		Uncharacterized protein
K4CA71	7	4	400.35		Uncharacterized protein
K4BA95	6	3	164		Thioredoxin reductase
K4BTJ3	5	3	149.12		Uncharacterized protein
K4CIW8	4	1	67.52		Nucleoside diphosphate kinase
K4DAD0	2	1	27.96		Uncharacterized protein
K4BW47	5	1	161.16		Uncharacterized protein
K4CPN9	5	3	127.55		Nucleoside diphosphate kinase
K4BM62	7	4	174.67		Uncharacterized protein
K4D3T6	36	1	2223.86		Uncharacterized protein
K4CFE7	7	5	194.33		Isocitrate lyase
K4CUA5	4	1	34.15		Uncharacterized protein
K4CQ40	6	4	356.91		Uncharacterized protein
K4BIC8	7	1	256.87		Uncharacterized protein
K4C8X1	8	2	297.08		Uncharacterized protein
K4DB95	1	1	29.31		Uncharacterized protein
Q2VY16	5	3	128.03		Peptidyl-prolyl cis-trans isomerase
K4BXX0	19	16	617.1		Uncharacterized protein
K4C8T4	10	2	799.1		40S ribosomal protein AS
K4B9J6	7	5	422.43		Uncharacterized protein
K4CCA9	2	1	29.8		Uncharacterized protein
K4C2M0	12	2	604.52		Histone H2B
K4D324	2	1	72.2		Small nuclear ribonucleoprotein F
RS27A	11	2	630.71		Ubiquitin-40S ribosomal protein S27a
K4CGZ3	10	4	125.49		Uncharacterized protein
K4B407	14	12	575.29		Proteasome subunit alpha type
K4B3R5	4	2	72.13		Amidophosphoribosyltransferase
K4B123	2	2	55.26		Uncharacterized protein
K4C8V8	5	4	130.03		Uncharacterized protein
K4BD40	8	4	261.56		Uncharacterized protein
K4CC14	7	5	165.94		Uncharacterized protein
K4CC89	4	2	100.57		Uncharacterized protein
K4B2B1	3	2	181.09		Uncharacterized protein
K4B4Z0	5	3	209.53		Uncharacterized protein
K4D1Q1	4	2	87.67		Uncharacterized protein
K4DEQ8	11	6	492.58		Uncharacterized protein
K4D4G9	3	1	34.47		Cellulose synthase
K4CLI8	3	1	90.17		Uncharacterized protein
K4C363	4	1	182.41		Uncharacterized protein
K4BA13	3	2	136.99		Uncharacterized protein
K4B413	2	2	73.81		Uncharacterized protein
K4BZB1	11	5	415.96		Uncharacterized protein
K4C2K1	3	2	62.93		Uncharacterized protein
K4BNR2	38	6	3107.52		ATP synthase subunit beta
K4B9G5	3	1	114.29	Yes	Uncharacterized protein
K4B2T2	2	1	33.97		Uncharacterized protein
K4D5S0	3	1	37.78		Uncharacterized protein
K4C3Y3	4	3	103.71		Uncharacterized protein
K4D5E1	1	1	24.79		Beta-hexosaminidase
K4C926	2	1	24.68		Uncharacterized protein
K4C9J5	11	2	437.45		Histone H2B
K4BU76	6	4	150.98		NADPH--cytochrome P450 reductase
K4BNA9	4	2	59.21		Uncharacterized protein
K4C874	23	4	1461.73		Uncharacterized protein

K4AW47	4	4	66.55	Uncharacterized protein
K4C947	14	9	444.4	Uncharacterized protein
K4C2K2	1	1	65.44	Uncharacterized protein
K4CGU0	8	3	279.06	Fen-interacting protein 3
K4C7D0	4	2	36.89	Uncharacterized protein
K4C6R5	2	2	59.46	Ubiquitin carboxyl-terminal hydrolase
K4BRR1	8	3	512.04	Uncharacterized protein
K4BHCS	2	1	27.63	Uncharacterized protein
K4D613	2	2	66.01	Uncharacterized protein
K4COW6	6	4	119.16	Uncharacterized protein
K4CXQ8	46	9	1872.27	Uncharacterized protein
K4CEC3	2	2	36.87	Uncharacterized protein
K4DAF9	3	3	59.6	Uncharacterized protein
K4CX99	1	1	50.01	Uncharacterized protein
K4B831	1	1	31.71	Uncharacterized protein
K4C7W9	4	4	153.18	Uncharacterized protein
K4D4S7	6	3	148.17	Uncharacterized protein
K4B3H9	18	15	1130.61	Uncharacterized protein
K4BA40	8	7	499.55	Proteasome subunit alpha type
K4CA68	12	3	631.92	Uncharacterized protein
K4BB54	3	1	44.46	Uncharacterized protein
K4ATJ4	4	4	100.13	Peptidyl-prolyl cis-trans isomerase
K4BF07	6	5	109.26	Uncharacterized protein
K4D938	3	1	72.88	Signal recognition particle subunit SRP72
K4BJY3	8	3	342.02	Uncharacterized protein
K4DHA3	16	2	686.91	40S ribosomal protein S6
K4DA96	4	2	80.88	Protein disulfide-isomerase
K4CVX3	1	1	29.98	Uncharacterized protein
K4B8C3	3	1	67.96	Uncharacterized protein
K4CAS6	8	5	222.96	Uncharacterized protein
K4C2U9	17	12	443.91	Uncharacterized protein
K4C7H6	2	2	73.19	RNA-binding protein 8A
Q6IV07	22	4	912.69	UDP-glucose:protein transglucosylase-like protein SIUPTG1
K4B373	3	1	26.31	Uncharacterized protein
K4CW84	5	3	108.04	Uncharacterized protein
K4D102	6	1	230.3	Uncharacterized protein
K4B935	2	1	55.14	Uncharacterized protein
K4CWI5	3	3	58.56	Uncharacterized protein
K4B0P2	1	1	27.7	Uncharacterized protein
K4B117	5	2	232.31	Uncharacterized protein
K4BJG4	1	1	31.1	Uncharacterized protein
K4D7Y5	4	3	45.78	Uncharacterized protein
K4C731	3	2	137.15	Uncharacterized protein
DES	3	2	49.47	9-divinyl ether synthase
K4CG62	12	7	397.39	Uncharacterized protein
K4AT09	5	4	108.5	Uncharacterized protein
K4C669	8	2	177.68	Uncharacterized protein
K4D452	15	8	905.44	Uncharacterized protein
K4AT06	4	4	109.24	40S ribosomal protein S27
CYPH	13	6	796.52	Peptidyl-prolyl cis-trans isomerase
K4BZ35	7	4	259.62	Uncharacterized protein
K4CII8	2	1	33.03	Uncharacterized protein
K4AYJ8	11	11	414.93	Uncharacterized protein
K4CW92	6	5	91.6	Uncharacterized protein
K4CGD8	3	1	64.81	Uncharacterized protein

K4C286	9	2	295.18	Uncharacterized protein
K4D4J0	2	1	24.54	Uncharacterized protein
K4CJE1	3	1	62.4	Uncharacterized protein
K4DF02	8	1	335.05	Uncharacterized protein
K4C3Z3	3	3	109.55	Uncharacterized protein
K4D6D0	5	2	152.92	Uncharacterized protein
K4DE77	1	1	44.62	Uncharacterized protein
K4D5C8	6	2	68.9	Acyl-[acyl-carrier-protein] desaturase
K4C9U6	2	2	57.67	Uncharacterized protein
Q9FV21	8	1	246.31	Aldehyde oxidase (Fragment)
K4CTF6	7	2	402.12	40S ribosomal protein S8
K4BXK1	1	1	33.45	Uncharacterized protein
K4D888	5	2	47.25	Uncharacterized protein
K4D435	24	9	1208.78	Uncharacterized protein
K4CTW6	3	1	138.87	Uncharacterized protein
K4CN52	5	1	63.28	Uncharacterized protein
K4CXT9	6	1	217.3	Uncharacterized protein
K4DHT1	17	5	887.42	Dihydrolipoyl dehydrogenase
K4C740	5	3	98.6	Uncharacterized protein
K4DGU3	13	7	351.54	Uncharacterized protein
K4B0Q2	2	1	52.03	Uncharacterized protein
K4CUW3	10	8	473.64	Uncharacterized protein
K4D530	13	7	449.39	Pyruvate kinase
K4DEU5	19	4	892.6	Uncharacterized protein
K4BJY1	12	8	250.13	Uncharacterized protein
K4C1Z4	7	4	200.69	Uncharacterized protein
K4CGB9	6	4	56.83	Uncharacterized protein
K4CIA3	6	1	51.63	Uncharacterized protein
K4CP17	6	2	310.25	Uncharacterized protein
K4CW09	5	1	65.33	Uncharacterized protein
K4AZY8	7	1	56.72	Uncharacterized protein
K4BXU9	5	2	84.47	Purple acid phosphatase
K4C3D8	10	2	475.65	40S ribosomal protein S8
K4BXJ9	9	5	454.5	Uncharacterized protein
K4D1F7	22	2	1236.38	Uncharacterized protein
K4BTC7	4	1	57.08	Uncharacterized protein
K4D7R1	6	3	203.94	Uncharacterized protein
K4CIH6	11	8	214	Uncharacterized protein
K4BRN5	5	4	117.01	Uncharacterized protein
K4BXT9	2	2	118.27	Uncharacterized protein
K4BIB5	7	5	168.09	Uncharacterized protein
K4BS82	5	2	86.67	Uncharacterized protein
K4BC25	22	14	658.68	Uncharacterized protein
K4BYA8	13	2	277.39	Uncharacterized protein
K4D7F1	14	4	673.14	Uncharacterized protein
K4D9M3	9	2	349.92	Uncharacterized protein
K4B3Y8	5	4	113.31	Uncharacterized protein
K4AXC0	8	8	369.13	Citrate synthase
K4CYU9	10	6	367.35	Uncharacterized protein
K4D4E9	1	1	29.6	Uncharacterized protein
K4BAF0	2	1	59.5	Uncharacterized protein
K4D5N8	3	1	63.84	Uncharacterized protein
K4CMT7	8	1	400.68	60S ribosomal protein L13
K4AYJ2	21	17	751.48	Uncharacterized protein
C6K8M2	7	1	189.13	Plastid isopentenyl diphosphate isomerase
K4B9Y4	5	4	288.84	Uncharacterized protein

K4B504	9	6	224.99	Uncharacterized protein
K4B2Y6	1	1	23.39	Uncharacterized protein
K4B350	1	1	42.69	Uncharacterized protein
K4AYW0	4	3	125.67	Uncharacterized protein
K4CFR0	19	15	658.1	Uncharacterized protein
K4BWT6	7	1	62.36	Uncharacterized protein
K4CXV5	3	2	68.48	Uncharacterized protein
K4BI70	9	6	349.98	Uncharacterized protein
K4BM70	3	3	89.37	Uncharacterized protein
K4BSR7	4	3	61.44	Uncharacterized protein
K4BTZ3	5	2	120.54	Uncharacterized protein
K4CC52	2	1	91	Uncharacterized protein
K4C6Z0	1	1	39.66	Uncharacterized protein
K4AXJ0	2	2	68.67	Uncharacterized protein
K4B0Y8	4	4	130.15	Uncharacterized protein
K4CEP2	25	20	1154.16	Uncharacterized protein
K4BD93	4	1	132.79	Uncharacterized protein
K4B0X2	7	6	109.01	Uncharacterized protein
K4D7D0	2	1	108.11	Uncharacterized protein
K4BUC0	6	5	97.73	Uncharacterized protein
K4C3C9	6	6	320.61	Uncharacterized protein
K4AYW9	1	1	35.84	Uncharacterized protein
K4DHI9	11	8	455.73	Uncharacterized protein
K4BF64	1	1	27.45	Uncharacterized protein
E5L4Q6	6	1	76.04	ABA aldehyde oxidase
K4B9V1	4	3	126.72	Aminomethyltransferase
K4C9C7	1	1	37.39	Uncharacterized protein
K4B1L6	4	3	147.57	Uncharacterized protein
K4BX20	37	4	3190.71	ATP synthase subunit beta
Q93X45	9	6	243.83	Uncharacterized protein
K4BI42	2	1	32.54	Uncharacterized protein
K4BAZ4	16	3	1171.28	Peroxidase
Q9LEG5	5	3	148.29	Allene oxide cyclase
K4CAB8	11	8	543.38	Uncharacterized protein
K4BSH5	5	4	99.88	Uncharacterized protein
K4B612	1	1	30.31	Uncharacterized protein
K4BEJ6	4	2	114.62	Reticulon-like protein
PER2	3	1	131.23	Suberization-associated anionic peroxidase 2
K4BBY2	14	14	1060.73	Uncharacterized protein
K4CNP6	2	2	93.12	Uncharacterized protein
K4D1F3	3	2	253.99	Plasmamembrane intrinsic protein 29
K4BMW3	11	2	226.21	Uncharacterized protein
K4B3Q8	8	6	278.18	Uncharacterized protein
B6ECN9	19	17	730.21	Aminoaldehyde dehydrogenase 2
K4BJR2	1	1	36.89	Uncharacterized protein
K4CXU9	5	5	191.39	Uncharacterized protein
K4CAC2	12	1	478.42	Uncharacterized protein
K4CN15	3	2	67.53	Uncharacterized protein
K4CEB8	2	2	30.43	Eukaryotic translation initiation factor 3 subunit K
K4CK76	9	5	143.42	Delta-1-pyrroline-5-carboxylate synthase
K4CAB5	4	1	89.18	Uncharacterized protein
K4C7G6	3	2	59.79	Uncharacterized protein
K4CPJ1	2	1	73.97	Uncharacterized protein
K4BK90	5	4	98.3	Uncharacterized protein
K4C8Y0	1	1	102.45	Uncharacterized protein
K4C2H5	5	1	43.14	Uncharacterized protein

K4BNL4	6	3	191.83	Uncharacterized protein
K4C715	8	1	259.03	Uncharacterized protein
K4CW78	3	3	174.24	Uncharacterized protein
Q68HC8	23	15	681.77	Glucose-6-phosphate isomerase
K4B7H7	4	3	156.49	Uncharacterized protein
K4BXN9	8	3	185.96	Uncharacterized protein
K4AZ59	11	9	467	3-phosphoshikimate 1-carboxyvinyltransferase
K4BH59	6	1	76.48	Acyl-[acyl-carrier-protein] desaturase
K4B486	4	1	54.98	Uncharacterized protein
K4CB49	3	1	31.43	Uncharacterized protein
K4CNB0	6	3	114.96	Uncharacterized protein
K4DF79	2	2	105.17	Uncharacterized protein
K4BY24	9	6	259.42	Uncharacterized protein
Q9FV23	4	1	74.83	Aldehyde oxidase
K4CAS8	4	2	220.29	40S ribosomal protein S24
K4D860	5	1	167.83	Uncharacterized protein
K4B428	2	2	72.16	Plasmamembrane intrinsic protein 28
K4CFR4	3	1	44.32	Uncharacterized protein
K4CJE2	8	1	173.45	60S ribosomal protein L18a
K4CUE6	7	3	113.67	Uncharacterized protein
K4CLR0	1	1	39.15	Uncharacterized protein
K4DAZ1	13	11	748.34	Histone H4
K4BNF7	7	1	322.61	Uncharacterized protein
K4CR64	11	3	373.18	Uncharacterized protein
K4CJH4	14	2	677.6	Proteasome subunit alpha type
Q9MAZ6	2	1	66.69	Nonclathrin coat protein zeta2-COP
K4D9U0	2	2	52.93	Uncharacterized protein
K4CGY7	5	3	166.03	Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1
K4D0Y5	2	1	43.5	Uncharacterized protein
K4CUK9	5	4	134.95	Uncharacterized protein
K4BP02	10	7	426.58	Ribosomal protein L15
K4BFH1	6	2	110.58	Thioredoxin reductase
K4B513	4	2	45.03	DNA damage-binding protein 1
K4C2M1	5	2	86.85	Uncharacterized protein
K4BBU4	23	2	1620.17	Uncharacterized protein
K4C9L7	9	4	295.25	Uncharacterized protein
K4D3J1	33	2	1404.84	Uncharacterized protein
K4D249	6	3	47.14	Histone-lysine N-methyltransferase
K4CMV4	3	1	86.53	Uncharacterized protein
K4CA80	1	1	25.58	Uncharacterized protein
K4ATA6	6	2	146.76	Uncharacterized protein
K4CQE1	4	1	97.16	Peroxidase
K4CXJ6	3	2	172.45	Uncharacterized protein
K4BUA0	11	2	81.18	Uncharacterized protein
K4C7V7	3	1	86.44	Uncharacterized protein
K4DCU0	2	1	41.72	Uncharacterized protein
K4B124	5	3	359.04	Uncharacterized protein
E1U7P9	5	1	47.85	Glutathione synthetase
K4BF36	2	1	38.88	Uncharacterized protein
K4C6B2	5	4	214.27	Uncharacterized protein
K4DC02	13	10	604.58	Proteasome subunit alpha type
K4BS21	9	5	51.62	Uncharacterized protein
K4B8J2	6	1	196.97	Uncharacterized protein
K4B3K7	13	8	628.23	Uncharacterized protein
K4DH88	9	2	319.61	60S ribosomal protein L13

K4BR52	8	1	363.89	Uncharacterized protein
K4AZC8	3	1	108.98	ATPase ASNA1 homolog
K4CZS1	4	1	128.08	Uncharacterized protein
K4AV48	2	1	33.29	Uncharacterized protein
Q66MH8	2	1	34.35	MAPKK
K4B0A7	3	3	43.8	Uncharacterized protein
K4C6D5	3	3	74.56	Uncharacterized protein
K4BX96	10	4	184.02	Uncharacterized protein
K4D054	3	1	102.46	Uncharacterized protein
K4CH48	3	2	75.29	Ubiquitin carboxyl-terminal hydrolase
K4D0P0	2	1	52.3	Uncharacterized protein
K4CLG8	2	1	26.86	Uncharacterized protein
K4CV64	1	1	44.64	Uncharacterized protein
K4CWZ8	2	1	69.06	Eukaryotic translation initiation factor 3 subunit H
K4DF00	9	2	200.13	Uncharacterized protein
K4CC22	5	1	209.94	Uncharacterized protein
K4CBV6	16	6	689.63	Uncharacterized protein
K4CDN0	2	1	39.03	Uncharacterized protein
K4CF13	1	1	23.63	Uncharacterized protein
K4ASY4	9	5	429.08	Uncharacterized protein
K4AYH4	5	1	108.52	Uncharacterized protein
K4D810	7	3	129.43	Uncharacterized protein
K4BAG0	3	2	42.72	Uncharacterized protein
K4B089	4	4	146.3	Uncharacterized protein
K4D2T4	3	3	82.49	Uncharacterized protein
K4CBW8	4	4	73.04	Uncharacterized protein
K4DHU7	16	6	993.87	Uncharacterized protein
K4BSP7	3	1	145.15	Uncharacterized protein
K4CQP7	4	2	83.26	Uncharacterized protein
K4B9R3	6	1	109.68	Uncharacterized protein
K4CMU2	2	2	49.72	ATP-dependent Clp protease proteolytic subunit
K4DHU5	4	3	71.57	Uncharacterized protein
K4C3B5	14	8	320.56	Uncharacterized protein
V5YN05	16	4	778.31	Plasmamembrane intrinsic protein 15
K4B063	6	1	64.78	AGO4D
K4CC33	9	6	248.88	Uncharacterized protein
K4D831	10	3	491.12	Uncharacterized protein
K4B3G7	16	15	681.01	Coatomer subunit gamma
K4B0I9	3	1	46.14	Uncharacterized protein
K4ARQ3	2	2	26.3	Uncharacterized protein
K4DFC1	6	1	405.61	Uncharacterized protein
K4CZP2	2	1	34.7	Uncharacterized protein
K4BD63	4	1	80.07	Uncharacterized protein
MAF1	4	3	135.28	MFP1 attachment factor 1
K4BHX0	1	1	41.04	Uncharacterized protein
K4AQU9	4	2	42.86	Uncharacterized protein
K4DG11	3	2	58.87	Uncharacterized protein
Q8LRN7	4	2	32.97	Cell-wall invertase
K4C3E8	10	4	519.69	Uncharacterized protein
K4CYV9	2	1	78.25	Uncharacterized protein
K4DG12	1	1	31.9	Uncharacterized protein
K4BT41	3	2	35.34	Uncharacterized protein
K4AZT0	1	1	42.03	Uncharacterized protein
K4BTP3	3	2	95.4	Uncharacterized protein
K4BVU1	10	6	328.78	Uncharacterized protein
K4C3T2	19	17	945.96	Uncharacterized protein

K4B1W9	5	3	72.21	Uncharacterized protein
K4BC61	3	3	87.81	Eukaryotic translation initiation factor 3 subunit M
K4BVU3	3	2	77.66	Uncharacterized protein
K4B9Y6	26	25	1202.15	Uncharacterized protein
K4C7W2	3	2	58.73	Uncharacterized protein
K4C4N6	4	4	250.79	Uncharacterized protein
K4C2W3	8	4	267.95	Uncharacterized protein
K4B0S9	4	2	100	Mitochondrial Rho GTPase
K4AZ32	4	3	157.37	Uncharacterized protein
K4C9T0	1	1	21.91	Tonoplast intrinsic protein 12
K4BNE0	21	5	1123.53	Uncharacterized protein
K4BJ51	5	1	286.49	Uncharacterized protein
A0A097PLA9	9	5	296.59	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (Fragment)
K4C1T2	52	11	2508.51	Clathrin heavy chain
K4BKL0	3	1	139.78	Uncharacterized protein
K4CCJ2	32	12	1333.95	Uncharacterized protein
Q6LB28	7	1	386.81	Histone H3
K4B832	14	2	694.66	Proteasome subunit alpha type
K4ASZ8	13	1	603.29	Uncharacterized protein
K4CFR7	5	5	148.88	Uncharacterized protein
K4C320	5	4	230.63	Uncharacterized protein
Q645N0	4	1	182.76	Malate dehydrogenase
K4CGL1	3	1	25.59	Uncharacterized protein
K4BVZ1	1	1	31.15	Uncharacterized protein
K4AYP7	1	1	51.93	Acyl carrier protein
K4BMP7	8	1	151.59	Uncharacterized protein
K4BPV3	1	1	64.08	Uncharacterized protein
K4DA01	1	1	113.98	Uncharacterized protein
K4BIW5	7	3	49.34	Uncharacterized protein
K4BE00	6	1	315.64	Uncharacterized protein
K4CVK9	10	9	254	Uncharacterized protein
K4D553	11	1	584.91	Histone H2B
K4CRL4	2	1	39.87	Uncharacterized protein
K4C779	15	2	610.99	Uncharacterized protein
K4AXM7	4	3	103.94	Uncharacterized protein
K4CZY4	1	1	34.02	Uncharacterized protein
K4D0F3	1	1	32.66	Uncharacterized protein
K4B960	1	1	28.28	Uncharacterized protein
K4C0D4	3	1	51.03	Uncharacterized protein
K4BVR7	3	3	116.43	Uncharacterized protein
14310	19	9	1150.37	14-3-3 protein 10
K4BDP2	17	5	898.37	Phosphorus transporter
K4CEY5	10	2	321.59	Uncharacterized protein
K4AR02	1	1	54.33	Uncharacterized protein
K4ATM2	1	1	50.23	Uncharacterized protein
K4CJ46	6	2	227.25	Uncharacterized protein
K4AVG8	1	1	26.08	Uncharacterized protein
K4AVW3	2	1	36.21	Uncharacterized protein
K4BKN1	6	6	94.89	Uncharacterized protein
K4BJP3	12	4	309.51	Protein argonaute
K4BPW1	7	4	147.35	Uncharacterized protein
Q9SPD5	23	3	688.93	Plasma membrane ATPase 2
K4B6G9	8	4	111.6	Signal recognition particle subunit SRP68
K4C755	6	4	83.16	Uncharacterized protein
K4AYQ1	2	2	33.46	Uncharacterized protein

K4CJX8	3	3	154.1	Uncharacterized protein
K4B3Q2	5	5	187.67	Uncharacterized protein
K4BJJ7	3	2	140.67	Uncharacterized protein
K4BMT5	3	2	38.27	Uncharacterized protein
K4BAY4	1	1	29.31	Uncharacterized protein
K4D3L7	7	4	323.69	Uncharacterized protein
K4D4M0	3	3	55.16	Peptidyl-prolyl cis-trans isomerase
K4AT91	6	1	574.02	Uncharacterized protein
K4CWX9	2	1	40.73	Uncharacterized protein
K4C882	12	3	655.35	Uncharacterized protein
K4B172	8	6	225.48	Uncharacterized protein
K4C998	9	1	382.55	Uncharacterized protein
K4C7I8	7	1	144.7	60S ribosomal protein L18a
K4BA70	9	5	566.8	Uncharacterized protein
OPR1	5	1	41.61	12-oxophytodienoate reductase 1
K4D9K1	11	2	64.28	Uncharacterized protein
K4CS26	4	1	56.65	Uncharacterized protein
K4BDU9	5	1	134.09	Uncharacterized protein
PROF2	5	2	215.37	Profilin-2
K4BWY8	1	1	28.77	Uncharacterized protein
K4CPE5	1	1	38.8	Uncharacterized protein
K4C258	2	2	56.55	Uncharacterized protein
K4BFE4	4	1	165.12	Uncharacterized protein
K4BMZ6	2	1	22.58	Uncharacterized protein
K4CMI6	36	10	1234.27	Uncharacterized protein
K4CYM9	4	2	76.27	Uncharacterized protein
ACCD	7	3	209.66	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic
K4BA92	8	5	216.5	Uncharacterized protein
K4BSE0	3	3	146.5	Uncharacterized protein
K4DAX6	6	2	122.5	Uncharacterized protein
K4BB06	6	5	329.87	Proteasome subunit beta type 1
K4BVD8	12	11	565.72	Proteasome subunit alpha type
K4BCK6	5	3	92.3	Uncharacterized protein
A8DUB0	4	1	93.25	Glutathione S-transferase-like protein
K4AUB9	2	2	105.58	Uncharacterized protein
K4BJ22	41	2	1875.19	Clathrin heavy chain
Q66MH9	5	2	65.02	MAPKK
K4DAT4	7	2	196.95	Uncharacterized protein
K4C0U8	3	2	63.75	Uncharacterized protein
K4CMG1	7	5	135.78	Uncharacterized protein
K4B188	8	6	198.03	Uncharacterized protein
K4D5E7	31	19	1441.43	Methylenetetrahydrofolate reductase
K4BJJ6	14	12	835.77	Uncharacterized protein
K4APN5	2	2	75.28	Uncharacterized protein
K4CGU4	2	1	113.87	Uncharacterized protein
K4B8G4	6	4	158.5	Histidinol dehydrogenase, chloroplastic
IMP3	1	1	28	Inositol monophosphatase 3
K4BFU0	16	1	1159.65	Uncharacterized protein
Q40151	31	3	1828.81	Hsc70
K4DFY4	5	2	165.71	Uncharacterized protein
K4CR83	4	2	36.69	Uncharacterized protein
K4BPJ0	28	10	975.92	Uncharacterized protein
D7S016	2	1	35.54	Glycosyltransferase
K4D3R4	7	5	200.35	Uncharacterized protein
K4AT29	8	8	176.67	Uncharacterized protein

K4C627	5	1	134.74	Uncharacterized protein
K4BVH7	21	10	668.5	Coatomer subunit alpha
K4AQY8	7	1	124.9	Uncharacterized protein
K4CL64	29	2	1715.52	Uncharacterized protein
K4CWK0	8	2	216.24	Uncharacterized protein
K4B3K6	1	1	32.01	Uncharacterized protein
D1MAF2	10	6	186.71	Exportin-1
K4BKD8	7	1	204.68	Uncharacterized protein
K4DCP0	1	1	32.62	Uncharacterized protein
K4BM95	1	1	30.13	Uncharacterized protein
K4D518	3	2	40.59	Uncharacterized protein
K4CN59	3	3	97.44	Uncharacterized protein
K4CAE2	11	6	574.09	Uncharacterized protein
K4D3Y2	5	2	214.64	Uncharacterized protein
K4DBF1	4	1	43.35	Uncharacterized protein
K4CV66	3	2	95.53	Uncharacterized protein
K4B4Y5	3	1	30.91	Uncharacterized protein
K4AZG5	2	1	34.89	Uncharacterized protein
K4BW50	13	1	694.47	Uncharacterized protein
K4CKP3	7	2	206.57	Uncharacterized protein
K4CIP0	1	1	62.53	Uncharacterized protein
K4CPS1	2	1	26.55	Uncharacterized protein
K4AYM7	9	7	341.03	Eukaryotic translation initiation factor 3 subunit B
K4BYA3	5	2	155.1	Proteasome subunit beta type
G8IIJ5	6	3	410.46	Histone H2A (Fragment)
K4CWH3	9	5	293.68	Uncharacterized protein
K4D025	2	2	63.08	Uncharacterized protein
K4DB31	5	2	386.12	Histone H2A
K4DEV1	8	1	306.78	Uncharacterized protein
K4D2A4	12	4	501.81	Uncharacterized protein
K4D2F4	4	1	58.49	Uncharacterized protein
K4BSG5	1	1	44.45	Uncharacterized protein
K4AXF7	9	1	352.45	Histone H3
K4DHY1	1	1	25.62	Uncharacterized protein
K4BWQ2	3	2	51.67	Ribulose-phosphate 3-epimerase
K4BT18	4	3	55.46	Uncharacterized protein
K4AQH2	3	2	113.69	Uncharacterized protein
K4CRB9	2	2	95.87	Uncharacterized protein
K4CBY0	4	4	137.78	Uncharacterized protein
K4DF90	10	1	173.45	Uncharacterized protein
K4B496	5	1	43.98	Uncharacterized protein
K4BP97	4	3	132.11	Proteasome subunit beta type
K4CBN0	11	6	488.22	Uncharacterized protein
K4B6V2	1	1	43.8	Uncharacterized protein
K4CXY8	4	3	154.72	Acyl-coenzyme A oxidase
K4BLV3	38	11	1470.58	Uncharacterized protein
K4D2D4	6	3	151.92	Uncharacterized protein
K4BG21	4	1	81.8	Uncharacterized protein
K4CPR6	8	8	333.55	Uncharacterized protein
K4D2I8	6	2	56.44	Uncharacterized protein
K4DBC4	42	14	2442.5	Aconitate hydratase
K4BP24	4	1	70.81	Uncharacterized protein
K4B331	3	1	22.79	Uncharacterized protein
K4CI93	15	1	709.84	40S ribosomal protein S6
K4CGB7	3	1	53.05	Citrate synthase
G8Z246	2	1	66.54	Hop-interacting protein THI002

K4B433	15	13	251.95	Uncharacterized protein
K4C9L4	32	2	1543.6	Uncharacterized protein
K4AYC6	4	3	48.4	Uncharacterized protein
K4CHD8	3	2	41.43	Uncharacterized protein
K4D2M9	8	5	224.6	Eukaryotic translation initiation factor 3 subunit E
K4D616	14	6	490.21	Uncharacterized protein
K4B6T2	2	1	29.43	Peroxidase
K4BBU9	4	1	112.5	Uncharacterized protein
K4C6Q6	6	2	407.6	Tonoplast intrinsic protein 23
K4DHC7	12	2	451.93	v-type proton ATPase subunit a
K4C3B9	10	1	249.01	40S ribosomal protein S4
K4BNL9	4	3	168.41	Uncharacterized protein
K4BSC6	5	1	36.03	Uncharacterized protein
K4BBN2	7	3	146.42	Uncharacterized protein
K4CAJ9	2	1	136.22	Uncharacterized protein
C6K2L0	16	4	613.09	GDP-mannose 3',5'-epimerase
K4D318	6	6	156.5	Uncharacterized protein
H6WYS2	10	5	301.69	Sulfite reductase
K4C3K6	7	1	300.76	Uncharacterized protein
O65917	13	8	490.06	Dehydroquinase dehydratase/shikimate:NADP oxidoreductase
K4C7N4	8	2	252.8	Uncharacterized protein
K4B9P3	24	2	1853.72	Pectinesterase
K4C8M5	7	1	197.82	Uncharacterized protein
K4CJ79	4	2	46.82	Uncharacterized protein
K4CV83	3	1	59.67	Uncharacterized protein
K4BDD3	1	1	37.8	Uncharacterized protein
K4CHY4	12	6	597.3	Phosphoglycerate kinase
K4DI33	1	1	25.69	Uncharacterized protein
K4B1A3	7	1	276.47	Importin subunit alpha
K4CHI8	3	1	63.22	Uncharacterized protein
K4AXN9	3	1	57.22	Uncharacterized protein
K4B307	9	2	632.39	Uncharacterized protein
K4B3M5	21	20	817.26	V-type proton ATPase subunit a
K4BV98	2	1	36.14	Uncharacterized protein
K4C2H3	3	2	37.53	Uncharacterized protein
K4DAC8	31	1	1407.36	Uncharacterized protein
K4D5M2	12	1	83.07	Uncharacterized protein
K4BCY6	2	2	86.58	Uncharacterized protein
K4C128	1	1	40.51	Small nuclear ribonucleoprotein-associated protein
K4CJB4	17	4	699.8	Uncharacterized protein
B5M9E4	6	5	294.38	Beta-glucosidase 01
K4D9Z8	4	3	147.17	Uncharacterized protein
K4C455	19	9	1117.22	Uncharacterized protein
K4CND7	6	2	117.61	Uncharacterized protein
V5YNW6	8	6	451.45	Plasmamembrane intrinsic protein 21
K4DA24	5	5	106.03	Uncharacterized protein
K4B2J4	21	2	951.61	Uncharacterized protein
K4C949	6	3	312.72	60S ribosomal protein L27
K4C745	13	9	439.12	Uncharacterized protein
K4C203	5	1	225.28	Uncharacterized protein
K4BIM9	4	2	138.01	Uncharacterized protein
K4C247	11	1	426.45	Uncharacterized protein
K4BZW2	4	2	60.31	Uncharacterized protein
K4BUD9	30	1	2377.47	Uncharacterized protein
K4CB31	7	5	196.77	Uncharacterized protein

K4C2F3	17	10	749.57	Uncharacterized protein
K4B3H5	3	1	43.83	Uncharacterized protein
K4D5Q6	3	1	71.11	Uncharacterized protein
K4BLT8	4	2	92.24	Uncharacterized protein
K4AT35	5	5	195.93	Uncharacterized protein
K4BBN6	5	2	35.89	Alpha-mannosidase
K4CNF1	13	1	865.42	Isocitrate dehydrogenase [NAD] subunit, mitochondrial
K4CAR4	3	1	94.35	Histone H2A
K4BV04	9	7	297.46	Uncharacterized protein
K4C2S4	2	1	24.91	Uncharacterized protein
K4B264	7	5	131.04	Uncharacterized protein
K4C7L1	3	1	65.51	Uncharacterized protein
K4BI34	4	2	148.43	Uncharacterized protein
K4CMQ7	3	3	78.76	Uncharacterized protein
K4C5P4	2	2	82.42	Uncharacterized protein
K4BM06	1	1	37.55	Uncharacterized protein
K4D2W1	13	8	297.37	Uncharacterized protein
K4AYT8	9	5	752.27	Nucleoside diphosphate kinase
K4BEF0	3	1	42.44	Uncharacterized protein
K4CXI7	4	1	218.91	Histone H2A
K4C3D5	2	1	55.46	Uncharacterized protein
Q66YT8	6	3	63.7	DWARF1/DIMINUTO
K4B101	12	2	449.11	Uncharacterized protein
K4D3B5	11	8	422.62	Uncharacterized protein
K4CIV5	12	2	468.81	Uncharacterized protein
K4BI36	4	3	113.95	Uncharacterized protein
K4BYG6	30	4	2248.56	Glyceraldehyde-3-phosphate dehydrogenase
Q8SA58	4	3	87.37	Putative uncoupling protein
K4CB99	1	1	61.33	Uncharacterized protein
K4CI40	7	4	147.34	Uncharacterized protein
K4B3E9	1	1	52.85	Uncharacterized protein
ATP9	1	1	70.81	ATP synthase subunit 9, mitochondrial
K4DAG1	3	3	101.2	Uncharacterized protein
Q8H0Q2	3	1	61.02	Hexokinase
K4BXW2	2	1	51.36	Uncharacterized protein
K4BJE6	15	8	385.36	Alanine--tRNA ligase
K4AZN6	3	1	80.8	Mitogen-activated protein kinase
K4DCV8	3	2	44.26	Uncharacterized protein
K4B139	6	1	63.43	Uncharacterized protein
K4AX33	3	1	106.2	Peroxidase
K4D740	6	5	187.74	Uncharacterized protein
K4BJS3	3	3	81.62	Uncharacterized protein
K4D304	6	1	566.04	Uncharacterized protein
K4BWI5	4	2	133.01	Serine/threonine-protein phosphatase
K4CXN6	4	1	61.57	Uncharacterized protein
K4BM13	11	7	291.04	Uncharacterized protein
K4BK69	8	2	299.22	Elongation factor Tu
AROC1	13	2	459.22	Chorismate synthase 1, chloroplastic
K4DDY5	2	1	41.32	Uncharacterized protein
K4BMY9	7	1	214.78	Uncharacterized protein
K4B047	6	3	291.85	Uncharacterized protein
K4BPD2	5	1	84.17	Uncharacterized protein
K4B892	1	1	24.68	Uncharacterized protein
K4BG34	2	1	87.7	Uncharacterized protein
K4BM53	24	5	1393.93	Uncharacterized protein
K4CXH1	6	3	74.15	Uncharacterized protein

K4C858	1	1	30.09	Uncharacterized protein
K4CV84	2	1	62.24	Uncharacterized protein
K4BD39	5	1	173.63	Uncharacterized protein
K4BM85	12	3	487.64	Uncharacterized protein
K4D8V2	2	1	66.71	Uncharacterized protein
K4D5D1	5	1	65.36	Uncharacterized protein
K4C1B2	3	2	76.66	Uncharacterized protein
K4BJ57	3	3	170.5	Uncharacterized protein
K4BYL6	6	2	216.45	Uncharacterized protein
K4CMT6	9	7	300.15	Uncharacterized protein
K4CPC9	12	10	406.02	Uncharacterized protein
K4B1H9	5	2	36.29	Uncharacterized protein
K4BBJ0	2	1	29.54	Uncharacterized protein
K4D3H4	2	2	53.75	Uncharacterized protein
K4B1B7	13	1	700.85	Uncharacterized protein
K4BWA5	10	1	86.05	Uncharacterized protein
K4C6K7	5	2	144.35	Uncharacterized protein
K4DHK7	11	1	409.49	Uncharacterized protein
K4CSL7	4	1	72.47	Uncharacterized protein
K4CZ51	3	1	33.76	Uncharacterized protein
K4C245	9	2	173.86	Uncharacterized protein
K4B8Y5	5	1	135.17	Uncharacterized protein
G1EN31	1	1	25.57	LysM receptor-like kinase variant SlBti9-1a
K4ARN4	3	1	38.83	Uncharacterized protein
K4D5S8	5	1	98.69	Uncharacterized protein
K4D378	17	2	396.49	Coatomer subunit beta
K4BMS2	4	1	141.94	Uncharacterized protein
K4B893	3	2	95.67	Uncharacterized protein
K4CYN1	7	5	113.81	Uncharacterized protein
K4AXH0	5	1	73.62	Uncharacterized protein
K4B854	3	1	36.19	Uncharacterized protein
K4CHX2	1	1	39.51	Uncharacterized protein
K4B1S1	19	8	495.57	Uncharacterized protein
K4AY75	9	1	418.48	Histone H3
K4BME7	4	3	80.83	Uncharacterized protein
K4AXI7	3	2	214.11	Uncharacterized protein
K4BAZ5	15	2	1053.17	Peroxidase
K4BJE2	3	3	76.41	Uncharacterized protein
K4BDZ0	8	1	63.36	Uncharacterized protein
K4CIF3	2	2	73.94	Uncharacterized protein
K4BMT2	5	3	105.32	Uncharacterized protein
K4B7Q8	5	2	99.58	Protein argonaute
K4D930	25	10	1481.5	Uncharacterized protein
K4CCK0	4	2	75.95	Uncharacterized protein
K4BJC8	2	2	63.06	Uncharacterized protein
K4CQ71	5	1	61.22	Uncharacterized protein
K4CLA3	12	11	264.43	Uncharacterized protein
Q152U8	3	1	55.85	Multiprotein bridging factor 1b
K4D7W0	5	3	144.78	Cytochrome b-c1 complex subunit Rieske, mitochondrial
K4CWK1	9	3	249.09	Uncharacterized protein
B1Q3F0	6	1	193.36	Glutamate decarboxylase
K4CHD1	4	2	158.36	Uncharacterized protein
K4DF88	13	5	275.83	Uncharacterized protein
Q40159	6	3	143.55	Late embryogenesis (Lea)-like protein
K4B6D9	5	1	303.18	Peroxidase

K4CGI2	8	7	219.47	Uncharacterized protein
K4CLC9	8	2	59.5	Serine hydroxymethyltransferase
METK1	13	2	840.93	S-adenosylmethionine synthase 1
A0A097PJ88	8	2	44	Structural maintenance of chromosomes protein 2 (Fragment)
K4CGA2	3	1	27.43	Uncharacterized protein
K4AZL9	3	3	41.78	Cysteine synthase
K4B276	5	5	169.55	Uncharacterized protein
K4DFV4	4	4	148.61	Glutathione peroxidase
K4CN87	1	1	32.31	Uncharacterized protein
K4D2D7	8	2	235.36	Uncharacterized protein
K4CMQ6	5	3	76.44	Uncharacterized protein
K4CHJ6	11	3	537.89	40S ribosomal protein S8
K4BJK7	16	1	893.52	40S ribosomal protein S3a
K4AXL3	4	2	101.59	Uncharacterized protein
K4BIZ6	2	1	42.79	Uncharacterized protein
G8Z278	5	3	99.81	Hop-interacting protein THI111
K4CDF4	16	5	379.23	Coatomer subunit alpha
K4CPC6	4	1	29.36	Uncharacterized protein
K4BAY1	1	1	23.95	Uncharacterized protein
K4C311	3	1	32.03	Uncharacterized protein
K4CE04	17	2	902.51	Uncharacterized protein
K4D4H5	4	1	41.61	Uncharacterized protein
K4B1D4	10	6	477.34	Uncharacterized protein
K4CHK7	1	1	72.28	Uncharacterized protein
K4B3E8	3	2	35.57	Uncharacterized protein
K4CL50	14	8	213.23	Uncharacterized protein
K4BDK7	5	4	182.29	Uncharacterized protein
K4AQH0	5	5	73.4	Uncharacterized protein
K4C6Y4	2	1	75.55	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B
K4CXQ6	6	1	146.62	Ubc13-type ubiquitin-conjugating enzyme 2
Q76LU4	4	3	78.96	Alpha-L-arabinofuranosidase
K4CQR5	8	2	268.85	Uncharacterized protein
K4BDD0	3	2	57.24	Uncharacterized protein
K4BRP6	1	1	45.85	Uncharacterized protein
K4AW29	2	1	27.97	Uncharacterized protein
K4D4A7	35	1	2083.63	Uncharacterized protein
K4CV89	7	2	142.61	Uncharacterized protein
K4BA10	4	3	287.06	Uncharacterized protein
CALM	5	1	425.37	Calmodulin
K4B7U1	1	1	68.42	Uncharacterized protein
K4DA61	3	3	92.51	Uncharacterized protein
K4C219	1	1	96.06	Uncharacterized protein
K4D131	1	1	41.98	Uncharacterized protein
CLPP	1	1	72.63	ATP-dependent Clp protease proteolytic subunit
K4CVM9	12	2	457.23	40S ribosomal protein S3a
K4B9T4	14	12	598.79	Lactoylglutathione lyase
K4DH95	16	2	554.9	Uncharacterized protein
E3VWN6	7	1	125.38	1-aminocyclopropane-1-carboxylic acid oxidase
K4CRJ0	2	1	34.04	Uncharacterized protein
K4B6W4	12	6	252.13	Uncharacterized protein
K4D300	9	9	294.53	Proteasome subunit alpha type
K4D2U9	7	1	149.16	Uncharacterized protein
K4BLM8	3	1	28.66	Uncharacterized protein
K4BNL0	19	13	607.22	Uncharacterized protein

K4D5B1	3	1	148.52	Uncharacterized protein
K4C5Y9	6	3	251.89	Uncharacterized protein
K4BKB2	21	3	912.9	Uncharacterized protein
K4BVD6	8	6	311.67	Uncharacterized protein
K4CG68	5	1	147.34	Uncharacterized protein
K4C3A3	12	2	549.15	Uncharacterized protein
K4APY0	4	3	42.7	Eukaryotic translation initiation factor 6
K4CP37	3	3	104.36	Uncharacterized protein
K4B8C0	2	1	42.74	Uncharacterized protein
K4CCD7	8	8	346.12	Proteasome subunit beta type
K4CMC4	3	2	29.97	Uncharacterized protein
K4BF61	3	1	54.09	Uncharacterized protein
K4C875	9	5	192.15	Uncharacterized protein
K4B6K0	4	2	166.63	Uncharacterized protein
K4AU58	8	2	275.82	Uncharacterized protein
K4BJB9	5	1	42.73	Uncharacterized protein
K4BMF8	3	2	57.19	Uncharacterized protein
K4AT92	23	11	596.31	AGO4A
K4BUK4	3	2	42.91	Uncharacterized protein
A8Y6N6	7	1	139.11	ATP synthase subunit beta (Fragment)
K4CLN4	3	2	24.63	Uncharacterized protein
K4B816	18	4	742.86	40S ribosomal protein S4
A9LRT6	4	1	147.38	3-hydroxy-3-methylglutaryl coenzyme A synthase
K4BV02	7	5	413.12	Uncharacterized protein
K4B9B8	2	1	45.66	Uncharacterized protein
K4BQC1	6	1	59.05	Uncharacterized protein
K4C807	14	13	632.3	Uncharacterized protein
K4C8W9	16	1	877.38	40S ribosomal protein S3a
K4D2R0	3	2	83.74	Uncharacterized protein
K4AWS0	5	3	91.98	Uncharacterized protein
PSBD	4	4	48.51	Photosystem II D2 protein
K4B0H4	4	1	193.93	40S ribosomal protein S24
K4BV01	2	2	16.97	Uncharacterized protein
RBS2A	4	1	88.47	Ribulose biphosphate carboxylase small chain 2A, chloroplastic
K4B3W9	2	2	72.56	Uncharacterized protein
Q3SC85	12	2	411.61	60S ribosomal protein L10
K4D9A2	5	3	61.33	Uncharacterized protein
K4D348	6	2	114	Ubiquitin carboxyl-terminal hydrolase
K4D7X4	12	7	870.99	Uncharacterized protein
K4BB89	5	3	45.83	Uncharacterized protein
K4C839	5	1	55.68	Uncharacterized protein
K4B0R5	2	1	35.49	Uncharacterized protein
E7EC27	7	5	329.8	Aquaporin
K4ATQ2	16	9	507.44	Uncharacterized protein
K4C7J6	7	1	90.9	Uncharacterized protein
K4DEW2	4	1	39.95	Uncharacterized protein
K4B015	1	1	100.39	Uncharacterized protein
K4B5K9	4	1	38.57	Uncharacterized protein
K4BB18	4	2	125.45	Uncharacterized protein
K4CSA9	11	8	282.14	Uncharacterized protein
K4CNH9	13	1	356.2	Uncharacterized protein
DHQS	5	4	203.27	3-dehydroquinate synthase, chloroplastic
K4CU73	9	8	459.4	Uncharacterized protein
K4AZL0	7	2	456.83	Plasmamembrane intrinsic protein 12
K4DD89	19	5	732.64	Uncharacterized protein

K4DDG7	3	1	27.98	Uncharacterized protein
K4B0V5	6	2	55.96	Lipoxygenase
K4BNK4	5	2	121.39	Uncharacterized protein
K4DBZ9	2	2	51.4	Uncharacterized protein
K4C6I9	2	2	50.88	Uncharacterized protein
K4C844	3	1	57.67	Uncharacterized protein
K4CTF8	4	2	110.21	Peptidyl-prolyl cis-trans isomerase
K4BEI8	5	1	126.9	Uncharacterized protein
COLIR4	5	2	104.78	Sulfurtransferase
K4B8W8	6	3	143.07	Uncharacterized protein
K4D6I9	8	5	268.77	Uncharacterized protein
K4BG13	2	1	36.9	Uncharacterized protein
K4B0H5	1	1	35.26	Uncharacterized protein
K4CG46	30	1	917.12	Uncharacterized protein
H2BJQ1	5	1	156.72	Putative steroid 5beta-reductase
K4AV57	3	2	79.98	Uncharacterized protein
K4DAP8	4	1	44.72	Uncharacterized protein
K4CTF7	6	2	178.52	Uncharacterized protein
K4BYB6	5	1	105.95	Uncharacterized protein
K4C8V0	9	3	245.94	Protein argonaute
G8Z288	3	2	102.6	Hop-interacting protein THI141
K4BAN8	6	2	51.29	Alpha-mannosidase
K4DHM2	21	2	1143.04	Serine hydroxymethyltransferase
K4CM61	1	1	45.38	Uncharacterized protein
K4C9I3	7	4	198.87	Uncharacterized protein
K4C9L0	4	1	90.97	Uncharacterized protein
K4BY91	4	2	44.52	Uncharacterized protein
K4DCH1	9	2	490.52	Ketol-acid reductoisomerase
K4B4N0	8	4	117.29	Uncharacterized protein
K4BZA6	6	5	174.81	NADH-cytochrome b5 reductase
K4DI40	8	2	180.74	Uncharacterized protein
K4DHC5	1	1	29.28	Uncharacterized protein
K4BT62	7	1	395.28	Uncharacterized protein
K4BDI6	5	3	220.11	Uncharacterized protein
K4BIB1	7	1	47.54	Uncharacterized protein
K4CA81	5	3	117.77	Uncharacterized protein
K4C273	5	2	204.81	Uncharacterized protein
Q8H272	7	1	195.37	Metacaspase 1 (Fragment)
K4AST1	15	2	374.3	Coatomer subunit beta
K4CM42	5	1	100.73	Ribosomal protein L37
K4BML9	5	1	72.1	Uncharacterized protein
K7T8S0	8	5	144.41	Eukaryotic translation initiation factor iso4G
K4DGX0	5	2	89.56	Uncharacterized protein
K4B0V7	6	1	59.77	Lipoxygenase
LGUL	6	4	134.24	Lactoylglutathione lyase
K4BG20	4	1	169.21	Uncharacterized protein
K4DAZ4	7	6	223.19	Uncharacterized protein
K4DCN6	10	1	572.93	Histone H2B
K4AYG4	5	1	77.19	Uncharacterized protein
K4BWK1	6	6	187.14	Uncharacterized protein
K4CAM8	2	1	72.24	Uncharacterized protein
K4DH92	3	3	40.21	Uncharacterized protein
K4CA83	2	1	70.46	Laccase
K4BIG0	4	1	40.1	Uncharacterized protein
K4C9E8	11	3	487.65	Ribosomal protein
K4B427	6	1	152.08	Uncharacterized protein

K4DED3	3	2	79.43	Uncharacterized protein
K4CAU9	6	4	82.76	Uncharacterized protein
K4CQA5	3	1	30.41	Uncharacterized protein
K4BL51	3	1	63.9	Uncharacterized protein
K4DFR4	5	2	209.41	Uncharacterized protein
K4BS59	2	1	134.72	Uncharacterized protein
K4C0M5	4	4	101.49	Uncharacterized protein
K4CHP7	4	2	48.06	Uncharacterized protein
K4CR69	3	2	66.33	Arginine biosynthesis bifunctional protein ArgJ, chloroplastic
K4BLQ1	5	5	68.9	Uncharacterized protein
K4BG62	6	3	66.66	Uncharacterized protein

APPENDIX F Proteins detected in less tolerant genotype TTO in different Cd exposure periods in roots.

Accession	Peptide count	Peptides used for quantitation	Confidence score	DAP	Description
K4CC21	5	1	244.32	Yes	Uncharacterized protein
K4D3M6	13	11	700.03	Yes	Uncharacterized protein
K4CGI0	4	1	56.13		Uncharacterized protein
K4AT60	8	6	326.49	Yes	Uncharacterized protein
K4C131	5	3	195.73	Yes	Uncharacterized protein
K4CNZ0	19	5	1026.16	Yes	Uncharacterized protein
K4CRI1	3	2	108.9	Yes	Uncharacterized protein
K4CNF0	7	7	583.66	Yes	Uncharacterized protein
K4CUC1	8	6	292.85	Yes	Uncharacterized protein
K4D203	11	7	352.67	Yes	Lysine--tRNA ligase
O48625	6	5	203.45	Yes	Lemir
Q38JE1	6	5	119.03		Temperature-induced lipocalin
K4CRH8	4	3	167.47	Yes	Uncharacterized protein
Q9LWA3	18	13	992.54	Yes	Subtilisin-like protease
K4CWC5	12	8	760.28	Yes	PR10 protein
K4D4Y1	4	4	371.05	Yes	Uncharacterized protein
Q6A1K7	9	8	464.95		1-aminocyclopropane-1-carboxylate oxidase
K4B7W2	2	2	82.54		Uncharacterized protein
K4CX40	10	9	296.11	Yes	Uncharacterized protein
K4BKZ7	6	3	138.89		Uncharacterized protein
K4CF67	6	3	123.66	Yes	Uncharacterized protein
K4D4V2	2	1	168.7	Yes	Uncharacterized protein
K4D1H1	12	7	1014.07	Yes	Uncharacterized protein
K4CWL0	15	10	657.6	Yes	Uncharacterized protein
K4C1S8	1	1	56.24	Yes	Ferritin
K4CVR2	7	2	193.97		Uncharacterized protein
K4B2X0	10	6	316.84	Yes	Uncharacterized protein
K4BRF6	3	3	83.6	Yes	Uncharacterized protein
Q0H8U4	7	3	417.07		Pathogenesis-related protein
Q9AWA9	14	10	821.47		Non-symbiotic hemoglobin class 1
K4D5T8	16	10	761.12		Uncharacterized protein
K4BM69	10	10	358.52		Uncharacterized protein
Q4W8D2	2	1	96.92		2-oxoglutarate-dependent dioxygenase
K4C4Z6	24	2	1394.79		Uncharacterized protein
K4B030	4	2	166.52	Yes	Uncharacterized protein
K4ATR9	7	3	241.78	Yes	Uncharacterized protein
K4BBL4	7	5	162.01	Yes	Uncharacterized protein
L7Q568	9	6	286.32	Yes	Glycine rich RNA binding protein 1a
K4B3Y5	2	2	148.4	Yes	Uncharacterized protein

K4CNZ7	8	5	159.73	Yes	Uncharacterized protein
K4C376	21	17	1058.36		Protein disulfide-isomerase
P43282	27	12	1206.54	Yes	S-adenosylmethionine synthase 3
K4B2X5	17	13	690.51		Uncharacterized protein
K4CM55	3	3	111.83		Uncharacterized protein
K4C8H3	15	11	453.42	Yes	Uncharacterized protein
K4CQW8	28	23	1918.66	Yes	Uncharacterized protein
K4B553	23	19	840.95		Uncharacterized protein
B1Q3F1	22	13	875.24	Yes	Glutamate decarboxylase
K4C7W1	6	4	227.94		Uncharacterized protein
K4BV08	1	1	41.7		Patatin
K4CC17	4	2	93.62	Yes	Uncharacterized protein
AOA097PJV1	5	1	45.08	Yes	Minichromosome maintenance 5 protein (Fragment)
B1Q3F8	12	8	356.42		Succinic semialdehyde dehydrogenase
K4D1W6	20	12	792.86	Yes	Peroxidase
K4B7M2	15	14	683.5	Yes	Uncharacterized protein
K4CFM5	19	11	1169.61		Ketol-acid reductoisomerase
K4BUC5	20	11	821.57		Uncharacterized protein
K4CQF3	3	2	75.79		Carboxypeptidase
K4BJ73	9	7	847.62	Yes	Uncharacterized protein
K4CC42	7	7	441.48		Uncharacterized protein
K4CC70	2	2	271.02		Uncharacterized protein
K4AY19	4	3	141.48	Yes	Uncharacterized protein
K4CJW3	19	8	643.32	Yes	Lipoxygenase
K4CQN4	3	1	103.07	Yes	Uncharacterized protein
P12670	7	5	743.98		Protein NP24
O80432	4	4	205.47		Mitochondrial small heat shock protein
K4B277	14	12	1240.26	Yes	Peroxidase
K4BT79	6	3	160.07	Yes	Uncharacterized protein
K4BQ77	3	1	24.27		Uncharacterized protein
K4C2U7	5	4	170.71	Yes	Uncharacterized protein
K4CVH1	10	5	279.23	Yes	Amine oxidase
K4D7V9	16	7	356.17	Yes	Uncharacterized protein
K4DG37	10	5	177.22		Uncharacterized protein
K4BNL2	10	6	157.66		Uncharacterized protein
K4BBF4	10	6	146.89	Yes	Uncharacterized protein
K4C145	2	2	106.17		Uncharacterized protein
K4BSL7	7	6	189.39	Yes	Uncharacterized protein
K4CW30	2	1	58.34	Yes	Uncharacterized protein
K4CVC0	7	1	309.87	Yes	Ribosomal protein L19
K4D1H0	16	8	1697	Yes	Uncharacterized protein
K4CNZ3	22	12	1620.85	Yes	Uncharacterized protein
K4BIC0	30	19	1047.39	Yes	Uncharacterized protein
K4C144	39	21	2433.81	Yes	Malic enzyme
K4B9B4	2	1	30.45		Uncharacterized protein

Q7Y0S1	2	1	97.28	Yes	Chitinase
E0XN34	14	12	412.62		Alpha-mannosidase
K4BKR7	16	8	812.94		Uncharacterized protein
K4BW77	3	1	83.25		Uncharacterized protein
K4BP02	10	8	427.35		Ribosomal protein L15
K4B031	4	2	162.54	Yes	Uncharacterized protein
Q4W5U7	14	12	741.37	Yes	Calnexin-like protein
K4C2F8	8	2	320.93		Uncharacterized protein
K4BAN9	4	3	296.71	Yes	Uncharacterized protein
K4CRI2	1	1	37.68	Yes	Uncharacterized protein
K4CU14	6	3	228.55		Uncharacterized protein
K4BK64	4	3	46.75		Uncharacterized protein
K4CVS3	4	4	69.51	Yes	Pyruvate kinase
K4BCC3	10	10	208.72	Yes	Uncharacterized protein
K4DBV8	2	2	77.98		Uncharacterized protein
K4CUU6	17	12	719.88	Yes	Uncharacterized protein
K4CN56	3	2	97.24	Yes	Uncharacterized protein
K4BG34	2	2	37.47		Uncharacterized protein
K4B778	10	6	500.1	Yes	Uncharacterized protein
B2LW68	10	6	760.48		PR1 protein
K4C310	6	5	272.51		Uncharacterized protein
K4CV78	9	8	377.82		Uncharacterized protein
K4AR66	14	8	714.64	Yes	Peroxidase
K4CEY6	7	5	215.43	Yes	Uncharacterized protein
O49877	12	10	824.04		CYP1
K4BN73	2	1	39.93	Yes	Uncharacterized protein
K4CMV0	8	5	396.26	Yes	Peroxidase
K4B8E6	6	6	212.75		Uncharacterized protein
K4C8F8	4	1	109.07		Uncharacterized protein
K4CVE4	8	7	170.63	Yes	Uncharacterized protein
K4CWR9	4	3	152.33		Uncharacterized protein
K4DAD5	24	15	1174.42		Uncharacterized protein
K4AS65	19	15	1265.79		Uncharacterized protein
K4BTY6	21	14	791.14		Uncharacterized protein
K4B808	10	1	55.68		Uncharacterized protein
K4DHE9	10	7	392.51		Uncharacterized protein
K4BK90	7	5	202.78		Uncharacterized protein
K4D3B7	4	1	85.21		Uncharacterized protein
K4CK47	16	8	507.57		Aspartate aminotransferase
K4B9Y9	5	3	224.91		1-aminocyclopropane-1-carboxylate oxidase 4
K4BH22	3	3	269.83		Uncharacterized protein
K4B383	2	2	28.33	Yes	Uncharacterized protein
K4B962	2	2	75.6		Uncharacterized protein
K4BWS2	5	2	53.18	Yes	Uncharacterized protein
K4DAX6	5	3	72.56		Uncharacterized protein

K4BVH5	4	4	103		Uncharacterized protein
K4CWW8	7	2	137.14		Uncharacterized protein
K4DFH8	5	4	126.76	Yes	Uncharacterized protein
K4CXY9	14	11	504.24		Uncharacterized protein
K4DCT6	1	1	28.56		Uncharacterized protein
K4CGH7	3	1	90.45	Yes	Uncharacterized protein
K4C0T4	15	7	934.87	Yes	Peroxidase
K4C3F2	2	1	36.85	Yes	Uncharacterized protein
K4B445	3	1	95.64		Uncharacterized protein
K4BNL0	24	14	858.96		Uncharacterized protein
K4CAX7	1	1	30.92	Yes	Uncharacterized protein
K4C6X6	3	2	135.68	Yes	Uncharacterized protein
K4AZ04	3	1	62.87		Uncharacterized protein
K4CP64	8	4	698.01		Uncharacterized protein
K4DF56	5	2	387.7		40S ribosomal protein S12
K4CH96	9	1	557.3		Uncharacterized protein
K4CP14	10	4	447.44		Uncharacterized protein
K4D1F8	3	1	49.89		Uncharacterized protein
Q40143	5	4	209.41	Yes	Cysteine proteinase 3
K4CN78	4	4	64.34	Yes	Pyruvate kinase
K4DGU7	3	1	72.27	Yes	Uncharacterized protein
K4BVD6	8	7	356.4	Yes	Uncharacterized protein
P32045	2	2	75.18		Pathogenesis-related protein P2
K4BI68	29	6	1453.79	Yes	Uncharacterized protein
K4B7W7	10	2	362.25		Uncharacterized protein
K4CYL4	6	4	131.81	Yes	Cysteine synthase
K4CQI3	13	6	536.2		Uncharacterized protein
K4BNC2	16	8	723.36	Yes	6-phosphogluconate dehydrogenase, decarboxylating
K4B9P2	32	7	2232.47		Pectinesterase
K4BRN5	4	3	98.12	Yes	Uncharacterized protein
K4BNT2	6	5	508.42		Uncharacterized protein
K4B978	5	4	197.99		Uncharacterized protein
K4CJ21	15	12	352.96	Yes	Malic enzyme
K4CQB7	5	2	343.43		Uncharacterized protein
K4C3V1	8	2	319.89	Yes	Ribosomal protein L19
K4B1J4	9	8	276.47		Uncharacterized protein
K4D1V6	1	1	44.86		Uncharacterized protein
K4CIH4	6	5	347.73		Patatin
K4CUX6	17	13	721.18	Yes	Elongation factor Tu
Q9S898	1	1	76.55		23 kDa heat-induced protein (Fragment)
K4D2N9	4	1	63.51		Uncharacterized protein
K4CA24	36	3	1981.09		Uncharacterized protein
K4B2X1	11	7	246.95	Yes	Uncharacterized protein
P28032	36	27	2546.95		Alcohol dehydrogenase 2
K4D0P3	19	13	681.86		Uncharacterized protein

K4B3Y8	7	5	150.48		Uncharacterized protein
K4D7Y5	3	2	52.85	Yes	Uncharacterized protein
K4BPB5	2	2	106.48		Uncharacterized protein
G8XSL1	7	6	74.52	Yes	GSH1
Q42896	26	19	1765.86		Fructokinase-2
Q38MV0	39	4	2283.35		Beta-tubulin
Q9FT22	13	4	330.83	Yes	Putative glutathione S-transferase T2
K4AXP6	11	7	627.27		Uncharacterized protein
K4AXC0	8	8	368.96	Yes	Citrate synthase
K4CW40	20	14	1644.54		Malate dehydrogenase
K4CXS7	20	10	674.35		Uncharacterized protein
P15004	3	1	108.21		Suberization-associated anionic peroxidase 2
K4BDN9	3	3	144.67	Yes	Translocon-associated protein subunit beta
K4C869	1	1	52.42		Uncharacterized protein
K4BMW9	1	1	26.31		Uncharacterized protein
K4CBX5	17	7	545.01	Yes	Purple acid phosphatase
Q5NE18	19	17	1048.17		Formate dehydrogenase
K4BA78	1	1	34.11		Uncharacterized protein
K4CDF4	13	4	339.71		Coatomer subunit alpha
K4BAP8	3	2	34.13	Yes	Uncharacterized protein
K4B2Z8	4	3	110.47		Uncharacterized protein
K4CWC6	10	6	391.07		Uncharacterized protein
C6K2K9	15	3	539.82		GDP-mannose 3',5'-epimerase
K4AWA0	7	5	356.44	Yes	Uncharacterized protein
K4BEL1	26	3	1063.31		Uncharacterized protein
K4B496	8	3	41.68		Uncharacterized protein
K4C8C6	2	1	24.86		Uncharacterized protein
K4B0P2	2	2	41.58		Uncharacterized protein
K4C891	11	7	350.33	Yes	Uncharacterized protein
K4B137	2	2	54.29		Uncharacterized protein
K4BMM7	5	5	97.73		Ribosomal protein L37
K4AYN8	2	2	61.43	Yes	UMP-CMP kinase
K4C2E1	22	7	971.34		Uncharacterized protein
K4CGY7	1	1	69.2	Yes	Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1
K4CEV0	5	5	113.86	Yes	Uncharacterized protein
O64439	4	3	343.19	Yes	Germin-like protein
K4CR90	47	10	3054.44		Uncharacterized protein
K4C5F4	3	3	281.26		Superoxide dismutase
K4AWF0	15	10	624.42		Importin subunit alpha
K4B860	2	1	43.17	Yes	Uncharacterized protein
K4DBQ4	11	9	129.26	Yes	Uncharacterized protein
K4AYA3	9	7	535.08	Yes	Uncharacterized protein
K4AXS2	11	6	435.61	Yes	Glutamine synthetase
K4CRQ5	2	2	81.64		Uncharacterized protein

K4BBN1	11	8	419.23		Uncharacterized protein
K4CC22	5	1	194.57	Yes	Uncharacterized protein
K4BMN4	9	1	170.81		Uncharacterized protein
K4D1X7	3	2	79.9		Uncharacterized protein
K4C8R4	18	7	1243.04		Glyceraldehyde-3-phosphate dehydrogenase
K4BHZ4	9	7	286.71		Uncharacterized protein
K4C730	4	1	43.78		Uncharacterized protein
K4DBP0	9	7	293.06	Yes	Uncharacterized protein
K4BLV4	5	3	70.89		Uncharacterized protein
K4DBB7	7	3	255.26	Yes	Uncharacterized protein
K4AQ32	16	13	615.79	Yes	Uncharacterized protein
K4B1G7	3	3	152.65	Yes	Uncharacterized protein
K4BGT9	3	1	172.23	Yes	Uncharacterized protein
K4B1M0	9	6	162.53	Yes	Uncharacterized protein
K4B124	6	4	398.01		Uncharacterized protein
K4AS30	4	1	107.45		Phenylalanine ammonia-lyase
K4D297	25	16	1219.47		Glutamate dehydrogenase
K4D3I3	20	4	1014.4		S-adenosylmethionine synthase
K4ASJ4	13	12	347.67		Uncharacterized protein
K4BLN8	4	1	48.71	Yes	Uncharacterized protein
K4CWC4	14	10	1143.32		PR10 protein
K4CMI7	10	7	348.82		Uncharacterized protein
K4B171	5	4	291.46		Uncharacterized protein
K4CVI4	22	17	1401.71		Cysteine synthase
K4B504	9	4	242.73	Yes	Uncharacterized protein
K4D1Z3	12	9	792.06		Uncharacterized protein
K4AYE5	2	1	23.95		Uncharacterized protein
K4B8W9	6	2	93.69		Uncharacterized protein
K4C2D7	12	3	382.81	Yes	Uncharacterized protein
K4AVE6	4	2	54.56		Pyruvate kinase
K4BX93	5	3	109.18		Uncharacterized protein
K4CID1	6	4	140.06	Yes	Uncharacterized protein
K4BF68	3	2	106.12	Yes	Uncharacterized protein
K4CAN4	18	12	902.12	Yes	Succinyl-CoA ligase subunit beta
K4DBV1	19	15	1300.06		Uncharacterized protein
K4B9G0	3	2	48.7	Yes	Uncharacterized protein
K4D7N0	1	1	87.64		Uncharacterized protein
K4BLN5	8	1	356.04		Uncharacterized protein
K4BCQ9	8	8	154.46	Yes	Uncharacterized protein
K4BLT8	7	3	87.95		Uncharacterized protein
K4C3B7	2	1	80.38		Uncharacterized protein
K4B123	2	1	52.5	Yes	Uncharacterized protein
Q49B52	24	20	1244.08		Monodehydroascorbate reductase
K4B854	3	1	37.34		Uncharacterized protein
Q84P53	8	2	196.57		Gamma aminobutyrate transaminase 2

K4BQ64	1	1	45.31		Uncharacterized protein
K4C7V4	3	3	65.99	Yes	Uncharacterized protein
K4B3H9	18	15	1167.75	Yes	Uncharacterized protein
K4D451	7	3	299.41		Phenylalanine ammonia-lyase
K4B8R0	3	1	43.67	Yes	Uncharacterized protein
K4B170	11	9	412.72		Uncharacterized protein
K4CNR8	4	4	136.26		Uncharacterized protein
K4B8B1	4	2	127.42	Yes	Uncharacterized protein
K4CDL3	19	12	785.67		Aspartate aminotransferase
K4DDF6	2	2	38.7	Yes	Uncharacterized protein
K4AY17	2	1	54.66	Yes	Uncharacterized protein
K4C284	9	1	392.47		Glutamate decarboxylase
K4BBY2	13	13	931.65	Yes	Uncharacterized protein
K4CFF0	24	17	1822.96		Peroxidase
K4AZN6	3	1	84.06	Yes	Mitogen-activated protein kinase
K4CDW6	2	1	33.19	Yes	Uncharacterized protein
K4CEJ1	28	22	911	Yes	Uncharacterized protein
A0RZC9	6	4	72.18		Constitutive plastid-lipid associated protein
K4ASM4	5	2	38.84	Yes	Uncharacterized protein
K4C9A8	5	4	161.06		Uncharacterized protein
K4BUC0	3	3	73.39		Uncharacterized protein
K4CAY2	9	6	376.56		Uncharacterized protein
K4BDH9	21	14	628.51	Yes	Glucose-6-phosphate 1-dehydrogenase
K4B3F4	8	5	241.75		Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit
K4BNB4	11	1	283.36		Pyruvate dehydrogenase E1 component subunit alpha
K4D9S9	8	2	412.76		Uncharacterized protein
K4CB65	13	10	648.77	Yes	Uncharacterized protein
K4BJ74	8	7	661.2		Uncharacterized protein
K4C234	4	1	102.1		Uncharacterized protein
K4DG11	2	2	33.42		Uncharacterized protein
K4CPG9	3	1	54.89	Yes	Reticulon-like protein
K4BAW0	4	1	76.41	Yes	Fructose-bisphosphate aldolase
K4DHC5	2	1	54.64	Yes	Uncharacterized protein
Q01413	20	16	1884.54		Glucan endo-1,3-beta-glucosidase B
K4AZ59	10	8	423.36		3-phosphoshikimate 1-carboxyvinyltransferase
O65917	12	6	412.61		Dehydroquinase dehydratase/shikimate:NADP oxidoreductase
K4DFR4	5	5	222.39		Uncharacterized protein
K4C288	3	2	128.76		Uncharacterized protein
K4DFV6	11	10	412.64		Uncharacterized protein
K4B166	15	9	561.88	Yes	Uncharacterized protein
Q3I5C4	15	1	943.5		Cytosolic ascorbate peroxidase 1
K4C4X4	6	3	145.63		60S ribosomal protein L36
D2KQJ9	8	5	253.05		Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial

K4DHD5	11	8	390.5		Uncharacterized protein
Q0PY39	3	3	133.41		Auxin repressed/dormancy associated protein
K4BNE0	22	7	1166.51		Uncharacterized protein
K4DC18	36	12	1555.81		Uncharacterized protein
K4DGL5	7	6	356.53		Uncharacterized protein
K4BMU5	1	1	21.23		Uncharacterized protein
K4D5V2	26	19	772.95	Yes	Uncharacterized protein
K4BVN6	26	16	1115.85		Uncharacterized protein
K4BWA5	9	1	86.8		Uncharacterized protein
K4BBN2	11	5	152.2	Yes	Uncharacterized protein
K4B3A1	8	5	157.84		Uncharacterized protein
K4B7P2	5	5	197.29	Yes	Uncharacterized protein
K4CDC2	3	3	73.12	Yes	Uncharacterized protein
K4CR64	11	2	349.09	Yes	Uncharacterized protein
K4D5B1	4	4	146.24	Yes	Uncharacterized protein
K4C635	7	4	235.16		Acyl-[acyl-carrier-protein] desaturase
K4C6Q9	2	1	46.67		Uncharacterized protein
K4CUK9	6	4	153.04		Uncharacterized protein
K4BPK4	17	15	1571.25		Triosephosphate isomerase
Q9FT17	9	1	131.37	Yes	Lipoxygenase
K4CQ01	2	1	89.88		Uncharacterized protein
K4C6Z0	3	1	38.62		Uncharacterized protein
K4BW98	6	1	151.21		Uncharacterized protein
K4D389	6	4	258.01		Uncharacterized protein
K4C2A2	3	2	87.09		Uncharacterized protein
K4BTH7	14	7	625.34		Peroxidase
K4CF87	18	15	876.53		Uncharacterized protein
K4BVZ4	2	2	54.16		Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
K4CGZ3	7	4	93.13		Uncharacterized protein
K4CR73	17	9	382.91	Yes	Eukaryotic translation initiation factor 3 subunit A
Q9FPM6	6	5	73.64	Yes	9-divinyl ether synthase
K4BTL1	10	9	413.06		Uncharacterized protein
Q3SC84	9	6	492.37		Oxoglutarate/malate translocator
K4BLG1	2	2	86.53		Uncharacterized protein
O81536	23	20	1346.63		Annexin
K4C6V9	3	2	39.88		Uncharacterized protein
K4C2K4	2	1	97.37	Yes	Uncharacterized protein
K4D9G1	4	3	108.64	Yes	Uncharacterized protein
K4B0S9	4	3	88.55		Mitochondrial Rho GTPase
K4C2W4	9	4	275.61		Protein disulfide-isomerase
K4AXL3	5	3	119.11		Uncharacterized protein
K4BN62	22	14	1205.69		Pectinesterase
K4BSP7	3	2	93.99		Uncharacterized protein
Q8GZD8	23	17	1306.71		Leucine aminopeptidase 2, chloroplastic

K4C7C4	11	9	473.3		Uncharacterized protein
K4CIH8	3	1	103.97		Uncharacterized protein
K4CGI1	4	1	47.13		Uncharacterized protein
K4C2X8	8	4	319.85		Uncharacterized protein
K4DG12	3	2	28.61	Yes	Uncharacterized protein
O22478	8	2	294.7		Importin subunit alpha
K4BCF4	3	1	52.7		Uncharacterized protein
K4D3R4	9	5	247.36		Uncharacterized protein
K4BYA8	9	2	167.42		Uncharacterized protein
A6N6K8	8	6	381.17	Yes	Phenylacetaldehyde reductase
K4CL66	3	2	64.37		Uncharacterized protein
K4BAY6	3	1	51.06		Thioredoxin
Q645N0	4	2	200.1	Yes	Malate dehydrogenase
K4C1C9	31	25	1699.84		Uncharacterized protein
P43280	15	2	756.96		S-adenosylmethionine synthase 1
B6RQ70	3	3	54.86		Asr2
K4C0Y7	3	2	38.94	Yes	Uncharacterized protein
K4CP63	7	3	654.39		Uncharacterized protein
K4C8P4	4	2	141.77		Uncharacterized protein
K4AZ93	2	2	57.03		Uncharacterized protein
K4CHJ0	4	4	226.28		Uncharacterized protein
K4ASQ6	6	4	281.32		Uncharacterized protein
K4CGI2	6	4	207.11		Uncharacterized protein
K4BNL4	8	4	233.26		Uncharacterized protein
Q7Y1Y6	6	2	71.39		Mitogen-activated protein kinase
K4C3C9	6	1	311.26	Yes	Uncharacterized protein
K4B8D2	6	5	215.13		Uncharacterized protein
K4BHX1	2	2	54.16		Uncharacterized protein
K4DHU7	14	4	883.8		Uncharacterized protein
K4BM30	1	1	38.47		Uncharacterized protein
K4B1F9	8	8	280.4		Uncharacterized protein
K4CMQ3	4	1	41.09		Uncharacterized protein
K4CQ40	6	4	240.73		Uncharacterized protein
K4C034	6	3	153.5		Uncharacterized protein
K4BKH5	7	3	169.95		Uncharacterized protein
K4CSX3	1	1	36.4		Uncharacterized protein
K4CNR6	8	5	169.64		Uncharacterized protein
K4AX22	6	5	305.94	Yes	Superoxide dismutase [Cu-Zn]
K4ASX2	6	4	209.52		Uncharacterized protein
K4CJP1	3	2	47.22		Methylthioribose-1-phosphate isomerase
K4AZG6	2	1	52.77		Uncharacterized protein
K4CMT7	8	1	398.7		60S ribosomal protein L13
K4AXB5	9	8	223.11	Yes	Uncharacterized protein
K4C726	10	10	380.14		Uncharacterized protein
K4BU76	6	4	109.77		NADPH--cytochrome P450 reductase

K4B1Y6	9	9	427.95		Uncharacterized protein
K4D331	10	10	281.69	Yes	NADH-cytochrome b5 reductase
Q2PQI9	5	3	223.61		Nascent polypeptide-associated complex subunit beta
K4BNL3	15	8	480.17		Uncharacterized protein
K4CG60	10	8	240.25		Aspartate aminotransferase
Q7Y240	6	5	476.18		Thioredoxin peroxidase 1
K4BEB0	2	2	42.18		Uncharacterized protein
K4B9J6	8	6	498.99		Uncharacterized protein
K4D3F2	5	4	220.72		Uncharacterized protein
Q52QQ4	13	4	815.83		Ascorbate peroxidase
K4C5P4	6	3	200.48		Uncharacterized protein
K4BGC0	3	3	85.53		Uncharacterized protein
K4B8W8	6	2	101.41		Uncharacterized protein
K4CQ64	5	4	92.11	Yes	Uncharacterized protein
K4CGH9	3	1	28.18		Uncharacterized protein
K4C7V7	7	4	82.65		Uncharacterized protein
K4C3E8	10	3	496.83		Uncharacterized protein
K4BDZ7	10	9	296.58	Yes	Uncharacterized protein
K4C2M1	5	1	71.67	Yes	Uncharacterized protein
A8DUB0	3	1	54.98	Yes	Glutathione S-transferase-like protein
K4D6E8	7	5	255.97		Eukaryotic translation initiation factor 3 subunit F
K4D0H2	8	2	501.39		Uncharacterized protein
K4C320	6	4	264.81		Uncharacterized protein
K4B089	5	5	128.21		Uncharacterized protein
K4CJ91	5	3	198.99		Uncharacterized protein
Q05538	13	7	1398.77		Basic 30 kDa endochitinase
K4D9N5	5	5	131.92		Xyloglucan endotransglucosylase/hydrolase
K4BSE0	2	2	140.7		Uncharacterized protein
K4D2I8	10	2	59.29		Uncharacterized protein
K4CIV5	12	1	424.97		Uncharacterized protein
K4B1V5	4	1	340.04		40S ribosomal protein S12
K4CME9	4	1	105.37	Yes	Uncharacterized protein
K4BPR4	26	3	1757.63		Uncharacterized protein
K4D3M1	15	1	804.5		Uncharacterized protein
K4BN60	15	9	701.15		Uncharacterized protein
K4BQD6	7	5	280.33		Uncharacterized protein
K4AZ16	10	8	444.36		T-complex protein 1 subunit alpha
K4BLV3	37	8	1410.6		Uncharacterized protein
K4BSR4	26	21	1598.11	Yes	Annexin
K4BJ06	9	6	192.77		Uncharacterized protein
K4DI33	3	3	65.3		Uncharacterized protein
K4CHD8	2	1	36.69	Yes	Uncharacterized protein
K4BTP3	2	1	50.36	Yes	Uncharacterized protein
K4BLA1	14	9	791.76		Uncharacterized protein
K4B3E9	2	1	41.65		Uncharacterized protein

K4CH48	4	3	64.97		Ubiquitin carboxyl-terminal hydrolase
P93214	15	5	927.87		14-3-3 protein 9
P38415	23	14	768.71		Linoleate 9S-lipoxygenase A
Q6X1D0	4	2	49.65	Yes	Superoxide dismutase
K4B489	5	3	84.27		Aminoacylase-1
Q76LU4	6	4	177.47		Alpha-L-arabinofuranosidase
K4CMC4	4	2	38.35	Yes	Uncharacterized protein
K4C3T2	16	15	935.07		Uncharacterized protein
K4B7U1	1	1	69.43		Uncharacterized protein
H6WYS2	13	7	374.14		Sulfite reductase
K4BV98	2	1	63.13	Yes	Uncharacterized protein
K4BU58	3	3	49.62		Uncharacterized protein
K4BPW1	6	2	125.4		Uncharacterized protein
K4BPX0	1	1	30.73		Uncharacterized protein
K4B0G3	13	1	487.73		Uncharacterized protein
K4CLR4	3	3	109.08		Uncharacterized protein
K4AXP3	5	2	115.35		Uncharacterized protein
K4D3W3	3	1	50.79		Uncharacterized protein
K4DAZ4	9	4	180.55		Uncharacterized protein
K4C3Y3	4	1	29.55		Uncharacterized protein
K4B8V1	12	8	882.51		Uncharacterized protein
K4B7E5	5	4	124.66		Uncharacterized protein
K4CGI6	6	1	115.54		Uncharacterized protein
K4D4Q9	5	3	213.36		Uncharacterized protein
K4CBW8	4	3	71.76		Uncharacterized protein
K4C2W3	8	2	225.49		Uncharacterized protein
K4DC87	2	1	22.52	Yes	Uncharacterized protein
K4CIP0	3	2	76.49		Uncharacterized protein
K4D3H4	2	2	79.62		Uncharacterized protein
K4BPH8	7	1	294.22		Uncharacterized protein
K4CA55	11	7	403.26		Peptidyl-prolyl cis-trans isomerase
K4BPX5	8	2	272.6		Uncharacterized protein
K4CJ67	12	7	430.95	Yes	Uncharacterized protein
K4B2I9	27	9	1374.6		Uncharacterized protein
A9QNE7	3	1	23.5		ABA 8'-hydroxylase
K4BYA0	6	2	38.57	Yes	Uncharacterized protein
K4CVP1	3	2	77.81	Yes	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
K4CET6	5	1	65.88		Uncharacterized protein
K4CA36	12	6	202.4		Uncharacterized protein
K4BIH2	7	7	295.2		Uncharacterized protein
K4CAH4	13	6	365.35		Uncharacterized protein
K4B8C3	6	2	103.95		Uncharacterized protein
K4BJY1	5	3	141.72		Uncharacterized protein
K4CFE7	4	2	49.36		Isocitrate lyase
K4AX94	9	5	41.72		Uncharacterized protein

K4CHA8	2	1	22.04		Uncharacterized protein
K4D0Y5	6	5	103.14	Yes	Uncharacterized protein
Q40131	8	6	208.52		Uncharacterized protein
K4CIH6	7	5	104.72		Uncharacterized protein
K4CEW0	5	2	67.18		Glucose-6-phosphate 1-dehydrogenase
K4BP37	7	2	313.11	Yes	Uncharacterized protein
K4D0F3	3	2	59.74		Uncharacterized protein
K4C275	6	6	286.59		Uncharacterized protein
K4CTJ3	2	2	42.53		Uncharacterized protein
K4C7H6	2	2	91.68		RNA-binding protein 8A
K4BTH5	2	1	66.32		Uncharacterized protein
K4DH49	25	8	1088.29		Uncharacterized protein
K4BMV8	10	7	179.37		Protein ROOT HAIR DEFECTIVE 3 homolog
K4CGA2	3	2	77.36		Uncharacterized protein
K4CZS1	5	1	183.6		Uncharacterized protein
K4DFY4	4	2	134.95		Uncharacterized protein
K4BL40	6	1	297.63	Yes	UDP-glucose 6-dehydrogenase
K4CCD2	13	7	661.1		Uncharacterized protein
K4DA65	6	4	75.31		Uncharacterized protein
Q9S9G8	7	3	367.49	Yes	TOM P14C pathogenesis-related PR-1 protein (Fragments)
K4CNU7	3	3	69.25		Uncharacterized protein
P62980	10	3	559.7		Uncharacterized protein
K4B989	15	11	795.67		Uncharacterized protein
K4DHJ5	14	2	358.75		Uncharacterized protein
K4DAS6	18	12	1212.07		Uncharacterized protein
K4D435	24	9	1247.73		Uncharacterized protein
K4C2D6	15	10	1015.18		Uncharacterized protein
K4D810	6	3	213.31		Uncharacterized protein
K4B7P1	3	2	34.38		Uncharacterized protein
K4B740	15	8	820.63		UDP-glucose 6-dehydrogenase
K4AYJ2	20	15	758.56		Uncharacterized protein
K4BM13	11	8	329.31		Uncharacterized protein
K4CRG8	5	3	337.69		Uncharacterized protein
H6V7A0	7	1	384.3		MIP (Fragment)
K4C2U9	16	10	493.85		Uncharacterized protein
K4BJF8	2	1	37.7		Uncharacterized protein
K4AZG1	10	8	438.17		Malic enzyme
K4CG62	12	6	453.46		Uncharacterized protein
K4C227	31	16	1549.28		Uncharacterized protein
K4DEQ8	10	5	470.65		Uncharacterized protein
K4AXJ9	7	1	295.81		Uncharacterized protein
K4C258	4	3	185.68		Uncharacterized protein
K4CGP6	11	3	335.58		Uncharacterized protein
K4AXR6	3	3	120.36	Yes	Uncharacterized protein
K4B414	4	2	67.42		Uncharacterized protein

K4BSR7	4	3	49.44		Uncharacterized protein
K4AYV3	2	2	126.53		Uncharacterized protein
K4B7J7	1	1	29.74	Yes	tRNA (guanine-N(7)-)-methyltransferase
K4CLR0	1	1	25.2		Uncharacterized protein
K4DFR1	45	37	2764.77		Uncharacterized protein
K4D9L5	40	4	2792.73		Uncharacterized protein
K4APU2	14	11	997.13		Uncharacterized protein
K4C1V8	2	1	55.83	Yes	Uncharacterized protein
K4B8U9	3	2	131.79		Uncharacterized protein
Q66MH8	2	1	61.13		MAPKK
K4B413	1	1	58.7	Yes	Uncharacterized protein
K4DAT4	5	1	161.89		Uncharacterized protein
Q2QJT5	9	9	265.15		ASR4
K4D9Y7	4	2	152.69		Uncharacterized protein
K4C8H8	5	1	149.64		Uncharacterized protein
K4BI25	3	2	56.61		Uncharacterized protein
O82777	12	3	407.98		Subtilisin-like protease
K4BRS6	1	1	22.94		Uncharacterized protein
K4AT31	13	10	348.46		Uncharacterized protein
K4CQV5	23	9	1704.58		Fructose-bisphosphate aldolase
P43281	15	2	731.18		S-adenosylmethionine synthase 2
K4CG46	31	3	1134.53		Uncharacterized protein
K4AZ32	4	3	159.51		Uncharacterized protein
K4D340	10	7	346.75		Uncharacterized protein
K4D5S3	1	1	39.45		Uncharacterized protein
K4BQ24	9	4	122.02		Uncharacterized protein
D9J1Y9	2	1	32.02	Yes	Mitogen-activated protein kinase
Q40159	6	4	161.27		Late embryogenesis (Lea)-like protein
K4B3G7	17	14	689.31		Coatomer subunit gamma
K4BFP1	6	1	245.66		Peroxidase
K4B172	10	9	391.67		Uncharacterized protein
K4D530	15	8	603.37		Pyruvate kinase
K4AV63	22	15	1097.41		Uncharacterized protein
K4BBJ0	2	2	39.99		Uncharacterized protein
K4CB31	4	2	132.74		Uncharacterized protein
K4BQC4	4	2	32.08		Uncharacterized protein
K4DHC7	12	2	402.34		Uncharacterized protein
K4DBU7	3	3	187.95		Profilin
K4DFC1	7	2	529.77		Uncharacterized protein
E0Z1D0	52	25	2984.62		Sucrose synthase isoform 3
P38547	11	8	648.59		GTP-binding nuclear protein Ran2
K4B1L4	3	1	40.62		Uncharacterized protein
K4CGW4	3	2	65.82	Yes	Uncharacterized protein
Q08306	15	1	692.59	Yes	Polyphenol oxidase D, chloroplastic
K4C6Q6	6	2	437.55		Tonoplast intrinsic protein 23

Q7XAV2	4	4	159.9	Yes	Superoxide dismutase [Cu-Zn]
K4CEG6	6	1	67.5		Uncharacterized protein
K4CSH4	7	2	237.27		Uncharacterized protein
K4CHG7	5	5	179.74		Small ubiquitin-related modifier
K4CHY3	29	21	1818.7		Phosphoglycerate kinase
K4D473	37	2	2570.31		Uncharacterized protein
K4CBF4	1	1	24.62	Yes	Uncharacterized protein
K4ATR8	11	11	368.92		Uncharacterized protein
K4CQ62	14	9	378.53		Uncharacterized protein
K4B433	17	10	404.83		Uncharacterized protein
Q8GT30	17	5	609.46	Yes	Dihydrolipoyl dehydrogenase
K4CNM8	3	1	22.29		Uncharacterized protein
K4BFW3	2	1	53.92		Uncharacterized protein
K4BAE6	11	7	369.56		Catalase
K4CGH0	5	2	46.24		Uncharacterized protein
K4BN59	6	1	139.83	Yes	Uncharacterized protein
K4D9A2	7	6	103.74		Uncharacterized protein
K4CND8	1	1	48.44		Uncharacterized protein
K4BWI5	4	2	78.91		Serine/threonine-protein phosphatase
K4D9V7	5	1	70.97		Uncharacterized protein
K4C839	5	1	58.73		Uncharacterized protein
K4AX21	2	1	59.68	Yes	Acyl carrier protein
K4BUD9	29	6	2192.35		Uncharacterized protein
K4DG42	5	2	88.48		Uncharacterized protein
K4B2B1	2	1	200.39		Uncharacterized protein
Q94K24	9	7	482.23		Ran binding protein-1
K4CX88	11	3	511.21		Uncharacterized protein
K4BLU5	3	3	76.26		Uncharacterized protein
K4DF99	34	6	1209		Uncharacterized protein
K4CWQ0	14	3	95.19		Uncharacterized protein
K4CQB5	29	14	1475.08		Uncharacterized protein
K4B2M8	7	5	629.83		Uncharacterized protein
K4B5K9	5	2	44.68	Yes	Uncharacterized protein
K4B893	1	1	56.65		Uncharacterized protein
O65004	6	5	181.49		Farnesyl pyrophosphate synthase
K4BM40	19	11	500.98		T-complex protein 1 subunit delta
K4CQR9	11	4	558.01		Pyruvate kinase
K4B3G5	7	4	235.15		Uncharacterized protein
K4BUL5	3	1	41.61	Yes	Uncharacterized protein
K4CRJ3	8	5	318.89		Uncharacterized protein
K4C627	5	3	201.1		Uncharacterized protein
K4D1W4	18	7	829.28		Peroxidase
K4DFU3	24	14	1414.13		6-phosphogluconate dehydrogenase, decarboxylating
K4CHH4	2	1	34.51		Uncharacterized protein
K4B1S8	3	2	97.87		Uncharacterized protein

P15003	5	4	230.2		Suberization-associated anionic peroxidase 1
K4BAF3	9	8	361.29	Yes	Phosphoserine aminotransferase
K4C755	4	3	56.93		Uncharacterized protein
K4D3X7	2	1	48.88		Uncharacterized protein
K4CU16	4	1	155.25		Uncharacterized protein
K4B440	10	8	283.53		Uncharacterized protein
K4DGU3	11	8	349.99		Uncharacterized protein
K4DE77	1	1	52.32		Uncharacterized protein
K4CHM9	6	3	99.7	Yes	Uncharacterized protein
K4BBU9	4	1	124.94		Uncharacterized protein
K4CVA6	5	1	209.88		Uncharacterized protein
K4D5E1	2	2	40.43		Beta-hexosaminidase
K4CFF2	8	1	442.2		Peroxidase
K4ATD4	3	1	66.39		Uncharacterized protein
K4CEB3	40	23	1643.01		Uncharacterized protein
K4ASF2	3	1	45.66		Uncharacterized protein
K4C8T4	10	2	818.9		40S ribosomal protein SA
K4AR83	3	2	53.31		Uncharacterized protein
K4C1Z7	1	1	22.24		Uncharacterized protein
K4D6L1	8	6	199.25		Eukaryotic translation initiation factor 3 subunit I
K4AX34	7	5	215.1		Peroxidase
K4CLY7	5	1	85.87		Uncharacterized protein
K4D553	10	1	583.39		Histone H2B
Q8VWR0	6	2	216.94		Profilin
Q41350	13	13	887.75		Osmotin-like protein
K4CCH1	1	1	19.67		Uncharacterized protein
K4BTY8	4	1	39.87		Uncharacterized protein
K4D4M0	4	4	155.92	Yes	Peptidyl-prolyl cis-trans isomerase
K4D9Q6	2	2	41.28		Uncharacterized protein
K4AXU7	2	1	41.62		Uncharacterized protein
K4BV02	8	6	489.42		Uncharacterized protein
K4BTY9	25	5	1564.14		14-3-3 protein 3
Q53Z32	46	8	3042.27		Molecular chaperone Hsp90-2
K4CP65	8	2	874.29		Uncharacterized protein
Q672Q8	3	1	90.99		Adenylyl-sulfate reductase
K4C740	7	3	129.69		Uncharacterized protein
K4C5G0	4	4	127.27		Alpha-galactosidase
O82575	5	4	205.45		Fruit-ripening protein
K4D318	6	5	173.96		Uncharacterized protein
K4BT42	3	1	130.01		Uncharacterized protein
K4AXX8	2	1	51.99		Uncharacterized protein
K4CSD7	10	8	479.57		Uncharacterized protein
K4BOW1	2	1	51.51		Uncharacterized protein
K4BX34	17	11	1150.5		Fructose-bisphosphate aldolase
Q9ZS45	4	4	94.26		Spermidine synthase

K4CA69	5	2	79.15		Uncharacterized protein
K4DAA0	8	3	451.54		Uncharacterized protein
K4B0D2	1	1	25.78	Yes	Uncharacterized protein
K4CP17	4	2	202.08		Uncharacterized protein
K4D888	6	3	77.34		Uncharacterized protein
K4BT19	13	11	828.76		Uncharacterized protein
K4B3M5	21	17	755.28		V-type proton ATPase subunit a
K4BZB1	11	5	399.28	Yes	Uncharacterized protein
K4C6W9	11	8	628.41		Uncharacterized protein
K4BP30	22	15	997.19		Pyruvate kinase
K4BT18	5	4	63.44		Uncharacterized protein
Q84KJ2	6	6	345.76		Copper chaperone
K4DH61	4	1	140.18		Uncharacterized protein
K4C2M0	11	2	602.4		Histone H2B
K4CFR0	19	14	697.26		Uncharacterized protein
K4BXV0	10	6	347.02		Uncharacterized protein
K4CW09	5	1	65.42	Yes	Uncharacterized protein
K4CRI4	3	1	73.35		Uncharacterized protein
K4B4Y5	5	1	34.24		Uncharacterized protein
H2BJQ1	7	6	182.59		Putative steroid 5beta-reductase
K4CJG6	3	1	49.32		Uncharacterized protein
K4DC11	2	1	40.96		Uncharacterized protein
K4CV89	5	1	149.49		Uncharacterized protein
K4CGY4	2	1	33		Uncharacterized protein
K4BQ70	5	3	142.37		Uncharacterized protein
K4AR02	1	1	32.02		Uncharacterized protein
K4BJD6	7	3	80.46		Uncharacterized protein
K4CR69	4	3	96.6		Arginine biosynthesis bifunctional protein ArgJ, chloroplastic
K4D1P2	14	11	464.28		Uncharacterized protein
K4CNB0	5	3	128.7		Uncharacterized protein
K4D3H1	4	2	45.2	Yes	Uncharacterized protein
K4AS98	4	1	42.13		Uncharacterized protein
K4D2D4	6	4	156.63		Uncharacterized protein
K4B9B8	4	2	79.61		Uncharacterized protein
Q6SKP4	22	5	729.16		Ribosomal protein L3
K4AU58	8	2	276.88		Uncharacterized protein
K4ATN9	4	3	68.9		Uncharacterized protein
K4BHA1	16	10	227.63		Uncharacterized protein
K4B4Z2	10	6	238.53		Uncharacterized protein
K4CGB9	3	2	34.1		Uncharacterized protein
K4CV09	3	3	27.37		Serine/threonine-protein phosphatase
K4DAG1	3	3	61.27		Uncharacterized protein
K4BEU1	3	3	92.88		Uncharacterized protein
K4BA58	1	1	54.85		Uncharacterized protein

P93212	17	4	836.78		14-3-3 protein 7
K4CNF2	13	1	668.38		Isocitrate dehydrogenase [NAD] subunit, mitochondrial
K4C779	16	2	592.82		Uncharacterized protein
K4C8R3	7	6	311.66		Uncharacterized protein
K4CE22	6	3	142.19		Uncharacterized protein
K4B8S7	6	4	109.55	Yes	Uncharacterized protein
D2Y3F4	9	8	254.35		Alcohol dehydrogenase class III
K4BE93	17	10	871.32		Peroxidase
K4CXZ1	8	6	412.89		Uncharacterized protein
K4B9P3	23	1	1735.23		Pectinesterase
K4CRJ2	5	3	150.9		Uncharacterized protein
K4DHK7	9	1	322.86		Uncharacterized protein
K4AZL0	7	3	504.7		Plasmamembrane intrinsic protein 12
K4CR71	2	1	95.89		Uncharacterized protein
K4CN52	6	2	139.36	Yes	Uncharacterized protein
K4D249	6	2	52.81		Histone-lysine N-methyltransferase
K4DB46	12	4	328.82		Uncharacterized protein
K4CXH1	5	1	45.77	Yes	Uncharacterized protein
K4BVZ0	3	3	57.57		Glyceraldehyde-3-phosphate dehydrogenase
K4ATC7	2	2	30.95		Uncharacterized protein
K4B2J4	23	4	931.03		Uncharacterized protein
K4D2W1	16	11	389.35		Uncharacterized protein
K4BX77	6	3	164.75		3-isopropylmalate dehydrogenase
K4AQH0	2	2	43.87		Uncharacterized protein
AOA097PM10	8	6	177.81		LOS4 (Fragment)
K4CL75	52	41	3168.05		Uncharacterized protein
K4DBS7	4	2	48.96		Uncharacterized protein
K4CWK0	6	1	174.75		Uncharacterized protein
K4CAL8	1	1	77.9		Uncharacterized protein
K4D930	25	11	1215.28		Uncharacterized protein
K4CBV4	5	4	93.21		Uncharacterized protein
K4CFP5	6	2	193.24		Uncharacterized protein
K4BEI8	6	5	118.42		Uncharacterized protein
K4BYA6	9	1	169.7		Uncharacterized protein
K4BVG4	7	4	370.49		Thioredoxin
K4CIU0	10	2	719.37		Uncharacterized protein
K4B9T4	13	10	652.07	Yes	Lactoylglutathione lyase
K4D2S2	12	7	287.02		Adenylosuccinate synthetase, chloroplastic
K4B0C2	4	1	51.29		Uncharacterized protein
K4AVZ9	3	1	36.88	Yes	Uncharacterized protein
K4BYC0	10	7	266.99		Uncharacterized protein
K4DHW5	9	5	175.71		Uncharacterized protein
K4BM58	7	7	131.65		Uncharacterized protein
K4BXX0	16	11	415.67		Uncharacterized protein
K4C8V8	5	5	86.78		Uncharacterized protein

K4ASR4	2	1	39.83		Uncharacterized protein
K4CF48	12	8	438.84	Yes	Uncharacterized protein
K4CNF1	13	1	671.33		Isocitrate dehydrogenase [NAD] subunit, mitochondrial
K4CI40	3	1	94.9	Yes	Uncharacterized protein
K4AXN9	4	3	158.06		Uncharacterized protein
K4BJJ7	2	2	84.51	Yes	Uncharacterized protein
K4CRI5	8	6	186.76		Uncharacterized protein
K4C1C0	4	3	110.63		Peroxidase
K4CIG1	2	2	48.76		Uncharacterized protein
Q5D8D3	10	7	154.23		Acyl-coenzyme A oxidase
K4CAG8	1	1	55.83		Uncharacterized protein
K4BPJ2	3	1	180.97		Uncharacterized protein
K4B894	3	2	64.12		Uncharacterized protein
K4DAV2	11	7	318.18	Yes	Uncharacterized protein
K4D5G8	7	1	269.15		Uncharacterized protein
K4CKH7	3	1	35.05		Uncharacterized protein
K4CUR8	6	1	276.4		Uncharacterized protein
Q9LEG5	5	3	158.94	Yes	Allene oxide cyclase
K4BAG0	3	2	74.96		Uncharacterized protein
K4C108	7	2	98.62		Phosphomannomutase
K4D9K2	4	1	51.67		Uncharacterized protein
K4BTJ3	6	3	166.49	Yes	Uncharacterized protein
K4AXI7	3	3	198.95	Yes	Uncharacterized protein
K4B169	7	1	294.39		Uncharacterized protein
E5LBC4	10	8	365.91		Prephenate aminotransferase
K4CHE0	4	1	83.44		Uncharacterized protein
K4BMZ6	2	1	21.28	Yes	Uncharacterized protein
K4C6B2	4	4	173.9		Uncharacterized protein
K4B0B4	6	5	507.06		Uncharacterized protein
K4BF34	5	4	100.54		Uncharacterized protein
K4CA25	3	1	54.77		Uncharacterized protein
K4DA09	4	3	195.12	Yes	Uncharacterized protein
K4BVD4	4	4	50.17		Uncharacterized protein
Q8LRN7	5	2	108.42		Cell-wall invertase
Q9XEX8	6	5	106.18		Remorin 1
K4BUT9	12	7	436.87		Uncharacterized protein
K4D3K7	3	2	46.93		Uncharacterized protein
K4BWY8	2	1	39.35	Yes	Uncharacterized protein
K4B7P7	3	1	44.73		Uncharacterized protein
K4C6L0	17	14	434.02	Yes	Protein disulfide-isomerase
Q9M726	5	1	68.13		SNF1
K4D4S9	6	2	48.84	Yes	Uncharacterized protein
K4DB71	9	1	417.01		Uncharacterized protein
K4BYA3	4	2	95.86		Proteasome subunit beta type
K4C9I3	8	4	204.34		Uncharacterized protein

K4CC33	10	6	247.9		Uncharacterized protein
K4D324	2	2	83.03	Yes	Small nuclear ribonucleoprotein F
K4D4B8	1	1	34.97	Yes	Uncharacterized protein
Q9M7N6	4	2	116.34	Yes	MFP1 attachment factor 1
K4C128	2	2	51.57		Small nuclear ribonucleoprotein-associated protein
K4BS21	6	2	47.95		Uncharacterized protein
K4DCV3	7	1	396.07		Malate dehydrogenase
K4CP11	2	1	25		Uncharacterized protein
K4C3V8	10	1	160.41		Uncharacterized protein
K4CIK9	3	3	80.49		Uncharacterized protein
K4DBW0	6	5	89.24		Uncharacterized protein
K4C6R5	2	2	80.46		Ubiquitin carboxyl-terminal hydrolase
K4D7W0	6	5	126.6		Cytochrome b-c1 complex subunit Rieske, mitochondrial
K4C7K0	6	3	95.98		Uncharacterized protein
K4CRT0	3	3	86.02		Uncharacterized protein
K4DAT6	2	1	32.54		Uncharacterized protein
K4B8B0	7	2	171.9		Uncharacterized protein
K4D9S4	2	1	52.23		Uncharacterized protein
K4BG20	6	3	151.28		Uncharacterized protein
K4BDL5	2	2	197.64		Uncharacterized protein
K4AXN3	4	3	200.17		Uncharacterized protein
K4B1S4	15	12	383.51		Uncharacterized protein
K4APN5	3	2	63.57		Uncharacterized protein
Q5NE21	10	9	404.89		Carbonic anhydrase
K4CH72	9	2	451.05		Uncharacterized protein
K4BVH7	16	7	569.42		Coatomer subunit alpha
K4B256	2	1	44.84	Yes	Uncharacterized protein
K4B3Q8	10	9	348.3		Uncharacterized protein
K4DH92	4	3	64.62		Uncharacterized protein
K4B546	13	10	332.34		Obg-like ATPase 1
K4CAM8	3	2	78.67		Uncharacterized protein
K4C1P5	4	2	162.69		Uncharacterized protein
K4CPS8	28	4	1623.99		Uncharacterized protein
K4C455	17	9	1018.92		Uncharacterized protein
K4CI69	14	13	901.32		Uncharacterized protein
K4B892	1	1	33.46		Uncharacterized protein
K4CK49	14	8	465.11		Importin subunit alpha
K4AYP1	4	2	139.67		Uncharacterized protein
K4DFA0	33	4	1205.54		Uncharacterized protein
K4CNI4	3	2	64.73		Uncharacterized protein
K4D2Z0	6	6	545.52		Uncharacterized protein
K4CYU9	10	6	348.56		Uncharacterized protein
K4D601	27	18	1452.72		Uncharacterized protein
P93213	11	6	384.72		14-3-3 protein 8
K4BLS9	4	1	113.34		Uncharacterized protein

K4DH69	5	4	204.02	Yes	Uncharacterized protein
K4BJ22	43	2	1716.53		Clathrin heavy chain
K4DA99	10	6	1115.1		Uncharacterized protein
K4BPJ4	18	7	793.25		Uncharacterized protein
K4CLE4	4	4	109.72		Uncharacterized protein
K4AS92	7	5	141.73		Uncharacterized protein
Q3SC85	9	2	394.48		60S ribosomal protein L10
K4CX43	6	4	291.24		Uncharacterized protein
K4BPS9	3	1	41.63		Uncharacterized protein
K4CBD6	2	2	80.7		Xylose isomerase
K4B6E8	6	4	135.9		Uncharacterized protein
K4DCX0	8	1	95.33	Yes	Uncharacterized protein
Q2MI93	5	1	100.68		ATP synthase subunit beta, chloroplastic
K4CR67	6	2	275.14		Histone H2A
K4D102	4	1	85.81		Uncharacterized protein
Q9FEW9	4	3	124.7		12-oxophytodienoate reductase 3
Q93X45	10	7	212.01		Uncharacterized protein
K4CJE1	3	1	63.97		Uncharacterized protein
K4DHU5	3	2	87.98		Uncharacterized protein
Q9SPD5	26	4	675.24		Plasma membrane ATPase 2
K4BA13	3	2	113.62		Uncharacterized protein
Q68HC8	24	16	733.03		Glucose-6-phosphate isomerase
K4B0I4	2	1	59.22		Uncharacterized protein
K4C9E8	10	3	476.16		Ribosomal protein
K4COW6	3	2	72.79		Uncharacterized protein
K4CXQ8	45	8	1736.76		Uncharacterized protein
K4CWH3	10	6	291.34		Uncharacterized protein
K4BEF0	1	1	35.15		Uncharacterized protein
K4DCC6	4	2	73.02		Uncharacterized protein
K4CXD9	10	2	498.25		40S ribosomal protein S8
E5L4Q6	6	1	87.79		ABA aldehyde oxidase
K4BA92	6	4	178.71		Uncharacterized protein
K4BV28	5	2	102.48		Uncharacterized protein
K4ASZ8	11	1	525.92	Yes	Uncharacterized protein
K4D7R1	8	4	210.22		Uncharacterized protein
K4DBI3	2	1	30.64		Uncharacterized protein
K4AZT0	1	1	35.72		Uncharacterized protein
K4BAF0	2	2	119.52		Uncharacterized protein
K4CRE0	3	2	49.42		Uncharacterized protein
K4CHJ6	11	4	507.16		40S ribosomal protein S8
K4C9T0	1	1	23.48		Tonoplast intrinsic protein 12
K4AT27	2	2	33.41		Dihydroorotate dehydrogenase (quinone), mitochondrial
K4D4T0	7	4	287.37		Uncharacterized protein
K4CPB3	7	5	165.88		Uncharacterized protein
K4BY24	7	6	280.49		Uncharacterized protein

K4CBS9	3	1	33.68		Uncharacterized protein
K4BDP2	16	11	758.2		Phosphorus transporter
K4AXU8	2	2	95.41		Uncharacterized protein
K4CN59	4	4	121.46		Uncharacterized protein
K4B9Y4	5	5	288.78		Uncharacterized protein
K4BMF0	9	3	258.9		Uncharacterized protein
K4CWE3	3	1	95.03		Uncharacterized protein
K4BJG4	3	3	46.65		Uncharacterized protein
K4BCV6	10	7	197.56		Uncharacterized protein
P93208	19	5	1193.49		14-3-3 protein 2
K4CE62	5	4	112.39		Uncharacterized protein
K4D0T6	8	4	123.4	Yes	Adenylyl cyclase-associated protein
K4B1X5	6	1	92.64		Serine hydroxymethyltransferase
K4B1D4	9	6	398.97		Uncharacterized protein
K4B7Q8	5	2	60.08		Protein argonaute
K4CHAO	8	1	89.36		Pectinesterase
K4CF13	1	1	41.61		Uncharacterized protein
K4BK69	8	1	336.56		Elongation factor Tu
K4CWK1	9	3	233.7		Uncharacterized protein
B1Q3F0	8	2	233.7	Yes	Glutamate decarboxylase
K4B212	1	1	107.16		Uncharacterized protein
K4DAL8	4	1	162.57		Uncharacterized protein
K4B3W9	1	1	54.49	Yes	Uncharacterized protein
K4BPV3	1	1	64.57		Uncharacterized protein
K4D3E4	21	7	1336.24		Fructose-bisphosphate aldolase
K4BKV2	14	9	619.81		Uncharacterized protein
K4CCJ2	33	11	1341.23		Uncharacterized protein
Q2VY16	4	2	143.07		Peptidyl-prolyl cis-trans isomerase
Q66YT8	8	5	105.07		DWARF1/DIMINUTO
K4BXN9	7	2	280.92		Uncharacterized protein
K4C9P9	5	4	75.13		Uncharacterized protein
K4CTF6	8	1	394.89		40S ribosomal protein S8
K4C2E8	9	8	278.3		Beta-hexosaminidase
K4BWK1	4	4	192.3		Uncharacterized protein
P42652	21	4	1257.3		14-3-3 protein 4
Q5GA61	2	1	56.1	Yes	Peptidyl-prolyl cis-trans isomerase
K4BAZ5	13	1	1000.46		Peroxidase
K4C8Q9	7	3	334.37		Uncharacterized protein
K4CHJ1	3	3	47.83		Uncharacterized protein
K4CI93	15	2	780.27		40S ribosomal protein S6
K4AX86	3	3	36.02		Uncharacterized protein
K4AXJ0	7	4	144.45		Uncharacterized protein
B5M9E5	4	2	105.53		Beta-glucosidase 08
K4B814	19	8	737.58		40S ribosomal protein S4
K4BMF8	3	2	83.26		Uncharacterized protein

Q8H0Q1	5	5	143.42		Proliferating cell nuclear antigen
K4CAM3	1	1	34.5		Uncharacterized protein
K4ATB4	21	2	1204.32		Uncharacterized protein
K4CPC2	20	17	623.39		Uncharacterized protein
K4C8R8	2	1	53.04		Uncharacterized protein
K4AWT4	4	4	363.65		40S ribosomal protein S21
K4CX83	21	14	1083.53		Glyceraldehyde-3-phosphate dehydrogenase
K4AVG8	1	1	25.54		Uncharacterized protein
K4B9V8	6	1	244.1		Uncharacterized protein
K4B267	13	10	552.18		Uncharacterized protein
K4CNZ8	4	3	44.59		Uncharacterized protein
K4C261	30	10	1647		Serine hydroxymethyltransferase
K4BIM9	5	1	104.88		Uncharacterized protein
K4AZP5	5	3	232.06		Uncharacterized protein
K4BCR8	2	2	55.69		Uncharacterized protein
K4C247	9	1	343.67		Uncharacterized protein
K4C5S4	43	3	1797.93		Clathrin heavy chain
K4DCY2	3	1	28.31		GrpE protein homolog
G1EN31	1	1	24.81		LysM receptor-like kinase variant SIBti9-1a
K4CFP9	3	3	158.37		Uncharacterized protein
K4BMT5	3	2	37.16		Uncharacterized protein
K4D7F1	13	5	722.68		Uncharacterized protein
K4BKD8	6	1	185.56		Uncharacterized protein
K4CHA9	5	1	47.64		Uncharacterized protein
K4CP92	7	6	142.27		Glutathione peroxidase
K4CJE2	10	2	203.17		60S ribosomal protein L18a
K4CBF0	21	13	677.28		Acetyltransferase component of pyruvate dehydrogenase complex
K4C1G0	2	2	67.64		Uncharacterized protein
K4B7H7	5	4	146.75		Uncharacterized protein
K4D9W7	5	4	551.21		Uncharacterized protein
K4DA61	3	3	96.02		Uncharacterized protein
K4CJ79	4	1	39.38		Uncharacterized protein
Q6EAL9	5	5	178.67		Arachidonic acid-induced DEA1
K4D5S8	6	1	88.71		Uncharacterized protein
P24157	8	1	184.95		1-aminocyclopropane-1-carboxylate oxidase 4
K4CAH3	11	4	541.68	Yes	40S ribosomal protein S8
K4C2V5	16	10	446.6		T-complex protein 1 subunit gamma
K4BXD4	16	8	710.97		Uncharacterized protein
K4B935	4	2	109.6		Uncharacterized protein
K4CKX4	17	5	953.75		Uncharacterized protein
K4D482	5	3	83.29		Uncharacterized protein
Q672Q3	6	6	280.97		Uncharacterized protein
K4BJA2	2	2	62.59		Uncharacterized protein
K4ATQ2	13	7	425.25		Uncharacterized protein

K4D3Y9	21	4	1738.95		Uncharacterized protein
K4BAZ4	15	1	1063.55		Peroxidase
K4D616	13	4	423.85		Uncharacterized protein
K4C6I9	2	2	40.95		Uncharacterized protein
K4BMK3	3	3	42.66		Uncharacterized protein
K4B891	4	4	139.39		Uncharacterized protein
P21568	15	7	851.61		Peptidyl-prolyl cis-trans isomerase
K4D2Y4	8	7	192.84		Uncharacterized protein
K4BTQ4	4	2	80.15		Uncharacterized protein
K4C245	7	1	178.91		Uncharacterized protein
K4B8M7	3	1	29.36		Non-specific serine/threonine protein kinase
K4BJR2	2	2	45.84		Uncharacterized protein
P20076	4	4	239.96		Ethylene-responsive proteinase inhibitor 1
P30264	28	15	1777.92		Catalase isozyme 1
K4CVQ4	12	10	412.79		Uncharacterized protein
K4BEX6	2	2	27.04		Uncharacterized protein
K4BU61	8	4	84.46		Uncharacterized protein
K4BE00	5	1	380.28		Uncharacterized protein
K4CMG1	5	3	124.08		Uncharacterized protein
Q8RU74	8	5	258.95		3-dehydroquinate synthase, chloroplastic
K4DDA8	4	1	23.78		Uncharacterized protein
K4D3L7	5	4	235.41		Uncharacterized protein
K4BPJ0	27	9	1092.64		Uncharacterized protein
K4ASG5	2	2	28.59		Uncharacterized protein
P17786	25	3	1845.04		Elongation factor 1-alpha
K4BPM8	1	1	53.92		Uncharacterized protein
K4BFN4	3	2	55.3		Uncharacterized protein
A8WBX7	2	1	36.82		Mevalonate disphosphate decarboxylase
K4B7E7	4	4	247.39		Uncharacterized protein
K4CVW4	5	2	136.07		Uncharacterized protein
K4D518	1	1	40.02		Uncharacterized protein
K4B8G4	5	2	138.46	Yes	Histidinol dehydrogenase, chloroplastic
K4D1B5	3	2	64.15		Uncharacterized protein
K4B318	2	1	36.83		Uncharacterized protein
K4CNT3	2	2	48.3		Uncharacterized protein
K4D9Y0	3	1	36.72		Uncharacterized protein
K4CU73	8	7	526.05		Uncharacterized protein
K4BU57	5	3	348.8		Uncharacterized protein
K4C241	11	2	423.55		Uncharacterized protein
K4BTI7	1	1	53.03		Uncharacterized protein
K4BV66	5	1	58.75	Yes	Uncharacterized protein
K4BDD0	5	2	74.39		Uncharacterized protein
K4DC13	8	7	208.46		Uncharacterized protein
K4C858	2	2	33.58		Uncharacterized protein
K4D5D1	2	1	34.25		Uncharacterized protein

K4AXX0	2	1	96.4		Uncharacterized protein
Q8H0Q2	5	3	129.06		Hexokinase
K4CBV6	14	6	653.79		Uncharacterized protein
K4C950	13	3	782.03		Uncharacterized protein
K4D5I0	8	3	297.15		Uncharacterized protein
K4CAS6	9	7	273.31		Uncharacterized protein
K4AT29	7	6	94.15		Uncharacterized protein
K4B110	14	9	614.35		26S protease regulatory subunit 6A homolog
Q8H272	8	6	260.22		Metacaspase 1 (Fragment)
K4BBN7	6	2	148		Uncharacterized protein
K4BNT3	10	7	616.96		Uncharacterized protein
K4DCD9	6	1	130.87		Uncharacterized protein
K4D8S6	19	16	827.06		Uncharacterized protein
K4D6I9	10	7	158.13		Uncharacterized protein
D1MAF2	9	7	131.96		Exportin-1
K4CHY8	1	1	43.35		Defective in cullin neddylation protein
K4CLQ6	5	2	93.91		Phospholipase D
K4DHT1	16	4	613.27		Dihydrolipoyl dehydrogenase
K4B9T8	3	1	23.77		Uncharacterized protein
K4C977	10	9	323.55		Uncharacterized protein
K4BB18	6	2	120.52		Uncharacterized protein
K4CEK6	6	4	201.97		Uncharacterized protein
K4D557	3	2	67.59		Uncharacterized protein
K4BKB2	22	3	920.65	Yes	Uncharacterized protein
K4AT78	2	1	63.2		Uncharacterized protein
K4C753	2	2	31.44	Yes	Uncharacterized protein
K4D338	55	33	4915.2		Uncharacterized protein
K4BF00	7	5	339.95		Uncharacterized protein
K4CM58	3	2	105.13		Eukaryotic translation initiation factor 3 subunit L
Q38JD4	4	1	69.32		Temperature-induced lipocalin
K4CP13	7	6	172.69		Phospholipase D
K4D2B6	5	4	170.44		Uncharacterized protein
E7EC27	6	4	398.51		Aquaporin
K4C8U3	4	2	158.04		Uncharacterized protein
K4C1T2	50	9	2157.17		Clathrin heavy chain
K4BSK2	4	4	146.64		Uncharacterized protein
K4C1B2	2	1	60.96		Uncharacterized protein
K4CW15	2	1	115.64		Uncharacterized protein
K4CLA3	9	6	193.72		Uncharacterized protein
K4CAB5	4	1	36.21		Uncharacterized protein
K4CB99	1	1	60.01		Uncharacterized protein
K4C4W6	35	4	1957.65		Uncharacterized protein
K4BJW4	15	4	722.01		Glyceraldehyde-3-phosphate dehydrogenase
K4DA30	3	2	88.09		Uncharacterized protein
K4DFF9	9	7	234.41		Ubiquitin carboxyl-terminal hydrolase

K4BMW3	10	2	234.96		Uncharacterized protein
K4AVB7	17	13	906.52		Uncharacterized protein
K4BIB1	7	3	51.02		Uncharacterized protein
K4BTE8	2	2	24.71		Uncharacterized protein
Q66MH9	4	1	37.54		MAPKK
K4CGT2	4	1	148.6		Uncharacterized protein
K4CP66	5	3	185.68		Uncharacterized protein
K4BAZ3	18	4	1125.46		Peroxidase
K4C5A8	7	5	88.72		Uncharacterized protein
K4BPV5	18	9	1433.13		Glutamine synthetase
K4BZ35	5	2	220.04		Uncharacterized protein
K4CA71	7	4	299.48		Uncharacterized protein
K4CPC9	14	12	460.42		Uncharacterized protein
K4BNL9	6	2	190.11		Uncharacterized protein
Q2VY17	1	1	30.48		CONSTANS interacting protein 2b
K4C6Y1	5	3	55.12		Uncharacterized protein
K4CX11	1	1	22.38		Uncharacterized protein
K4C2I3	3	1	38.74		Serine/threonine-protein phosphatase
K4AYT8	8	3	656.57		Nucleoside diphosphate kinase
K4BMT2	8	5	192.32		Uncharacterized protein
K4CC45	2	1	89.1		Uncharacterized protein
K4BG30	10	6	464.05		Peroxidase
K4B3Q2	4	4	157.39		Uncharacterized protein
K4B876	6	1	341.25		Uncharacterized protein
K4D444	5	5	407.29		Uncharacterized protein
K4BB54	2	2	39.58		Uncharacterized protein
K4B381	5	4	143.38		N-acetyl-gamma-glutamyl-phosphate reductase
K4D5U3	20	13	1355.33		Glutamine synthetase
K4BDD3	2	2	38.04		Uncharacterized protein
K4BMH6	11	2	367.77		Uncharacterized protein
K4B331	1	1	27.57		Uncharacterized protein
K4C3V9	9	2	163.52		Uncharacterized protein
K4CAC3	2	2	53.25		Uncharacterized protein
K4AXM7	3	2	77.12		Uncharacterized protein
K4BKE0	2	1	35.24		Uncharacterized protein
K4CSA9	12	9	348.61		Uncharacterized protein
Q2MIA4	1	1	40.97		Photosystem II CP43 reaction center protein
K4ATA6	5	5	126.91		Uncharacterized protein
K4DC84	10	5	210.68		Uncharacterized protein
K4DDC7	1	1	42.3		Uncharacterized protein
K4CX85	4	2	67.72		Uncharacterized protein
K4CFR7	5	5	105.2		Uncharacterized protein
K4CAL7	13	9	500.51		Uncharacterized protein
K4BXC7	8	4	253.74		Uncharacterized protein
K4B1H9	6	3	58.03		Uncharacterized protein

K4C630	2	2	49.37		Uncharacterized protein
K4BL13	17	12	817.48		Uncharacterized protein
K4C3B5	16	11	515.56		Uncharacterized protein
K4C715	8	1	256.54		Uncharacterized protein
K4CMI6	32	8	1262.92		Uncharacterized protein
K4B831	3	1	76.27		Uncharacterized protein
K4AWU1	1	1	25.82		Uncharacterized protein
K4DBU5	13	6	158.47		Uncharacterized protein
K4AWT6	4	3	100.86		Uncharacterized protein
K4C5M1	10	5	457.74		Uncharacterized protein
K4BTH6	23	16	1579.55		Peroxidase
K4B419	2	1	32.28	Yes	Uncharacterized protein
K4B6E2	1	1	24.04		Uncharacterized protein
K4CM99	2	1	70.25		Uncharacterized protein
K4BJY3	8	2	343.07	Yes	Uncharacterized protein
K4CVT4	13	9	339.65		Uncharacterized protein
K4D6I5	7	2	80.09		Nitrate reductase
K7T8S0	7	1	125.54	Yes	Eukaryotic translation initiation factor iso4G
K4BJE6	15	6	458.41		Alanine--tRNA ligase
K4BK61	17	7	502.63		Uncharacterized protein
K4CMJ7	7	5	230.34		Eukaryotic translation initiation factor 3 subunit G
B5M9E4	7	5	226.63		Beta-glucosidase 01
G8Z246	3	2	58.63	Yes	Hop-interacting protein THI002
K4C745	11	6	406.19		Uncharacterized protein
K4BI70	9	6	326.1		Uncharacterized protein
K4C3H8	5	2	168.76		Uncharacterized protein
K4BKM5	3	1	48.68		Uncharacterized protein
K4BMJ6	9	1	402.96		Uncharacterized protein
K4DC28	4	4	42.63		Pyruvate dehydrogenase E1 component subunit alpha
K4B3R6	3	1	40.27		Uncharacterized protein
K4CXT9	6	2	127.47		Uncharacterized protein
K4B1L6	5	3	141.28		Uncharacterized protein
K4CZ51	2	1	24.08		Uncharacterized protein
K4CTL7	5	2	141.73		Uncharacterized protein
K4C7G6	2	2	66.79		Uncharacterized protein
K4CQ60	2	2	45.52		Uncharacterized protein
K4BD54	16	14	1020.09		Peroxidase
K4BDF9	8	4	169.82		Uncharacterized protein
K4C9J1	4	1	43.04		Protein argonaute
K4BMY9	10	3	300.41		Uncharacterized protein
K4BF54	5	3	53.55		Uncharacterized protein
K4CGB4	3	1	32.72		Uncharacterized protein
P93207	21	9	1118.67		14-3-3 protein 10
K4CXX8	8	4	304.68		Proteasome subunit alpha type
K4CCB4	1	1	57.59		Uncharacterized protein

K4CMI0	4	2	74.38		Uncharacterized protein
K4BP76	5	4	48.15		Uncharacterized protein
K4B3Z2	9	7	643.79		Uncharacterized protein
K4BVE0	6	1	82.37		Uncharacterized protein
K4BUN4	7	3	410.72		Uncharacterized protein
K4DHP7	4	2	44.1		Uncharacterized protein
K4CBS3	5	2	63.87		Uncharacterized protein
K4DH05	2	1	24.59		Vacuolar protein sorting-associated protein 35
K4BL65	4	3	75.38		Uncharacterized protein
K4BX20	39	5	3073.32		ATP synthase subunit beta
K4AXH0	4	1	67.45	Yes	Uncharacterized protein
K4D9T0	4	1	33.67		Uncharacterized protein
K4B9V1	4	3	153.58		Aminomethyltransferase
K4B101	12	2	391.41		Uncharacterized protein
K4BIP4	2	1	20.35		Mago nashi protein
K4DH73	31	3	1688.32		Uncharacterized protein
K4BFU0	17	1	1042.55		Uncharacterized protein
Q9M5A8	8	6	234.94		Chaperonin 21
K4BF11	2	2	91.94		Peroxidase
K4BEV0	11	3	790.61		40S ribosomal protein SA
K4BDI6	7	2	214.89		Uncharacterized protein
K4B4Z0	6	3	238.34		Uncharacterized protein
B1N678	2	2	72.52		Defensin protein
A0A097PLA9	9	8	281.5		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (Fragment)
K4CV66	3	2	108.47		Uncharacterized protein
K4B6J6	16	2	455.65		Uncharacterized protein
K4AVW3	2	1	38.45		Uncharacterized protein
K4B438	26	4	1728.56		Uncharacterized protein
K4CHF9	7	4	317.83		Uncharacterized protein
K4DHE3	14	1	717.11		Uncharacterized protein
K4B3E8	3	2	30.77		Uncharacterized protein
Q8H6B5	7	5	194.46		Putative dehydrogenase
K4C4L0	5	1	71.15		Glutamate dehydrogenase
K4BVQ3	5	2	48.51		Uncharacterized protein
K4C9W3	35	1	2270.57		Uncharacterized protein
K4BA40	7	6	522.43		Proteasome subunit alpha type
K4BF36	2	1	34.15		Uncharacterized protein
K4CC14	6	4	139.45		Uncharacterized protein
K4BXT9	2	2	41.57		Uncharacterized protein
K4D4V8	7	4	157.04		Uncharacterized protein
K4CK38	1	1	25.5		Uncharacterized protein
K4ASG1	7	3	121.92		Serine/threonine-protein phosphatase
K4C2X3	2	1	31.23		Uncharacterized protein
K4BX96	9	2	153.21		Uncharacterized protein

K4BSI6	2	2	47.41		Uncharacterized protein
K4CNS8	2	1	73.91		Uncharacterized protein
Q9LEG3	8	6	523.71		Putative alcohol dehydrogenase
K4CAN7	11	3	402.58		Uncharacterized protein
K4AYJ8	8	7	270.08		Uncharacterized protein
K4ASG2	6	1	157.02		Uncharacterized protein
K4CMU5	4	2	87.41		Uncharacterized protein
K4CA80	1	1	33.82		Uncharacterized protein
K4DD79	16	11	526.98		Uncharacterized protein
Q93YH0	2	1	56.79		ATP-dependent Clp protease proteolytic subunit
Q94FW7	1	1	26.28		Heme oxygenase 1
K4CND0	4	4	176.59		Uncharacterized protein
K4B139	5	2	44.39	Yes	Uncharacterized protein
E5KBY0	2	2	87.11		Snakin-2
K4DDG8	3	2	25.38		Uncharacterized protein
K4CB49	3	1	36.22	Yes	Uncharacterized protein
K4AQH2	5	4	228.98		Uncharacterized protein
K4B3Q4	4	2	87.59		Uncharacterized protein
K4BS97	9	4	142.76		Uncharacterized protein
K4DF31	2	1	42.89		Uncharacterized protein
K4BVZ8	3	1	91.58		Uncharacterized protein
K4D5E7	26	15	1079.46		Methylenetetrahydrofolate reductase
Q6UJX4	45	6	2631.36		Molecular chaperone Hsp90-1
K4BDH8	6	1	36.99		Uncharacterized protein
K4BNR2	39	5	3033.44		ATP synthase subunit beta
K4CGT6	25	2	604.78		Uncharacterized protein
K4CJB4	14	3	593.53		Uncharacterized protein
K4D4F0	2	1	58.18		Uncharacterized protein
K4D9K1	9	1	67.83		Uncharacterized protein
K4D443	2	1	160.83		Uncharacterized protein
K4C9L7	9	3	289.79		Uncharacterized protein
K4CAI5	7	3	249.28		Uncharacterized protein
K4D7D0	2	2	140.63		Uncharacterized protein
A1X875	4	1	47.88		Putative nuclear GTPase
K4BCY6	2	2	100.74		Uncharacterized protein
K4BRG8	22	17	840.97		Uncharacterized protein
K4D7X4	14	6	909.78		Uncharacterized protein
K4CHP7	4	1	55.98		Uncharacterized protein
K4BCK6	8	5	106.47		Uncharacterized protein
Q41340	4	1	168.92		Small GTP-binding protein
K4D5Q6	2	1	54.28		Uncharacterized protein
K4CWV7	2	1	65.41		Uncharacterized protein
K4DHN6	5	1	55.93		Kinesin-like protein
K4BB06	7	7	457.87		Proteasome subunit beta type
Q5NE20	3	2	141.57		Carbonic anhydrase

P07179	6	2	195.16		Ribulose biphosphate carboxylase small chain 2A, chloroplastic
K4BXU9	7	3	116.28		Purple acid phosphatase
P54928	2	1	62.31		Inositol monophosphatase 3
K4CFS8	14	1	565.55		Uncharacterized protein
Q2MI91	6	4	214.41		Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic
K4BB89	3	1	35.78		Uncharacterized protein
K4C2K2	1	1	52.51		Uncharacterized protein
K4CWX0	5	1	106.04		Uncharacterized protein
K4BEU4	2	1	39.89		Uncharacterized protein
K4BT41	2	1	59.54		Uncharacterized protein
K4B3J8	14	10	535.78		Uncharacterized protein
K4CL64	31	3	1578.66		Uncharacterized protein
K4BU29	4	4	212.19		40S ribosomal protein S21
Q40164	8	1	464.02		Ubiquitin
K4DHQ5	3	1	181.08		Uncharacterized protein
K4BSC6	5	1	36.41		Uncharacterized protein
K4C1Z4	6	2	131.17		Uncharacterized protein
Q9AXQ3	11	3	410.01		Eukaryotic translation initiation factor 5A-4
K4CL50	14	11	228.41		Uncharacterized protein
Q4PS96	4	3	93.49		Plastidic hexokinase
K4B9E5	2	1	36.3		Uncharacterized protein
K4AYP7	1	1	43.9		Acyl carrier protein
K4D4E6	36	1	2379.22		Uncharacterized protein
K4BNL7	8	1	322.36		Uncharacterized protein
K4CJX8	4	3	149.87		Uncharacterized protein
K4DC02	13	11	617.94		Proteasome subunit alpha type
K4AZQ9	3	1	61.75		Reticulon-like protein
K4BZA6	4	2	74.4		NADH-cytochrome b5 reductase
Q53U42	4	4	139.25		Similar to aquaporin
V5YN05	12	2	830.46		Plasmamembrane intrinsic protein 15
K4B1L7	5	1	287.83		Uncharacterized protein
K4CKC6	2	1	58.46		Uncharacterized protein
K4C7M6	2	1	32.11		Uncharacterized protein
K4CB59	7	3	63.38		Uncharacterized protein
K4D2T4	3	2	92.36		Uncharacterized protein
K4BLV2	26	1	896.26		Uncharacterized protein
K4BRZ6	4	3	51.39		Uncharacterized protein
K4B1G1	4	3	147.24		Uncharacterized protein
K4BA70	11	5	575.58		Uncharacterized protein
K4C3D8	12	3	522.45		40S ribosomal protein S8
K4C7E6	5	1	32.03		Uncharacterized protein
K4BW47	5	1	127.85	Yes	Uncharacterized protein
K4BK43	9	9	181.6		Uncharacterized protein
P26300	32	15	2586.33		Enolase

K4AYM7	11	7	403.67		Eukaryotic translation initiation factor 3 subunit B
K4AX99	12	1	554.73		Uncharacterized protein
K4C947	14	11	551.75	Yes	Uncharacterized protein
K4AZ08	2	1	29		Uncharacterized protein
K4B3K7	8	4	359.82		Uncharacterized protein
K4C2H5	5	1	55.49		Uncharacterized protein
K4CWZ8	3	2	156.96		Eukaryotic translation initiation factor 3 subunit H
K4AT92	21	9	619.6		AGO4A
K4D2R0	4	1	90.6		Uncharacterized protein
K4BD39	5	1	182.73		Uncharacterized protein
K4B0X2	8	5	123.14		Uncharacterized protein
K4CPI7	12	3	399.8		Uncharacterized protein
K4CW86	14	10	490.22		Uncharacterized protein
K4DH53	5	2	60.64		Uncharacterized protein
K4BVR7	2	2	63.05		Uncharacterized protein
K4D3G9	3	1	39.44		Uncharacterized protein
K4CY71	9	1	175.74		Uncharacterized protein
V5YNW6	6	4	384.75		Plasmamembrane intrinsic protein 21
K4BHG4	6	4	218.81		Alpha-1,4 glucan phosphorylase
K4DFV3	10	2	619.85		Plasmamembrane intrinsic protein 13
H1ZXA9	28	3	1867.32		Heat shock protein 70 isoform 3
K4D5C8	5	3	67.26		Acyl-[acyl-carrier-protein] desaturase
K4D955	3	3	76.22		Uncharacterized protein
Q9SAN2	3	1	79.83		P69D protein
Q1PCD2	3	2	72.92		Glucose-6-phosphate isomerase
Q9AXQ4	11	2	375.58		Eukaryotic translation initiation factor 5A-3
Q9XGY1	2	2	191.81		Small zinc finger-like protein
K4AUB9	4	4	48.6		Uncharacterized protein
Q9AXQ5	9	3	256.76		Eukaryotic translation initiation factor 5A-2
K4ATF7	1	1	79.7		Uncharacterized protein
Q2MIC0	2	2	114.93		Photosystem II protein D1
K4D7U2	9	5	191.59		Uncharacterized protein
K4D027	2	2	127.42		Uncharacterized protein
K4B407	15	12	545.85		Proteasome subunit alpha type
K4C7N4	10	2	295.97		Uncharacterized protein
K4D3L8	4	1	77.38		Uncharacterized protein
K4AYW0	6	5	185.38		Uncharacterized protein
K4C263	3	3	87.72		Uncharacterized protein
K4CD72	4	2	32.17		Uncharacterized protein
K4DF88	12	3	307.88		Uncharacterized protein
K4D3J8	6	1	337.35		Plasmamembrane intrinsic protein 25
K4C9J5	8	2	344.26		Histone H2B
K4BR52	10	2	409.95		Uncharacterized protein
K4CYM9	2	1	49.29		Uncharacterized protein
K4BW14	18	3	697.07		Uncharacterized protein

K4AW95	14	2	722.74		Uncharacterized protein
K4D8V2	2	1	62.39		Uncharacterized protein
K4BGN7	1	1	28.33		Uncharacterized protein
K4CHY4	13	4	541.35		Phosphoglycerate kinase
K4BNP7	1	1	31.63		Uncharacterized protein
K4DA24	7	3	167.59		Uncharacterized protein
K4D452	13	6	798.37		Uncharacterized protein
K4B8C0	4	1	51.06	Yes	Uncharacterized protein
K4BTC7	6	1	46.57		Uncharacterized protein
Q6R8F6	5	5	150.93		Cystathionine gamma synthase
K4B2L1	6	1	203.51	Yes	Uncharacterized protein
K4BRS2	15	9	510.63		Protein disulfide-isomerase
K4DAU1	3	2	79.9		Uncharacterized protein
K4DCI6	4	2	90.22		Citrate synthase
K4CWE4	29	11	1226.53		Uncharacterized protein
K4BF07	4	3	62.88		Uncharacterized protein
K4CK76	9	5	183.06		Delta-1-pyrroline-5-carboxylate synthase
K4CCK0	5	1	80.62		Uncharacterized protein
K4BA95	7	3	223.78		Thioredoxin reductase
K4B1G9	12	6	248.72		Uncharacterized protein
K4CXP8	5	4	124.73		Uncharacterized protein
K4AV57	4	4	113.42		Uncharacterized protein
K4BL51	2	1	46.49		Uncharacterized protein
P27161	5	1	440.82		Calmodulin
K4BML9	6	2	49.01		Uncharacterized protein
K4CXV5	5	5	89.81		Uncharacterized protein
K4B8P9	7	3	45.52		Uncharacterized protein
K4B378	7	1	206.33		Uncharacterized protein
K4CG68	5	1	160.93		Uncharacterized protein
K4C8V0	13	3	327.41		Protein argonaute
K4BSG5	1	1	46.81		Uncharacterized protein
K4B428	2	2	62.01		Plasmamembrane intrinsic protein 28
P27065	8	7	363.38		Ribulose biphosphate carboxylase large chain
K4C9N7	2	1	22.95		Uncharacterized protein
K4DAZ1	13	11	741.27		Histone H4
K4BKN1	4	4	59.95		Uncharacterized protein
K4BA00	6	1	56.05		Uncharacterized protein
K4BDC5	4	2	66.03		Uncharacterized protein
K4BLW8	8	3	251.64		Uncharacterized protein
K4CLS8	10	7	330.99		Cytochrome b-c1 complex subunit 7
K4CUE6	6	3	83.51		Uncharacterized protein
K4BFH1	6	2	173.96		Thioredoxin reductase
K4AQU9	5	3	53.66		Uncharacterized protein
K4BU44	2	2	54.96		Uncharacterized protein
K4AYE4	7	7	429.93		Uncharacterized protein

O24025	1	1	47.1		PR protein
K4CPR6	6	6	332.11		Uncharacterized protein
K4C6W6	2	2	49.43		Uncharacterized protein
K4DD89	15	4	646.14	Yes	Uncharacterized protein
K4B464	3	1	35.89		Uncharacterized protein
K4BM57	6	2	253.73		Uncharacterized protein
K4D787	4	2	39.83		Uncharacterized protein
K4DH88	8	2	314.25		60S ribosomal protein L13
K4C203	4	1	181.73		Uncharacterized protein
K4BOR5	3	3	88.65		Uncharacterized protein
K4CEU2	6	2	215.42		Uncharacterized protein
K4CMQ6	6	1	107.34		Uncharacterized protein
K4C998	10	1	388.49		Uncharacterized protein
K4CNG6	6	3	184.52		Uncharacterized protein
K4B9Q0	3	2	33.34		Uncharacterized protein
Q42891	4	3	131.33		Lactoylglutathione lyase
K4CQE1	5	1	158.92		Peroxidase
K4CXI7	4	1	149.8		Histone H2A
K4BEW2	2	2	58.34		Serine/threonine-protein phosphatase
K4CAM4	3	2	29.48		Uncharacterized protein
K4B2V0	3	1	36.58		Uncharacterized protein
K4BP97	3	1	120.7		Proteasome subunit beta type
K4CB52	8	1	101.73		Uncharacterized protein
K4AT35	6	6	287.33		Uncharacterized protein
K4C2B0	4	1	60.75		Uncharacterized protein
K4C3A3	11	1	537.59		Uncharacterized protein
K4DH19	11	7	484.79		Uncharacterized protein
K4DCV6	4	2	114.83		Uncharacterized protein
K4BJI5	9	3	355.69		Uncharacterized protein
K4DAS7	8	6	144.84		Uncharacterized protein
K4DF90	5	1	120.3		Uncharacterized protein
K4CW69	5	4	228.71		Cyanate hydratase
K4DH95	16	4	507.25		Uncharacterized protein
K4CFU2	5	3	120.08		Uncharacterized protein
K4DFF7	1	1	23.39		Uncharacterized protein
K4AXJ5	3	2	22.39		DNA helicase
K4ASC2	24	9	2011.45		Isocitrate dehydrogenase [NADP]
K4BLK6	7	2	56.47		Uncharacterized protein
K4C8I8	1	1	24.52		Uncharacterized protein
K4AVE9	4	3	110.98		Uncharacterized protein
K4CJH4	14	3	804.55		Proteasome subunit alpha type
K4BZB6	4	3	44.2		Uncharacterized protein
K4B753	6	4	74.99		Uncharacterized protein
K4BXJ9	10	6	462.8		Uncharacterized protein
K4CAS8	6	2	243.61		40S ribosomal protein S24

K4D304	6	1	591.39		Uncharacterized protein
K4B3R5	3	1	58.14		Amidophosphoribosyltransferase
K4CMT6	10	7	328.44		Uncharacterized protein
K4BM62	7	5	187.27		Uncharacterized protein
K4BJL4	1	1	53.6		Uncharacterized protein
K4CGU0	6	2	210.01		Fen-interacting protein 3
K4CHA5	1	1	60.57		Uncharacterized protein
K4BW97	11	1	442.82		Uncharacterized protein
K4C192	10	2	216.17		Uncharacterized protein
K4B9R3	6	1	123.89		Uncharacterized protein
K4ASJ5	3	2	120.53		Peroxidase
K4DHM2	21	3	1037.1		Serine hydroxymethyltransferase
K4ARN4	3	2	27.71		Uncharacterized protein
K4B7K6	4	4	165.06		Uncharacterized protein
K4C0T5	15	2	873.57		Peroxidase
K4BY59	1	1	46.24		Uncharacterized protein
K4CUW3	11	10	468.58		Uncharacterized protein
K4BVG7	6	3	170.44		Uncharacterized protein
K4DFV4	2	1	68.68		Glutathione peroxidase
K4B0H4	5	1	201.78		40S ribosomal protein S24
K4BFL6	6	1	310.38		Uncharacterized protein
Q6IV07	22	5	1038.68		UDP-glucose:protein transglucosylase-like protein SIUPTG1
K4B1K6	7	4	93.01		Uncharacterized protein
K4B6Q6	4	1	50.55		Uncharacterized protein
K4BJD2	3	2	91.57		Inositol-tetrakisphosphate 1-kinase
K4B813	5	2	243.25		Uncharacterized protein
K4BLB3	2	2	89.36		Uncharacterized protein
K4D1R3	3	1	102.76		Uncharacterized protein
K4CBY0	3	3	121.2		Uncharacterized protein
K4B8U2	2	1	32.98		Uncharacterized protein
K4CQP7	3	2	56.39		Uncharacterized protein
K4CQE3	15	6	148.49		Uncharacterized protein
K4D4F5	10	7	280.98		Uncharacterized protein
K4C7I8	9	1	184.23		60S ribosomal protein L18a
K4B6X9	4	2	144.82		Uncharacterized protein
K4CV90	3	2	83.24		Uncharacterized protein
K4C242	3	3	50.5		Uncharacterized protein
K4CFD4	43	22	2221.77		Aconitate hydratase
K4B2Z1	4	1	50.81		Uncharacterized protein
K4B1Z2	11	9	717.2		Uncharacterized protein
K4CU87	2	1	36.01	Yes	Uncharacterized protein
K4C868	3	1	60.8		Uncharacterized protein
K4CX56	2	2	59.12		Uncharacterized protein
K4BK46	4	1	49.32		Uncharacterized protein

K4DGX0	5	2	80.61		Uncharacterized protein
K4DA71	4	3	155.77		Proteasome subunit beta type
K4CJ99	9	4	322.16		Uncharacterized protein
K4ATE8	8	1	363.38		Ribosomal protein
K4BUK4	4	3	62.31		Uncharacterized protein
K4BSK3	11	6	95.72		Uncharacterized protein
K4AVF0	2	1	30.01		Uncharacterized protein
K4D6E4	2	2	24.59		Uncharacterized protein
K4M461	17	1	378.3		Protein argonaute
K4BOH5	1	1	40.84		Uncharacterized protein
K4BJ57	2	1	111.45		Uncharacterized protein
A0A097	2	2	92.92		Homoserine kinase (Fragment)
K4D9U0	2	2	50.24		Uncharacterized protein
Q96569	5	3	147.91		L-lactate dehydrogenase
K4CGU8	20	15	1805.28		Malate dehydrogenase
K4B276	6	4	246.27		Uncharacterized protein
K4C398	4	1	36.85		Uncharacterized protein
K4BM85	11	3	447.13		Uncharacterized protein
K4B9D0	3	2	75.81		Eukaryotic translation initiation factor 3 subunit J
Q9FV21	5	2	100.08		Aldehyde oxidase (Fragment)
K4BIC8	6	1	258.93		Uncharacterized protein
K4C7D0	1	1	41.06	Yes	Uncharacterized protein
K4DA57	18	13	639.9		Uncharacterized protein
K4D2H3	3	2	59.01		Uncharacterized protein
K4CC51	1	1	28.35		Uncharacterized protein
K4CCM6	3	1	113.76		Uncharacterized protein
K4BD40	6	2	116.66		Uncharacterized protein
K4BIA5	4	1	276.85		40S ribosomal protein S12
K4D3T6	35	1	2135.38		Uncharacterized protein
K4CAU9	4	3	52.66		Uncharacterized protein
K4BK27	5	2	61.27		Uncharacterized protein
K4AZY6	9	1	176.83		Uncharacterized protein
K4CLI8	3	1	86.6		Uncharacterized protein
Q9XG54	2	2	34.59		12-oxophytodienoate reductase 1
K4B264	8	5	149.52		Uncharacterized protein
K4C882	11	3	554.03		Uncharacterized protein
K4DEV8	5	1	102.63		Uncharacterized protein
K4B307	9	2	574.12		Uncharacterized protein
K4D463	2	1	71.41		Uncharacterized protein
K4BD93	4	1	124.31		Uncharacterized protein
K4BHX0	2	1	51.65		Uncharacterized protein
K4CET1	5	4	139.99		Uncharacterized protein
K4C952	8	3	182.36		Lysine--tRNA ligase
A9LRT7	15	5	378.12		Isopentenyl diphosphate isomerase
K4DI03	3	2	35.01		Signal recognition particle 9 kDa protein

K4D0P0	3	1	36.59		Uncharacterized protein
K4D5K8	19	7	819.04		Uncharacterized protein
K4B1B7	12	1	629.82		Uncharacterized protein
K4BDK7	3	3	111.36		Uncharacterized protein
K4BYG6	32	16	2453.9		Glyceraldehyde-3-phosphate dehydrogenase
K4AWR0	1	1	22.94		Uncharacterized protein
K4BS82	7	3	156.44		Uncharacterized protein
K4AZC8	4	2	40.53		ATPase ASNA1 homolog
K4CKP3	10	3	211.46		Uncharacterized protein
K4D3Y2	6	1	231.1		Uncharacterized protein
K4BU45	6	1	42.22		Uncharacterized protein
K4B832	14	3	728.87		Proteasome subunit alpha type
K4CBP6	3	3	116.86		Uncharacterized protein
K4C8M5	7	1	150.55		Uncharacterized protein
K4BFE4	7	1	203.5		Uncharacterized protein
Q93YG7	5	2	187.4		Profilin-2
K4BWQ2	1	1	38.61		Ribulose-phosphate 3-epimerase
K4C4N6	3	2	92.96		Uncharacterized protein
K4D2J1	6	3	108.79		Inosine-5'-monophosphate dehydrogenase
K4BC25	21	13	627.47		Uncharacterized protein
K4C8X8	10	5	467.5		Uncharacterized protein
K4BTX8	1	1	27.17		Uncharacterized protein
K4CLT6	7	5	172.79		Uncharacterized protein
K4C2Q2	5	3	83.75		Uncharacterized protein
K4C8Y0	1	1	67.89		Uncharacterized protein
K4BB47	9	5	465.82		Uncharacterized protein
K4DF79	2	2	95.46		Uncharacterized protein
K4BBU4	21	1	1547.02		Uncharacterized protein
K4CR79	2	2	29.26		Uncharacterized protein
K4BKLO	3	2	150.82		Uncharacterized protein
K4BAN8	5	1	43.01		Alpha-mannosidase
K4JB9	4	2	41.44		Uncharacterized protein
K4C8B3	3	3	126.59		Uncharacterized protein
K4BYW1	10	6	183.17		Glucose-6-phosphate 1-dehydrogenase
K4BSH5	3	2	81.98		Uncharacterized protein
K4CNH9	14	1	335.04		Uncharacterized protein
K4B303	13	11	557.48		Uncharacterized protein
A0A060	1	1	25.56		Sugar-porter family protein 4
K4BJC4	12	7	232.59		Uncharacterized protein
K4B033	15	12	710.39		Uncharacterized protein
K4CA81	4	2	105		Uncharacterized protein
K4AZZ5	9	4	162.94		Uncharacterized protein
K4BAY1	3	2	58.37		Uncharacterized protein
A8Y6N6	5	1	101.67		ATP synthase subunit beta (Fragment)
K4BRK5	2	1	35.71		Uncharacterized protein

K4CQ30	3	3	115.23		Uncharacterized protein
K4DB31	5	2	331.91		Histone H2A
K4BQ85	18	10	515.18		Uncharacterized protein
Q2MIB5	9	3	243.53		ATP synthase subunit alpha, chloroplastic
K4CAJ9	2	1	123.67		Uncharacterized protein
K4D5Q9	5	4	49.39		Uncharacterized protein
K4C7I1	12	9	503.7		Uncharacterized protein
K4C286	11	2	289.17		Uncharacterized protein
K4AUD4	1	1	38.41		Uncharacterized protein
K4CEP2	26	21	1174.8		Uncharacterized protein
Q9SDZ6	16	11	482.62		Phospholipase D alpha (Fragment)
K4CR48	1	1	62.56		CASP-like protein
K4C874	22	4	1316.46		Uncharacterized protein
Q8SA58	2	2	50.19		Putative uncoupling protein
K4BK00	2	2	28.94		Uncharacterized protein
K4B9Y6	24	16	1132.73		Uncharacterized protein
K4CTF7	4	1	130.37		Uncharacterized protein
K4CP24	3	1	50.1		Uncharacterized protein
K4BJB8	2	1	24.96		Uncharacterized protein
K4B3H5	3	1	49.8		Uncharacterized protein
K4BN81	7	3	195.64		Uncharacterized protein
K4BA10	3	2	159.47		Uncharacterized protein
K4CQ71	5	1	74.13		Uncharacterized protein
K4CN15	2	2	66.96		Uncharacterized protein
K4CXU9	7	7	215.66		Uncharacterized protein
K4B937	7	4	119.49		Eukaryotic translation initiation factor 3 subunit D
K4CVC2	5	3	80.5		Uncharacterized protein
K4D465	7	2	185.59		Uncharacterized protein
K4D3H8	4	3	30.3		Uncharacterized protein
K4CMV4	5	1	100.74		Uncharacterized protein
K4B3X5	10	5	534.79		Triosephosphate isomerase
K4BQT7	1	1	26.1		Uncharacterized protein
P93211	24	1	1711.74		14-3-3 protein 6
K4B015	1	1	100.5		Uncharacterized protein
G8Z288	4	2	102.94		Hop-interacting protein THI141
K4B2K0	6	4	103.27		Uncharacterized protein
K4B7I5	4	2	46.7		Uncharacterized protein
K4ASY4	9	6	481.31		Uncharacterized protein
K4BC24	9	4	486.53		Uncharacterized protein
K4D1R1	6	4	131.36		Uncharacterized protein
K4AT06	2	2	87.86		40S ribosomal protein S27
K4CW78	1	1	105.82		Uncharacterized protein
K4CPM4	15	10	358.27		Uncharacterized protein
P37218	4	1	57.1		Histone H1
K4DBC4	39	16	2105.56		Aconitate hydratase

K4D2M9	7	4	247.09	Eukaryotic translation initiation factor 3 subunit E
K4B0S5	11	6	463.01	Uncharacterized protein
K4AT91	6	1	601.58	Uncharacterized protein
K4CIV8	7	1	51.46	Uncharacterized protein
K4C3K6	9	1	331.01	Uncharacterized protein
K4CND7	5	1	97.17	Uncharacterized protein
K4AT98	3	1	147	Uncharacterized protein
K4DF00	10	1	238.86	Uncharacterized protein
K4BN29	4	4	52.42	Uncharacterized protein
K4B1A3	7	2	250.12	Importin subunit alpha
K4D4S7	8	3	172.58	Uncharacterized protein
K4BM95	2	2	37.34	Uncharacterized protein
K4CMM7	15	3	551.92	Uncharacterized protein
K4CEY5	10	1	368.57	Uncharacterized protein
K4C5K3	4	3	117.56	Uncharacterized protein
K4CHX2	1	1	38.89	Uncharacterized protein
K4ATJ4	5	5	102.33	Peptidyl-prolyl cis-trans isomerase
K4BJC8	3	3	80.09	Uncharacterized protein
K4CW45	6	2	96.76	Uncharacterized protein
K4CQY0	4	3	68.46	Uncharacterized protein
K4AX35	3	1	37.55	Peroxidase
K4DAF9	4	4	120.07	Uncharacterized protein
K4BJY6	4	1	202.21	Uncharacterized protein
K4C7W2	3	1	84.57	Uncharacterized protein
K4ATD8	7	1	242.88	Uncharacterized protein
K4C7W9	4	3	141.62	Uncharacterized protein
K4CQR5	10	2	290.61	Uncharacterized protein
K4DA40	12	10	275.95	Uncharacterized protein
P60117	1	1	82.93	ATP synthase subunit 9, mitochondrial
K4BDY4	5	1	87.97	Uncharacterized protein
K4BNK4	9	6	157.38	Uncharacterized protein
K4CDQ9	1	1	30.39	Uncharacterized protein
K4BLQ1	5	5	70.92	Uncharacterized protein
K4C2U0	6	3	171.71	Proteasome subunit beta type
K4B1M7	12	5	175.73	Uncharacterized protein
K4CA68	12	2	600.04	Uncharacterized protein
K4CAB8	12	9	504.79	Uncharacterized protein
K4CW27	3	1	48.41	Uncharacterized protein
K4BEI9	6	4	201.26	SGT1-1
K4BVD8	11	10	533.37	Proteasome subunit alpha type
K4BJK7	19	1	951.84	40S ribosomal protein S3a
K4D4Z0	6	2	79.49	Uncharacterized protein
K4CAE2	10	4	537.38	Uncharacterized protein
K4ARQ3	1	1	60.12	Uncharacterized protein
K4DHA3	14	1	697.11	40S ribosomal protein S6

K4CBV3	4	1	66.56		Uncharacterized protein
K4CCA9	4	1	33.15		Uncharacterized protein
K4CNP6	4	2	164.76		Uncharacterized protein
K4C9G1	4	1	281.57		Uncharacterized protein
K4B112	5	1	358.63		Uncharacterized protein
K4CIF3	3	2	67.88		Uncharacterized protein
K4C949	6	2	276.54		60S ribosomal protein L27
K4D3B5	9	7	478.1		Uncharacterized protein
K4BU70	4	3	76.61		Uncharacterized protein
K4C1Q9	9	8	336.02		Peroxidase
K4CJ46	5	1	231.34		Uncharacterized protein
K4BL38	11	3	547.84		Uncharacterized protein
K4BI36	3	2	70.96		Uncharacterized protein
K4DHX7	3	1	84.59		Uncharacterized protein
K4C9U6	2	2	104.08		Uncharacterized protein
K4C3B9	10	1	225.61		40S ribosomal protein S4
K4D4D5	1	1	60.21		Uncharacterized protein
K4BPQ6	6	1	70.17		Uncharacterized protein
K4CH51	6	2	238.63		Uncharacterized protein
K4D4A7	34	1	1990.89		Uncharacterized protein
Q6LB28	8	1	440.56		Histone H3
K4BNE1	1	1	24.91		Uncharacterized protein
K4DHQ6	4	1	68.82		Uncharacterized protein
K4CHK7	1	1	54.51		Uncharacterized protein
K4BNA9	6	3	70.32		Uncharacterized protein
K4BVU1	7	4	228.84		Uncharacterized protein
K4BCU7	4	3	88.29		Uncharacterized protein
B6ECN9	19	17	834.72		Aminoaldehyde dehydrogenase 2
K4CNQ1	2	1	184.95		Uncharacterized protein
K4B1L5	5	1	305.82		Uncharacterized protein
K4C363	5	1	254.59		Uncharacterized protein
K4DB11	11	3	319.48		Uncharacterized protein
K4BYL6	8	3	250.48		Uncharacterized protein
K4C8W9	19	1	919.87		40S ribosomal protein S3a
K4D2A4	11	3	491.73		Uncharacterized protein
K4D1Q1	3	2	57.8		Uncharacterized protein
K4BC61	5	5	125.13		Eukaryotic translation initiation factor 3 subunit M
K4DI40	8	1	181.3		Uncharacterized protein
K4B929	3	2	51.14		Uncharacterized protein
COLIR5	4	1	69.61		Thiosulfate:cyanide sulfurtransferase-like protein (Fragment)
K4C5T5	2	1	62.59		Uncharacterized protein
K4D740	6	5	219.56		Uncharacterized protein
Q42884	12	1	400.45		Chorismate synthase 1, chloroplastic
K4AYF1	2	1	49.31		Uncharacterized protein

K4BIB9	3	2	41.1		Uncharacterized protein
K4B0Y8	3	3	100.13		Uncharacterized protein
K4CN87	2	1	34.49		Uncharacterized protein
K4AXF7	7	1	344.31		Histone H3
K4D1F3	4	2	271.44		Plasmamembrane intrinsic protein 29
K4D637	1	1	48.1		Uncharacterized protein
K4B9H4	4	1	49.41		Serine/threonine-protein kinase
Q9SMD3	13	1	808.87		Ascorbate peroxidase
K4B017	8	1	456.1		Uncharacterized protein
K4BJ51	4	1	344.4		Uncharacterized protein
K4D9Z8	4	4	115.71		Uncharacterized protein
K4BUB7	12	8	489.54		Serine hydroxymethyltransferase
K4B8Y5	8	1	171.13		Uncharacterized protein
K4B1V0	2	1	101.84		Uncharacterized protein
K4C807	16	10	726.81		Uncharacterized protein
K4D3Q1	9	1	71.97		Eukaryotic translation initiation factor 3 subunit A
K4CXY8	6	3	140.18		Acyl-coenzyme A oxidase
K4B215	3	3	109		Uncharacterized protein
K4DAP8	5	2	47.16		Uncharacterized protein
K4CH57	2	2	101.27		Uncharacterized protein
K4CHP2	2	1	104.96		Uncharacterized protein
K4CPN9	7	3	193.26		Nucleoside diphosphate kinase
K4D184	5	1	315.69		Peptidyl-prolyl cis-trans isomerase
K4B4N0	11	5	141.39		Uncharacterized protein
K4BH59	5	1	69.56		Acyl-[acyl-carrier-protein] desaturase
K4CEK7	5	4	113.42		Uncharacterized protein
K4CSN4	5	3	59.09		Uncharacterized protein
K4CG47	4	2	142.54		Proteasome subunit alpha type
Q43710	1	1	22.67		Proteinase inhibitor type-2 TR8
K4AW47	5	5	153.05		Uncharacterized protein
K4D348	5	3	91.98		Ubiquitin carboxyl-terminal hydrolase
K4B249	28	1	1615.59		Uncharacterized protein
K4CCD7	8	8	372.33		Proteasome subunit beta type
K4C223	2	1	37.24		DNA-directed RNA polymerase subunit
C6K2L0	16	3	552.13		GDP-mannose 3',5'-epimerase
K4CEH9	2	1	39.42		Uncharacterized protein
K4CGD8	3	1	58.55		Uncharacterized protein
K4BF26	1	1	25.44		Uncharacterized protein
K4D3J1	29	2	1272.39		Uncharacterized protein
O65820	4	1	79.61		Histone H1
K4CWJ2	9	1	261.23		Uncharacterized protein
K4BBT3	2	2	68.2		Aldose 1-epimerase
K4COD4	3	1	50.98		Uncharacterized protein
K4BIB5	5	3	177.97		Uncharacterized protein
K4B188	11	7	193.15		Uncharacterized protein

K4BHY1	10	8	205.13		Uncharacterized protein
K4CBN7	6	5	103.77		Uncharacterized protein
K4CV83	2	1	56.95		Uncharacterized protein
K4CP37	5	4	132.72		Uncharacterized protein
K4BP05	2	1	44.61		Uncharacterized protein
K4BVT9	4	2	37.82		Uncharacterized protein
K4CTF8	4	2	107.31		Peptidyl-prolyl cis-trans isomerase
K4BP03	1	1	25.45		Uncharacterized protein
K4CXQ6	5	1	133.47		Ubc13-type ubiquitin-conjugating enzyme 2
K4C1W0	2	1	77.45		Uncharacterized protein
K4BF64	1	1	22.32		Uncharacterized protein
K4D533	9	5	149.43		Uncharacterized protein
K4CX99	1	1	38.3		Uncharacterized protein
K4C875	11	5	196.99		Uncharacterized protein
K4CRB9	1	1	41.11		Uncharacterized protein
Q4A1N1	3	2	134.37		Non-specific lipid-transfer protein
K4C5Y9	4	1	173.02		Uncharacterized protein
K4DHM7	4	3	182.64		Uncharacterized protein
K4CJR2	1	1	34.68		Uncharacterized protein
K4CQT3	2	1	61.07		Uncharacterized protein
K4CAZ2	1	1	59.91		Uncharacterized protein
K4CMQ7	4	3	114.84		Uncharacterized protein
K4B103	3	2	30.84		ATP-dependent Clp protease proteolytic subunit
K4B6G9	3	1	75.17		Signal recognition particle subunit SRP68
K4B111	6	2	464.52		Translationally-controlled tumor protein homolog
K4BCI8	3	1	34.1		Uncharacterized protein
K4CE04	17	4	866.73		Uncharacterized protein
K4DHQ7	4	1	117.54		Uncharacterized protein
K4BTX6	6	1	65.94		Uncharacterized protein
K4BV04	9	8	295.54		Uncharacterized protein
K4CVU7	4	1	75.87		Uncharacterized protein
K4DEU5	19	4	855.63		Uncharacterized protein
K4CBN0	10	5	506.6		Uncharacterized protein
K4CLG9	5	1	45.67		Uncharacterized protein
K4CTW6	4	1	107.57		Uncharacterized protein
K4AYV8	4	1	197.94		Uncharacterized protein
K4CA83	2	1	79.16		Laccase
K4C956	12	3	622.65		Uncharacterized protein
K4D0E5	11	1	272.51		Uncharacterized protein
K4BJJ6	17	13	630.61		Uncharacterized protein
K4BIL3	6	3	237.98		Uncharacterized protein
K4BW50	12	1	621.04		Uncharacterized protein
K4CGJ8	3	1	42.44		Uncharacterized protein
K4B0Q2	1	1	21.85		Uncharacterized protein
K4BJE2	5	4	43.84		Uncharacterized protein

K4D6M6	2	1	21.37		Uncharacterized protein
K4BM70	2	1	82.25		Uncharacterized protein
K4D0G7	1	1	58.64		Uncharacterized protein
Q40144	10	9	323.18		Probable xyloglucan endotransglucosylase/hydrolase 1
K4D478	21	1	1238.09		Uncharacterized protein
K4DGY7	1	1	27.86		Uncharacterized protein
K4B0V7	6	1	66.8		Lipoxygenase
K4BCJ1	1	1	32.05		Uncharacterized protein
K4CLY8	6	1	69.31		Uncharacterized protein
K4CGU4	2	1	101.14		Uncharacterized protein
K4D5K6	2	1	44.21		Uncharacterized protein
K4D433	4	2	101.38		Uncharacterized protein
K4B2Y6	1	1	20.19		Uncharacterized protein
K4DF02	9	1	345.29		Uncharacterized protein
K4D3F8	14	5	779.63		Pyruvate kinase
K4B117	4	2	218.77		Uncharacterized protein
Q94KH6	4	1	72.74		Calcium-dependent protein kinase CDPK1
K4CAR4	3	1	158.11		Histone H2A
K4AZG5	2	1	49.03		Uncharacterized protein
K4DBD3	3	1	30.15		Uncharacterized protein
K4BFL3	3	1	78.73		Uncharacterized protein
K4BVU7	14	11	738.75		Uncharacterized protein
K4BHZ1	4	2	206.56		Peroxidase
K4D1F7	23	1	1321.39		Uncharacterized protein
K4C844	2	1	49.06		Uncharacterized protein
K4B0I7	9	2	456.68		Uncharacterized protein
K4CC89	2	1	68.53		Uncharacterized protein
K4DA01	1	1	66.81		Uncharacterized protein
K4CHD1	7	3	191.09		Uncharacterized protein
K4BDU9	4	2	127.6		Uncharacterized protein
K4B0A7	2	2	47.15		Uncharacterized protein
K4AYG4	5	1	116.54		Uncharacterized protein
P46301	10	1	390.37		40S ribosomal protein S25
K4BBM6	4	2	96.74		Peroxidase
K4CXJ6	2	1	213.41		Uncharacterized protein
K4ASE8	5	5	115.12		Uncharacterized protein
K4B6K0	4	2	203.18		Uncharacterized protein
K4D4H5	6	2	62.95		Uncharacterized protein
K4BVU3	2	1	60.2		Uncharacterized protein
K4CDQ8	1	1	24.98		Uncharacterized protein
K4D378	17	4	342.52		Coatomer subunit beta
K4AQC2	5	5	146.56		Uncharacterized protein
K4D5Z8	10	1	546.81		Isocitrate dehydrogenase [NADP]
K4BXW2	2	1	53.04		Uncharacterized protein
K4CC52	2	1	91.06		Uncharacterized protein

K4BQC1	3	1	45.64		Uncharacterized protein
K4AYE6	2	1	24.96		Uncharacterized protein
K4C2F3	14	11	566.75		Uncharacterized protein
K4C2K1	3	2	55.83		Uncharacterized protein
K4BAX2	2	1	67.24		Uncharacterized protein
K4BTZ3	8	4	154.17		Uncharacterized protein
K4B047	6	3	243.28		Uncharacterized protein
K4CVM9	14	1	424.88		40S ribosomal protein S3a
K4CC35	3	2	61.77		Uncharacterized protein
K4BGK0	10	4	319.71		Uncharacterized protein
K4DAM1	10	3	245.67		Uncharacterized protein
K4C6K7	6	2	169.03		Uncharacterized protein
G8IIJ5	6	3	349.13		Histone H2A (Fragment)
K4BHQ8	11	1	503.42		Uncharacterized protein
K4DFB5	4	3	40.96		Uncharacterized protein
K4CV84	5	4	182.79		Uncharacterized protein
C6K8M2	8	1	197.09		Plastid isopentenyl diphosphate isomerase
K4AYP6	4	1	140.9		Uncharacterized protein
K4B7P4	4	1	42.32		Uncharacterized protein
K4C669	10	1	169		Uncharacterized protein
K4CFR4	6	3	43.56		Uncharacterized protein
K4D613	3	3	83.56		Uncharacterized protein
K4D2B1	6	6	323.73		Uncharacterized protein
K4CV64	2	1	42.1		Uncharacterized protein
K4C9L4	30	2	1417.2		Uncharacterized protein
K4DHX8	2	2	52.94		Uncharacterized protein
K4D300	9	6	277.05		Proteasome subunit alpha type
K4B6W4	12	6	218.68		Uncharacterized protein
K4C0U8	2	1	39.59		Uncharacterized protein
K4BT78	3	1	56.43		Uncharacterized protein
K4CIF4	4	1	30.4		Uncharacterized protein
A9LRT6	4	1	51.17		3-hydroxy-3-methylglutaryl coenzyme A synthase
K4BRR1	7	3	434.92		Uncharacterized protein
K4CV92	3	1	107.03		Uncharacterized protein
D0EXD9	1	1	90.67		Hexose transporter 1
K4DB95	1	1	30.38		Uncharacterized protein
K4B3C8	4	1	32.13		Uncharacterized protein
K4CW98	4	1	91.71		Uncharacterized protein
K4CAC2	9	1	457.41		Uncharacterized protein
K4D2Y1	35	1	1981.42		Uncharacterized protein
K4BME7	3	2	35.73		Uncharacterized protein
K4BNY4	4	3	117.49		4-hydroxy-4-methyl-2-oxoglutarate aldolase
K4AUE2	3	1	46.26		Peroxidase
E3UVW5	5	1	43.18		Beta-galactosidase
K4BDV0	4	1	152.28		Uncharacterized protein

Q9XGI9	1	1	39.42		N-carbamoylputrescine amidase
K4B8J2	7	2	218.33		Uncharacterized protein
K4CW84	3	1	71.31		Uncharacterized protein
K4BWL6	2	1	46.15		Uncharacterized protein
K4BIZ6	1	1	49.15		Uncharacterized protein
G8Z278	5	4	106.93		Hop-interacting protein THI111
P08706	5	1	216.02		Ribulose biphosphate carboxylase small chain 1, chloroplastic
K4BF17	3	3	110.2		Uncharacterized protein
K4B5Z2	6	1	207.79		Uncharacterized protein
K4AW29	2	1	26.71		Uncharacterized protein
K4BMM4	4	1	112.32		Uncharacterized protein
K4BVM3	9	7	206.49		Uncharacterized protein
K4CNT4	10	9	296.28		Uncharacterized protein
K4D5N7	2	1	47.93		Uncharacterized protein
K4CPJ1	2	1	83.28		Uncharacterized protein
K4B9G5	4	1	125.63		Uncharacterized protein
K4BLG4	6	1	114.47		Phospholipase D
K4DCH1	10	3	478.51		Ketol-acid reductoisomerase
K4CVK9	9	8	228.53		Uncharacterized protein
K4D6D0	6	3	168.73		Uncharacterized protein
K4CYN1	4	2	97.15		Uncharacterized protein
K4C731	3	1	137.4		Uncharacterized protein
K4BM53	24	6	1329.97		Uncharacterized protein
K4D831	10	2	451.95		Uncharacterized protein
K4DGN7	9	1	374.84		Uncharacterized protein
K4CTZ5	3	1	62.43		Uncharacterized protein
K4BI34	3	2	149.05		Uncharacterized protein
K4CWX9	4	2	44.31		Uncharacterized protein
K4AST1	16	4	350.83		Coatomer subunit beta
K4BXG3	1	1	23.08		Uncharacterized protein
K4CQA7	4	2	103.63		Uncharacterized protein
K4B1S1	14	7	398.41		Uncharacterized protein