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Proteomic analysis upon peach fruit infection with *Monilinia fructicola* and *M. laxa* identify responses contributing to brown rot resistance

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Brown rot, caused by *Monilinia* spp., is a major peach disease worldwide. In this study, the response of peach cultivars Royal Glory (RG) and Rich Lady (RL) to infection by *Monilinia fructicola* or *Monilinia laxa*, was characterized. Phenotypic data, after artificial inoculations, revealed that 'RL' was relatively susceptible whereas 'RG' was moderately resistant to *Monilinia* spp. Comparative proteomic analysis identified mesocarp proteins of the 2 cultivars whose accumulation were altered by the 2 *Monilinia* species. Functional analysis indicated that pathogen-affected proteins in 'RG' were mainly involved in energy and metabolism, while, differentially accumulated proteins by the pathogen presence in 'RL' were involved in disease/defense and metabolism. A higher number of proteins was differentiated in 'RG' fruit compared to 'RL'. Upon *Monilinia* spp. infection, various proteins were down accumulated in 'RL' fruit. Protein identification by mass spectrometric analysis revealed that several defense-related proteins including thaumatin, formate dehydrogenase, S-formylglutathione hydrolase, CBS domain-containing protein, HSP70, and glutathione S-transferase were up-accumulated in 'RG' fruit following inoculation. The expression profile of selected defense-related genes, such as major latex allergen, 1-aminocyclopropane-1-carboxylate deaminase and UDP-glycoltransferase was assessed by RT-PCR. This is the first study deciphering differential regulations of peach fruit proteome upon *Monilinia* infection elucidating resistance responses.

Brown rot is one of the most important and common diseases of peach (*Prunus persica* (L) Batsch) causing devastating yield losses that can exceed 50% or even reach 100% under environmental conditions favorable for the development of the disease^{1,2}. The disease occurs wherever stone fruits are cultivated and causes blossom, twig or fruit blight and pre- or post-harvest fruit rots. The latter are associated with the most severe yield losses². On stone fruit the disease is caused by several *Monilinia* species, with *Monilinia fructicola* and *Monilinia laxa* being the predominant³. *M. laxa* is widely distributed around the world and considered to be the most common brown rot pathogen in Europe³. In addition, *M. fructicola* occurs mainly in America, Australia, China and Japan. However, several reports of the last 2 decades have confirmed the presence of *M. fructicola* in South and Central European countries^{4–7}.

The control of the disease relies mainly on the use of synthetic fungicides and thus, they are essential for providing stone fruits of high quality at affordable prices^{8–10}. However, the increased public concern about food safety and the potential impact on the environment, combined with concerns of the peach industry regarding fungicide resistance and the emergence of new resistant strains have led to extensive research for the development of disease management methods alternative to conventional fungicides^{11,12}. Such alternatives include biological

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control with microbial antagonists or use of resistance inducers, but none of these approaches has gained until now a commercial feasibility^{12–14}.

Host resistance to brown rot could be an attractive, cost effective and environmentally friendly alternative to chemical control. However, most of the commercial peach cultivars are susceptible to brown rot, although some differences exist among them in the level of susceptibility to the disease^{15–17}. The susceptibility of peach fruit is also associated with the stages of their development and appear more susceptible in the very early stages, during the development of the pericarp and later at the stage of ripeness of the fruit, after the endocarp and the mesocarp have been fully developed^{8,11}. The mechanisms behind the different sensitivity levels at different stages are allegedly due to physical and chemical reasons¹⁸. For instance, the high levels of resistance in the peach cultivar Bolinha are associated with the presence of higher concentrations of phenolic compounds, such as caffeic acid and its quinate ester, chlorogenic acid, located in the epidermis and mesocarp^{8,11–21}. While these substances have no direct effect on mycelial growth and spore germination, they inhibit the production of the cell wall degrading enzymes polygalacturonase and cutinase, by down regulating their respective genes⁸. Additional factors, also playing an important role in resistance to the disease, are associated with different levels of the environmental pH of the host, regulated by the pathogen and affecting the expression of genes, responsible for pathogenesis²². Despite intensive investigation, the mechanism of peach fruit brown rot resistance remains unknown.

In recent years, proteomics has gained popularity in understanding host–pathogen interactions^{23,24}. Comparative proteomics have been successfully used to study interactions of plants with a wide range of pathogens²⁵. However, no proteomic studies have been published to date investigating the interactions of peach fruit with *Monilinia* species. To address this issue, the responses of two peach cultivars, ‘RL’ and ‘RG’, differing in their level of resistance to infection by *M. fructicola* or *M. laxa*, was characterized. Using two-dimensional gel electrophoresis (2-DE) analysis, we compared the proteomic changes from the fruit mesocarp of the two cultivars following inoculation with either *M. fructicola* or *M. laxa* to identify proteins potentially involved in defense mechanisms.

Results

Disease incidence. The artificial inoculations of the fruit of the 2 different peach cultivars revealed a higher rate of disease incidence at ‘RL’ fruit compared to that observed at ‘RG’ fruit, either inoculated with *M. fructicola* or *M. laxa* isolates (Fig. 1a,b). However, the difference in the disease incidence between the 2 cultivars was lower, when the fruits were inoculated with *M. fructicola* isolates Mf 101 and Mf 167, with disease incidence values of 84.2 and 90.5% in ‘RL’ and 66.7 and 65.2% in ‘RG’, respectively (Fig. 1b). Moreover, a higher difference in disease incidence was observed, when fruits were inoculated with *M. laxa* isolates Ml 1 and Ml 66, with infected fruit rates reaching 90 and 100% in ‘RL’ and only 18.2 and 8.7% in ‘RG’, respectively (Fig. 1b).

Characterization of the peach fruit proteome. To obtain a better understanding of the mechanisms behind the disease incidence data, a two-dimensional gel electrophoresis (2-DE) analysis was conducted to detect the protein changes in both cultivars ‘RL’ and ‘RG’ (Fig. 2a,b). In both cultivars a total of 250 protein spots, were detected, while 120 of them showed significant differences in their volume in the presence of either *M. fructicola* or *M. laxa* (Fig. 2c,d, Supplementary Data Figs. S1 and S2), according to the Student’s t-test for 95% confidence further validated by the two-fold change threshold. Following mass spectrum analysis, 126 different peach proteins were identified, while 11 of them were detected in more than one spots. These proteins were aconitate hydratase (spots no.: 4828, 4829), adenylyl cyclase-associated protein (spots no: 8510, 8520), aminoacylase (spots no.: 2311, 3316), aspartate aminotransferase (spots no: 9214, 9216), HSP70 (spots no: 1705, 1821, 2701, 2704), malic enzyme (spots no: 3616, 5615, 8604), peptidyl-prolyl cis-trans isomerase (spots no: 1705, 9013), phosphoenolpyruvate carboxykinase [ATP] (spots no: 6708, 7707, 7709, 8711), phosphoglycerate kinase (spots no: 6206, 7301), S-adenosylmethionine synthase (spots no: 4208, 4313), thaumatin (spots no: 5008, 9103). Detailed information regarding the identified proteins are provided in Supplementary Data Table S1. Subsequently, proteins based on gene ontology and literature, were grouped into functional categories²⁶.

Functional analysis of proteins modulated by the presence of the pathogen relative to the control fruit, within the same peach cultivar. In order to identify the peach proteins whose abundance was significantly changed (increased or decreased) by the presence of the pathogen in relation to the control, within the same peach cultivar, proteins were grouped into four sets: (1) a set of 33 proteins modulated in ‘RG’ by the presence of *M. laxa* (RGC vs RGL) (Fig. 3a), (2) a set of 32 proteins modulated in ‘RG’ by the presence of *M. fructicola* (RGC vs RGF) (Fig. 3b), (3) a set of 20 proteins modulated by the presence of *M. laxa*, in ‘RL’ (RLC vs RLL) (Fig. 3c) and (4) a set of 15 proteins modulated by the presence of *M. fructicola*, in ‘RL’ (RLC vs RLF) (Fig. 3d). Functional analysis revealed that the *M. laxa* affected several proteins ($n = 33$) in ‘RG’ that were mainly involved in energy (24.2%), metabolism (21.2%) and protein destination and storage (15.1%) (Fig. 3a). Similarly, the *M. fructicola* affected proteins in the same cultivar were mainly involved in metabolism (25%), energy (21.8%) and protein destination and storage (18.7%) (Fig. 3b). In contrast, *M. laxa* affected proteins in ‘RL’ participated mainly in disease/defense (30%), energy (25%) and metabolism (20%) (RLC vs RLL) (Fig. 3c) while, the *M. fructicola* affected proteins in the same cultivar participated in disease/defense (26.7%), metabolism (26.7%), energy (13.3%), protein destination and storage (13.3%) and secondary metabolism (13.3%) (RLC vs RLF) (Fig. 3d).

Proteins functional analysis: ‘Royal Glory’ and ‘Rich Lady’ inoculated with *M. laxa* or *M. fructicola*, versus not inoculated cultivars. Information concerning distinct or common proteins affected by *M. fructicola* or *M. laxa* in the 2 peach cultivars, in relation to control fruits, are given in Fig. 3f. Among the 2 sets of proteins modulated in ‘RG’ by the presence of *M. fructicola* and *M. laxa*, 16 proteins were common, while 10 proteins were specifically modulated in response to *M. laxa* and 9 proteins were specifically modulated in

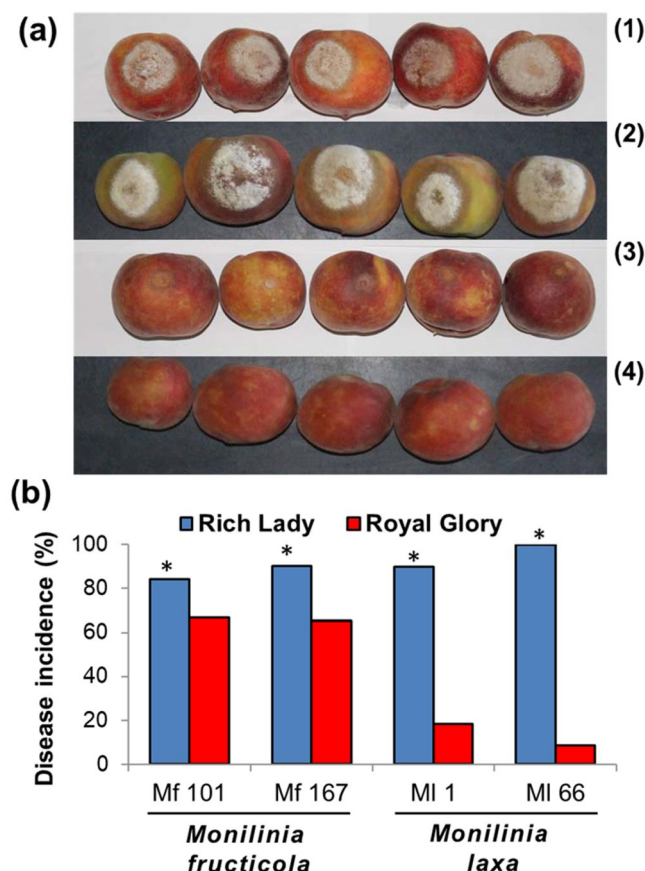


Figure 1. (a) Brown rot symptoms on peach fruit of Rich Lady (1, 2) and Royal Glory (3, 4) cultivars 6 days after the inoculation with isolates of *Monilinia fructicola* (1, 3) and *M. laxa* (2, 4). (b) Disease incidence on fruits of Rich Lady and Royal Glory cultivars artificially inoculated with *M. fructicola* (Mf 101, Mf 167) and *M. laxa* (MI 1, MI 66) isolates. Asterisks on the bars indicate significant differences between the disease incidence values in the 2 cultivars, according to a chi square analysis at $P = 0.05$.

response to *M. fructicola* (Fig. 3f). In 'RL' fruits, 6 and 5 proteins were individually changed by the presence of *M. laxa* and *M. fructicola*, respectively, while 8 proteins overlapped between the 2 sets of proteins (Fig. 3f).

Venn diagrams were further analyzed to determine the functional distribution of distinct or overlapping proteins. Proteins that were specifically modulated by *M. laxa* ($n = 10$) in 'RG' in relation with the control treatment were mainly involved in metabolism (30%), energy (20%) and intracellular traffic (20%) (Fig. 3e,f), while proteins specifically modulated by *M. fructicola* ($n = 9$), in 'RG' (RGC vs RGF) were mainly involved in metabolism (44.4%), protein destination and storage (22.2%), disease/defense (22.2%) (Fig. 3e,f). Proteins commonly affected by *M. laxa* and *M. fructicola* ($n = 16$) in 'RG' were involved in protein destination and storage (25%), energy (31.2%) and metabolism (12.5%) (Fig. 3e,f).

Proteins identified exclusively in 'RL' after inoculation with *M. laxa* ($n = 6$) were involved in energy (33.3%), disease/defense (33.3%), protein destination and storage (16.7%) and cell structure (16.7%) (Fig. 3e,f), while proteins ($n = 5$) exclusively identified in 'RL' after inoculation with *M. fructicola* were involved in metabolism (40%), energy (20%), intracellular traffic (20%) and secondary metabolism (20%) (Fig. 3e,f). Common targeted proteins among *M. laxa* and *M. fructicola* infected fruits of 'RL' ($n = 8$) were involved in disease/defense (37.5%), metabolism (25%) and protein destination and storage (25%) (Fig. 3e,f).

Comparing the proteins modulated by the pathogen in 'RG' (RGC vs RGL) 12 of the 33 proteins were up-regulated by *M. laxa* and they were involved mainly in energy (25%), cell growth/division (25%), disease/defense (16.7%) and transporters (16.7%), while, 21 proteins were down-regulated and participated mainly in metabolism (28%) and energy (24%) (Fig. 3a). In the presence of *M. fructicola* in the same cultivar (RGC vs RGF), 15 proteins were up-regulated, involved mainly in disease/defense (26%) and protein destination and storage (26%) whereas, 17 proteins were down-regulated mainly involved in metabolism (35%) and energy (29%) (Fig. 3b). Furthermore, in 'RL' (RLC vs RLL) out of the 20 proteins modulated by the presence of *M. laxa*, 10 of them were increased in abundance and involved mainly in energy (40%), disease/defense (20%) and metabolism (20%), while the remaining 10 down-regulated proteins were involved in disease/defense (40%) and protein destination and storage (30%) (Fig. 3c). Seven out of 15 proteins in the same cultivar (RLC vs RLF) were up-regulated by the presence of *M. fructicola* and involved in metabolism (28%), energy (28%), intracellular traffic (14%), disease/defense (14%), secondary metabolism (14%) while 8 of them were down regulated and involved in disease/defense (37%), metabolism (25%) and protein destination and storage (25%) (Fig. 3d).

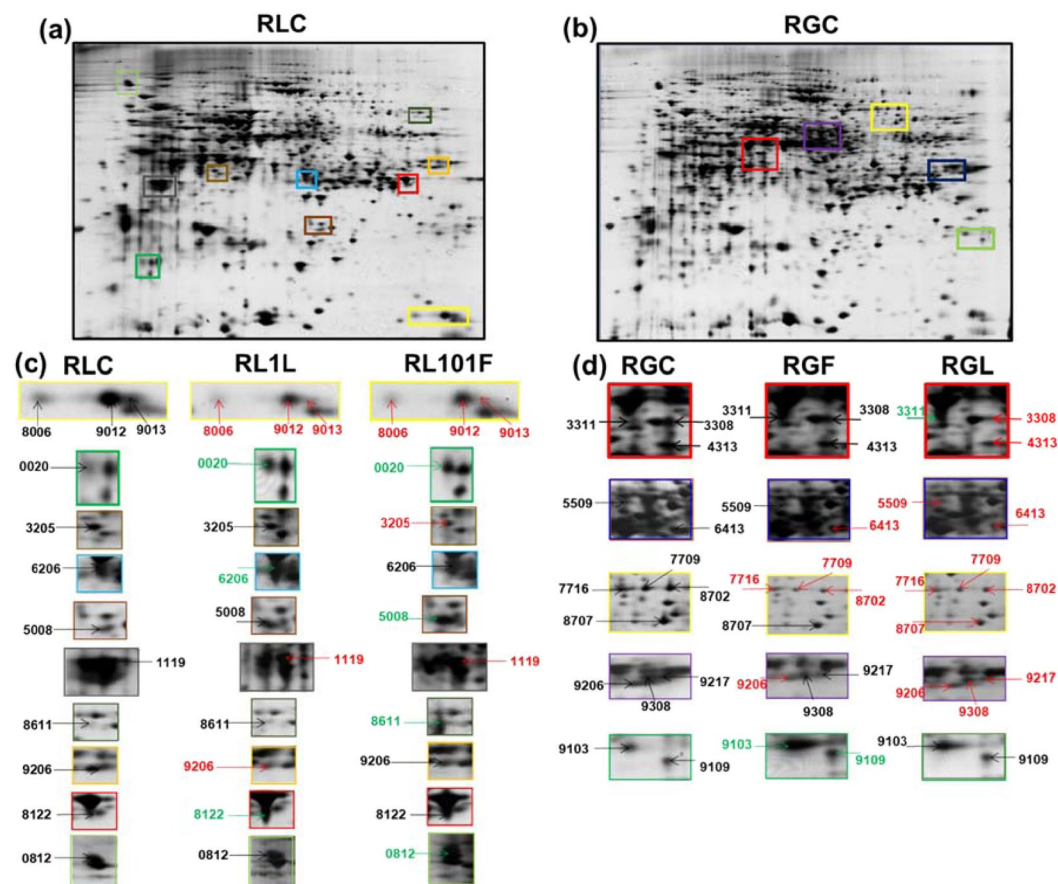


Figure 2. Representative silver-stained 2-DE map of total proteins from (a) Rich Lady (RLC) and (b) Royal Glory (RGC) control peach cultivars. (c) Zoomed in views of selected areas from RLC in relation to 'Rich Lady' fruits inoculated with *M. laxa* (RL1L) or *M. fructicola* (RL101F), showing differences in the protein spots intensity. (d) Enlarged views of RGC versus 'Royal Glory' fruits inoculated with *M. laxa* (RGL) or *M. fructicola* (RGF). Black, green and red arrows indicate protein spots whose abundance remained unchanged, increased, or decreased, respectively in comparison to control. Full-length gels of which zoomed in views of selected areas are given in Supplementary Data Fig. S2.

Proteins functional analysis: comparison between 'Royal Glory' and 'Rich Lady' inoculated with the same *Monilinia* species. Comparison of proteins that differed between the 2 cultivars due to the presence of the same pathogen, *M. fructicola* or *M. laxa*, 3 sets of proteins were defined: a set of 57 proteins varied due to the presence of *M. laxa* (RGL vs RLL), (Fig. 4a), a set of 42 proteins changed in response to *M. fructicola* (RGF vs RLF), (Fig. 4b) and a set of 71 proteins differed between 'RL' and 'RG' in the absence of any pathogen (RGC vs RLC) (Fig. 4c).

The *M. laxa* modulated proteins, which were differentiated between the inoculated 'RG' and 'RL' fruits ($n = 57$) were mostly involved in metabolism (24.6%), energy (21%), protein destination and storage (14%) and disease/defense (14%) (Fig. 4a). Of the 57 modulated proteins, 23 of them were up-regulated and involved in metabolism (26%) and disease/defense (26%), while 34 were down-regulated and participated in energy (32%) and metabolism (23.5%). In addition, proteins affected by *M. fructicola* differentially in the inoculated 'RG' and 'RL' fruits ($n = 42$) were involved in metabolism (38.1%) and energy (16.6%) (Fig. 4b). Of them 14 proteins were up-regulated and 28 down-regulated accounting majorly for the same functional categories. The proteomic maps of control fruits of 'RL' and 'RG' were varied in proteins ($n = 71$) mostly involved in metabolism (31%), energy (21.1%) and disease/defense (14.1%) (Fig. 4c). Of them, 25 proteins were up-regulated and participate mainly in metabolism (32%), protein destination and storage (16%) and disease/defense (16%), whereas the major categories for the 46 down-regulated proteins are metabolism (30%) and energy (26%).

Information on common and distinct proteins between the 'RG' and 'RL' peach cultivars inoculated with the same pathogen are provided in Fig. 4e. The commonly affected proteins ($n = 26$) between the 3 sets of proteins modified by the presence of the same pathogen or in the absence of pathogen, between 'RL' and 'RG' respectively, were mainly involved in metabolism (34.6%), energy (23.1%) and protein destination and storage (11.5%) (Fig. 4d). Proteins targeted specifically by the presence of *M. laxa* ($n = 17$) between 'RL' and 'RG' were mainly involved in metabolism (17.6%), energy (17.6%), protein destination and storage (17.6%) and disease/defense (17.6%) (Fig. 4a). Proteins related with metabolism (33.3%) and cell structure (22.2%) were predominant in

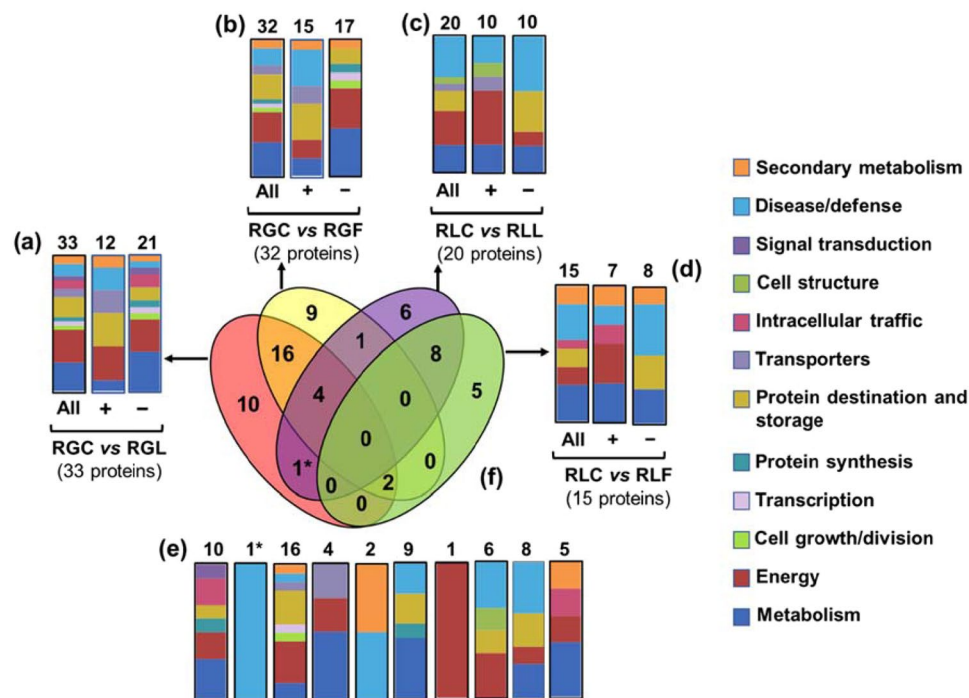


Figure 3. Venn diagram presenting the common and distinct differentially expressed proteins in peach cultivars after inoculation with *M. fructicola* and *M. laxa*, respectively. Graphical representation of the functional classification of the differentially expressed proteins in: (a) ‘Royal Glory’ inoculated with *M. laxa*, (b) ‘Royal Glory’ inoculated with *M. fructicola*, (c) ‘Rich Lady’ inoculated with *M. laxa*, (d) ‘Rich Lady’ inoculated with *M. fructicola*. (e) Functional classification of the unique and overlapping proteins presented in the Venn diagram (f). Symbols (+) and (−) indicate up-regulated and down-regulated proteins in each treatment. (RGC: ‘Royal Glory’ control fruits, RGL: ‘Royal Glory’ fruits inoculated with *M. laxa*, RGF: ‘Royal Glory’ fruits inoculated with *M. fructicola*, RLC: ‘Rich Lady’ control fruits, RLL: ‘Rich Lady’ fruits inoculated with *M. laxa*, RLF: ‘Rich Lady’ fruits inoculated with *M. fructicola*).

the set of proteins ($n = 9$) exclusively responsive to the inoculation with *M. fructicola* between ‘RL’ and ‘RG’ (Fig. 4e). Moreover, proteins individually identified between control conditions ($n = 28$) of the 2 peach cultivars were involved in metabolism (25%), energy (21.4%) and disease/defense (21.4%) (Fig. 4e).

Proteins functional analysis: comparison between ‘Royal Glory’ and ‘Rich Lady’ inoculated with different *Monilinia* species. Comparisons performed to identify proteins modulated within the same peach cultivar in response to the 2 different pathogens, *M. fructicola* and *M. laxa*, revealed a set of 2 proteins in ‘RG’ differed between the fruits which were inoculated by *M. fructicola* and *M. laxa* (RGF vs RGL) (Fig. 5b) and a set of another 2 proteins in ‘RL’ differed between the fruits which were exposed to *M. fructicola* and *M. laxa*, respectively (RLF vs RLL) (Fig. 5c).

Protein differences within ‘RG’ inoculated with either *M. fructicola* or *M. laxa*, were involved in energy (50%) and protein destination and storage (50%) (RGF vs RGL) (Fig. 5b) while differentiated proteins within ‘RL’ were participate in metabolism (50%) and disease/defense (50%) (RLF vs RLL) (Fig. 5c).

There were no common proteins among the 2 group of proteins modulated within the same cultivar by the presence of a different pathogen, *M. fructicola* and *M. laxa*, respectively (Fig. 5a). Only 2 proteins were specifically differentiated within ‘RG’ and ‘RL’, respectively (Fig. 5b,c).

Peach proteins of the mesocarp of ‘RL’ and ‘RG’ cultivars differentiated (up-accumulated or down-accumulated) after inoculation with *M. fructicola* or *M. laxa* are given as heat map profile in Fig. 6 and discussed below.

Quantitative RT-PCR assays. To investigate the correlation between proteins accumulation level and mRNA expression, a RT-qPCR analysis was performed for 6 representative defense-related genes, selected based on the data derived from the proteome analysis. Using this approach, we found that 4 of these 6 genes, namely thaumatin (Fig. 7a), glycosyltransferase_GTB_type (Fig. 7b), major latex allergen (Fig. 7c) and UDP-glycoltransferase (Fig. 7d) were in agreement with the corresponding protein levels as analyzed by proteomic analysis (Fig. 7; Supplementary Data Table S1). However, no correlation between mRNA expression and protein abundance of formate dehydrogenase (Fig. 7e) and 1-aminocyclopropane-1-carboxylate deaminase (Fig. 7f) was observed.

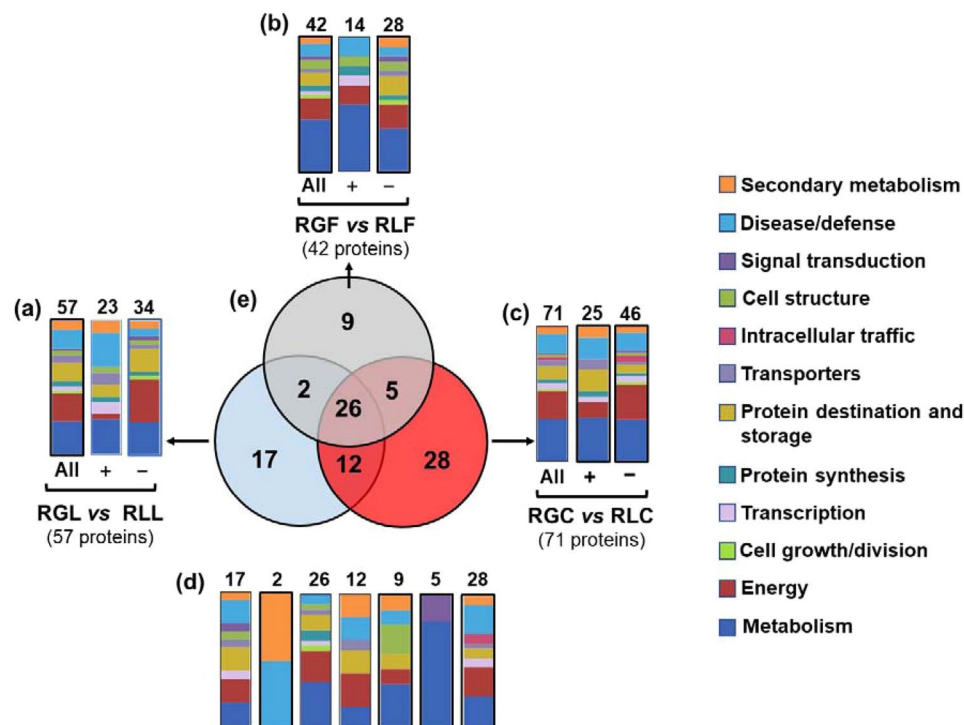


Figure 4. Venn diagram presenting the common and unique differentially expressed proteins among Royal Glory and Rich Lady cultivars inoculated with the same pathogen. Graphical representation of the functional classification of the differentially expressed proteins among the 2 varieties, (a) inoculated with *M. laxa*, (b) inoculated with *M. fructicola*, (c) control treatments. (d) Functional classification of the unique and overlapping proteins presented in the Venn diagram (e). Symbols (+) and (−) indicate up-regulated and down-regulated proteins in each treatment. (RGC: ‘Royal Glory’ control fruits, RGL: ‘Royal Glory’ fruits inoculated with *M. laxa*, RGF: ‘Royal Glory’ fruits inoculated with *M. fructicola*, RLC: ‘Rich Lady’ control fruits, RLL: ‘Rich Lady’ fruits inoculated with *M. laxa*, RLF: ‘Rich Lady’ fruits inoculated with *M. fructicola*).

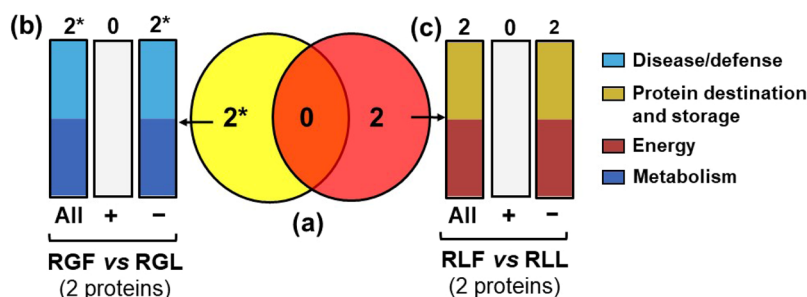


Figure 5. Venn diagram (a) presenting unique and common proteins within the same cultivar after inoculation with *M. fructicola* and *M. laxa* individually. Functional classification of differentially expressed proteins in ‘Royal Glory’ (b) and ‘Rich Lady’ (c), inoculated with *M. fructicola* and *M. laxa*, respectively. Symbols (+) and (−) indicate up-regulated and down-regulated proteins in each treatment. (RGL: ‘Royal Glory’ fruits inoculated with *M. laxa*, RGF: ‘Royal Glory’ fruits inoculated with *M. fructicola*, RLL: ‘Rich Lady’ fruits inoculated with *M. laxa*, RLF: ‘Rich Lady’ fruits inoculated with *M. fructicola*).

Discussion

This study represents a first attempt to investigate the response of peach fruit at proteomic level following infection by either *M. laxa* or *M. fructicola*, the two most common brown rot agents, and may constitute a groundwork for future studies. The phenotypical data acquired by artificial inoculations, revealed significant differences in the levels of resistance to brown rot between the two different peach cultivars used making them an interesting experimental model to characterize proteome-based responses to the disease.

In this work, the comparison of the proteomic profile of artificially-inoculated and non-inoculated control fruit of ‘RG’ and ‘RL’ cultivars, showed that a higher number of proteins was changed in the ‘RG’ fruit exposed to either *M. fructicola* or *M. laxa*. Such results suggest that the relatively resistant cultivar displayed a stronger

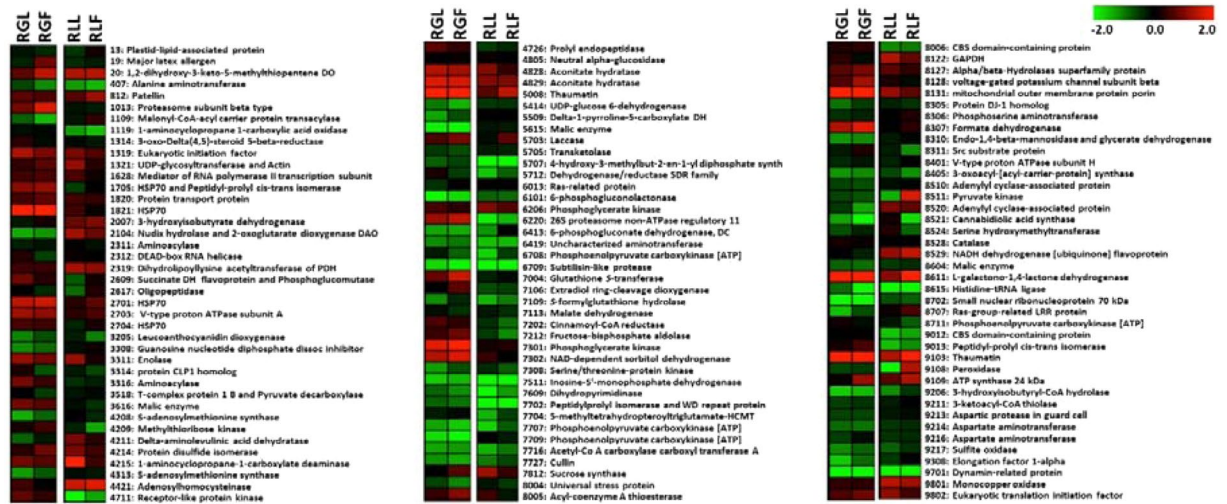


Figure 6. Protein abundance changes in ‘Royal Glory’ and ‘Rich Lady’ peach fruit inoculated with *Monilinia fructicola* or *M. laxa*. Heat map of proteins that demonstrated statistically significant differences among the different experimental conditions (RGC: ‘Royal Glory’ control fruits, RGL: ‘Royal Glory’ fruits inoculated with *M. laxa*, RGF: ‘Royal Glory’ fruits inoculated with *M. fructicola*, RLC: ‘Rich Lady’ control fruits, RLL: ‘Rich Lady’ fruits inoculated with *M. laxa*, RLF: ‘Rich Lady’ fruits inoculated with *M. fructicola*). Color scale shows the relative abundance of each protein across the experimental conditions as it has been calculated as log₂ of the ratio of the protein abundance of the RGL or RGF or RLL or RLF to the protein abundance of the corresponding control; red and green indicate respectively enhanced and reduced abundance in RGL or RGF or RLL or RLF samples in comparison to the corresponding control. Proteins correspond to that listed in Supplementary Table 1.

proteome-associated response to brown rot infection in relation to the more susceptible cultivar. Despite the differences in the disease incidence between *M. fructicola* and *M. laxa* observed in both cultivars, the artificial inoculations with both *Monilinia* species induced a similar proteomic response in the two cultivars. Thus, it is tempting to speculate that the peach fruit’s response to infection is presumably differentiated in terms of cultivar-specific protein changes that are involved in the resistance. On this basis, an interesting finding that emerged from this work is the overall accumulation of various defense-related proteins such as thaumatin, formate dehydrogenase, S-formylglutathione hydrolase, UDP-glycosyltransferase, 1-aminocyclopropane-1-carboxylate deaminase, CBS domain-containing protein, HSP70, L-galactono-1,4-lactone dehydrogenase, phosphoglycerate kinase, mitochondrial outer membrane protein porin, major latex allergen and glutathione S-transferase that observed in the relatively resistant ‘RG’ fruit following inoculation with either *M. fructicola* or *M. laxa*. For several of these proteins (thaumatin, major latex allergen, glutathione S-transferase or UDP-glycosyltransferase) their up-accumulation was confirmed by the over-expression of the respective genes using qPCR. However, there were also some of these proteins (1-aminocyclopropane-1-carboxylate deaminase, formate dehydrogenase) for which their over-accumulation was not confirmed by the qPCR data. This mismatch between the protein and gene expression can be due to various reasons such as post-transcriptional processes that may modify the active protein levels, such as synthesis, degradation, processing and post-translational modification, as shown in many studies^{23,27}. In the following, we discuss the changes of several of these defense-related proteins and their respective encoding genes that presented in Fig. 6, in an effort, to determine their biological functions and their contribution in the defense of peach fruits against brown rot.

Plant cells have displayed specific defense-related protein reprogramming to combat pathogen infection²³. One of the acquired modes in response to pathogen attack is the production of the pathogenesis-related (PR) proteins, which play key roles in plant disease-resistance responses²⁸. For example, thaumatin and thaumatin-like proteins with similar nucleotide sequences are considered pathogenesis-related (PR) proteins and are mainly involved in the induction of resistance against pathogens²⁹. Members of the thaumatin family have been reported to exhibit strong antifungal activity, participating in inhibition of mycelial or germ tube growth and in reduction of sporulation of many fungal pathogens in several fruits³⁰. The results of this study indicated that thaumatin was strongly over-accumulated in ‘RG’ fruits exposed to either *M. fructicola* or *M. laxa* as well as in ‘RL’ fruit treated with *M. fructicola*. In support to this observation we found that *thaumatin* expression was strongly induced in ‘RG’ fruits inoculated with *M. laxa* compared to control, suggesting that thaumatin plays an important anti-disease role in peach fruit against brown rot. Meanwhile, thaumatin proteins have been reported to be up-accumulated in chilled-injury resistant cultivars³¹. Thus, the accumulation of thaumatin might be a common response cascade during both abiotic and biotic stimuli in peach fruit.

Heat shock proteins (HSP) are a multi-gene family of stress proteins that protect the cell’s functions in response to stress conditions³². In this study, the abundance of HSP70 was increased in ‘RG’ fruit that had been inoculated with either *M. fructicola* or *M. laxa*, providing evidence of their involvement in resistance to these pathogens. In plants, HSP70 exhibit a protective role against these stresses acting as a molecular chaperone and playing an important role

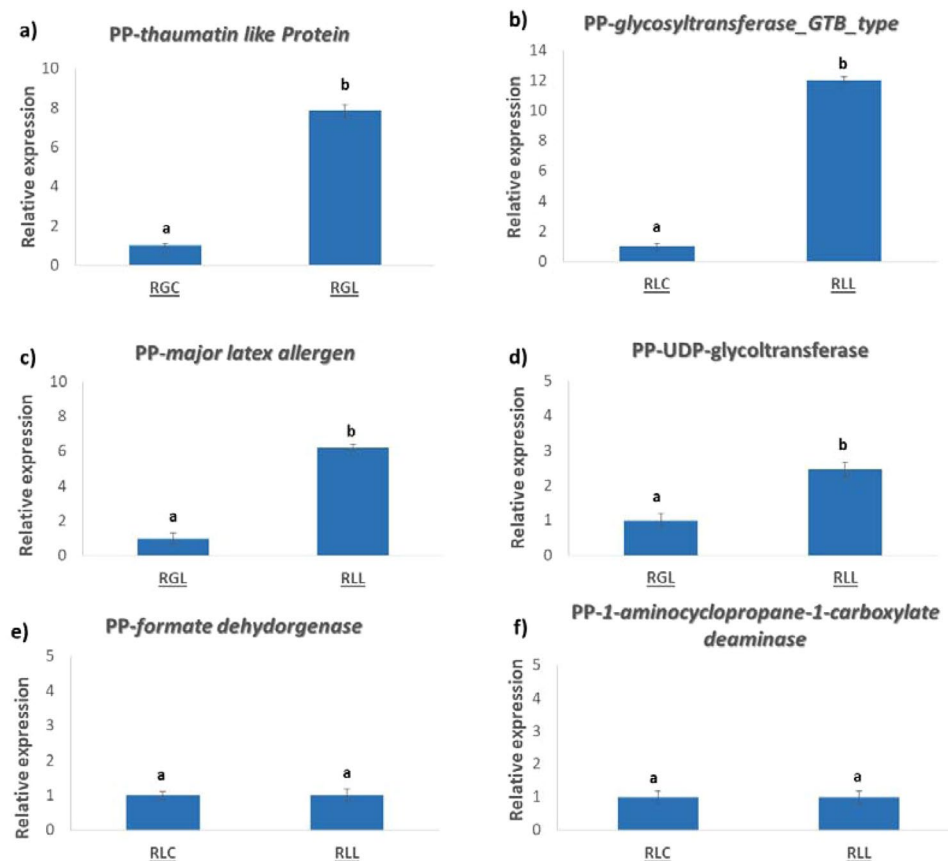


Figure 7. Transcript levels of *Prunus persicae* (PP) defense-related genes (a) thaumatococcal protein, (b) glycosyltransferase_GTB_type, (c) major latex allergen, (d) UDP-glycosyltransferase, (e) formate dehydrogenase and (f) 1-aminocyclopropane-1-carboxylate deaminase in fruits of 'Royal Glory' and 'Rich Lady' inoculated with *Monilinia fructicola* or *M. laxa*. Actin and ubiquinone were used as reference genes. (RGC: 'Royal Glory' control fruits, RGL: 'Royal Glory' fruits inoculated with *M. laxa*, RGF: 'Royal Glory' fruits inoculated with *M. fructicola*, RLC: 'Rich Lady' control fruits, RLL: 'Rich Lady' fruits inoculated with *M. laxa*, RLF: 'Rich Lady' fruits inoculated with *M. fructicola*). Different letters on the columns indicate significant differences according to analysis of variance (ANOVA) at $P = 0.05$.

in protein folding, intracellular trafficking of proteins and helping to refold proteins that were denatured due to abiotic cell stress³³. Overwhelming data support that HSP70 is also an important molecular chaperone during biotic stress responses. Cytoplasmic *Capsicum annuum* HSP70 (CaHSP70) significantly accumulates in pepper leaves, inducing the hypersensitive response (HR) by *Xanthomonas campestris* pv. *vesicatoria* (Xcv) infection. CaHSP70 silencing in pepper was shown to increase susceptibility to Xcv as well as alter the cell death response to Xcv infection³⁴.

Another interesting finding that emerged from this work is the fact that the 'RG' proteome status was differently modified by the two *Monilinia* species. For example, several proteins, such as major latex allergen and glutathione S-transferases (GST) were up-accumulated only in 'RG' fruits inoculated with *M. fructicola*, signifying their involvement in the defense of this cultivar to brown rot. In support to the role of GST in brown rot, our data disclosed that 'RG' fruit exposed to *M. fructicola* induced GST expression. GSTs are a large group of conserved enzymes, known for their ability to convert xenobiotic compounds to less reactive and more soluble substances, by facilitating their conjugation with glutathione and assisting to their discharge from the cells, via membrane-based glutathione conjugate pumps³⁵. Several studies reviewed by Gullner *et al.*³⁶, have shown that GSTs play a crucial role in plant-pathogen interactions, by suppressing ROS accumulation in the infected tissues of the host. In detail, it has been shown that infection of plant tissue by necrotrophic fungi leads to an up-regulation of GSTs that in subsequence, enhance the antioxidant plant system contributing to disease resistance to necrotrophic pathogens such as *Botrytis cinerea*, *Alternaria brassicicola* or *Sclerotinia sclerotiorum*^{36,37}.

The present proteomic study also identified several proteins, such as cystathionine- β -synthase (CBS) domains containing protein (CDCP), S-formylglutathione hydrolase, subtilisin-like protease, 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase, inosine-5'-monophosphate dehydrogenase, peptidylprolyl isomerase, peptidylprolyl isomerase and dynamin-related protein that are specifically decreased by brown rot in the relatively susceptible 'RL' fruit. Particularly, the observation that CDCPs abundance was decreased in 'RL' fruits inoculated with both *M. fructicola* and *M. laxa*, which, given the role of this enzyme in the regulation of redox homeostasis under pathogenic infection^{38–40}, prompts the question of whether this protein has an active function as a regulator of pathogen sensitivity in stressed plants.

Our proteomic analysis also provide evidence that S-formylglutathione hydrolase (SFGH) may be involved in fruit response to pathogen attack since we observed that this protein was down-regulated in 'RL' fruits inoculated with *M. laxa*. SFGH is a glutathione thiol esterase that hydrolyzes S-formylglutathione to glutathione and formate and participates in the formaldehyde detoxification pathway in plants⁴¹. However, we cannot speculate on its role in resistance to brown rot as there is little information regarding this protein. It is widely recognized that pathogen attack promotes the site-specific generation of reactive oxygen species (ROS) that can exacerbate the oxidative stress at the local site⁴². One of the consequences of the oxidative stress is lipid per-oxidation that might generate formaldehyde and other reactive lipid peroxidation products that can be provoke oxidative damage to peach fruit²⁷. We speculate that these differences in the SFGH abundance between cultivars reflect the differences in the ROS-originated oxidative damage contribution to brown rot sensitivity.

This study also documents that *Monilinia* species increased few proteins in 'RL' which are not affected in the 'RG' fruit, and involve, formate dehydrogenase (FDH), UDP-glycosyltransferase (UGT) and 1-aminocyclopropane-1-carboxylate. In this sense, FDH abundance was increased in the artificially-inoculated 'RL' fruit compared to the non-inoculated fruit, suggesting that it might be involved in fruit responses to brown rot agents.

In higher plants formate dehydrogenase is a mitochondrial, NAD-dependent enzyme that catalyzes the oxidation of formate to carbon dioxide⁴³. Formate results from photorespiratory glyoxylate and play a metabolic role as a signal in response to different stressful conditions⁴⁴. Formate dehydrogenase is induced by several abiotic stresses such as hypoxia, wounding, chilling and heat⁴³. There is convincing evidence that FDH may be involved in host-pathogen interactions^{45,46}; however, the role of FDHs in defense response to pathogen attack remain unclear. It has been reported that *FDH1* participates in the cell death signaling pathway, defense-related hormone and gene regulation, leading to hypersensitive cell death and defense response against pathogens⁴⁷. Particularly, in peach fruits it was evidenced that formate may derive from the conversion of methionine to ethylene as it was expressed in high levels during fruit ripening, coinciding with the start of the climacteric period^{48–50}. Therefore, FDH1 may regulate diverse peach fruit defense responses and ripening syndrome.

Glycosylation plays an important role in the phenylpropanoids by enhancing their solubility and stability, facilitating their storage and accumulation in living cells, and regulating their chemical properties and bioactivities⁵¹. Glycosylation is regulated by UDP-glycosyltransferase, which catalyzes the transfer of a saccharide moiety from an activated glycosyl donor to a nucleophilic glycosyl acceptor molecule, establishing natural glycosidic linkages⁵². Several lines of evidence show that phenylpropanoid compounds (i.e. chlorogenic acid) play a crucial role in peach resistance to *Monilinia* spp.^{20,21,53} while studies of UDP-glycosyl transferase in pathogen plant–pathogen interactions have revealed its function in disease resistance^{54,55}. Despite the increase in UDP-glycotransferase abundance and expression in the tissues of the 'RL' fruit in the presence of *M. laxa* the fruit of this cultivar remained extremely susceptible to the pathogen, suggesting that other factors contribute to this increased susceptibility, remaining to be elucidated.

The abundance of the 1-aminocyclopropane-1-carboxylate deaminase was increased in fruits of 'RL' inoculated with *M. laxa*. Recent studies have shown that on climacteric fruits such as kiwifruit or apple, it degrades 1-aminocyclopropane-1-carboxylate (ACC)^{56,57}. ACC constitutes the immediate precursor of ethylene and its degradation leads to a reduction in ethylene biosynthesis in these fruits. It is well established that ethylene plays a crucial role in the regulation of fruit defense against microbial pathogens⁵⁸. Depending on the pathogen type (necrotrophic vs biotrophic pathogens) and the plant species, ethylene can promote disease development acting as a virulence factor, while, in other cases, ethylene modulates resistance responses acting as a signaling compound for resistance to the pathogens^{59,60}. In several climacteric fruits has been shown that reduced ethylene production leads to an increase of their susceptibility to necrotrophic pathogens due to ethylene involvement into the regulation of defense-associated genes^{60,61}. However, in a recent study aiming to explore the role of ethylene during *Monilinia* spp. infection has been proposed that brown rot agents try to suppress ethylene biosynthesis aiming to an inhibition of fruit defense reactions⁶². The different level of 1-aminocyclopropane-1-carboxylate deaminase in the present work might be due to the spatial and temporal action of ethylene that was produced both during fruit-pathogen interactions and peach fruit ripening process. An alternate action, that needs to be considered, is whether ethylene directly affects the growth of *Monilinia* spp. as speculated by Sharon *et al.*⁶³ for *B. cinerea* in other types of fruits. A previous report suggested that applications of exogenous ethylene did not affect the development of *M. fructicola* on peach, nectarine and plum fruit⁶⁴. However, it has not been known yet what is the effect of endogenous ethylene produced within the host tissues. Thus, further research is required to highlight the precise role of the 1-aminocyclopropane-1-carboxylate deaminase, notably the ethylene metabolism, as a mechanism to account for fruit responses to *Monilinia* spp.

This study provides the first information concerning the peach fruit proteomic response to infection by brown rot pathogens such as *M. fructicola* and *M. laxa*. It is also illustrated the differential accumulation of proteins in response to both *M. fructicola* and *M. laxa* in peach cultivars with different resistance levels against brown rot. The significant up-accumulation of several proteins associated with defense in the disease-resistance cultivar and the down-accumulation of the defense proteins in the susceptible cultivar, may explain their differences in disease resistance levels. Further research should be conducted to determine their precise role and relationship of these proteins in peach fruit defense against brown rot, thereby enabling our ability to control this disorder using knowledge-based new peach breeding programs.

Methods

Fruit samples. Fruit used in the study were collected from an experimental orchard in Imathia (North Greece). Two medium-early harvest peach (*Prunus persica*) cultivars, Rich Lady and Royal Glory, grafted onto GF-677 (*Prunus persica* × *Prunus amygdalus*) rootstock, trained in an open vase, were used. Healthy with no visual defect fruits were sampled at commercial harvest stage (firmness 36.5 ± 5 N) and transported immediately

at the laboratory. All experimental fruit had received no previous fungicide applications during the vegetative period.

Artificial inoculations. Two isolates of *M. fructicola* (Mf 101, Mf 160) and two isolates of *M. laxa* (Ml 1, Ml 66) were used for the artificial inoculations. Isolates were recovered from infected peaches of commercial orchards in Imathia region and identified to species level with a PCR assay developed by Hily *et al.*⁶⁵. Artificial inoculation was conducted as described by Papavasileiou *et al.*³. Briefly, for conidia production, isolates were cultured in Petri dishes on V8 agar juice nutrient medium for 7 days at 25 °C, under continuous light. Five ml of sterile and distilled water were then added in each Petri dish, while the conidia were scraped off the cultures with a surgical scalpel. The conidial suspension was then filtered twice through a cheesecloth to withhold mycelia and adjusted to a concentration of 10^5 spores ml^{-1} with a Neubauer Haemocytometer. Before the inoculation, fruit were disinfected by dipping them in a 10% sodium chloride solution for 1 min and then rinsed twice using distilled water and let to dry. Fruit were then placed in sterilized plastic containers lined with wet paper towels. The inoculation was carried out by pipetting a drop of 20 μl spore solution on the un-wounded surface of each fruit. In total 15 replicate fruits (3×5 fruit, in 3 independent replications) of each peach cultivar were inoculated with each isolate. The containers were then sealed airtight with a plastic lid to ensure 100% relative humidity necessary for the infection. The fruit were incubated for 6 days at 22 °C. After the incubation period the disease incidence was determined by measuring the number of fruit showing typical brown rot symptoms. The observed frequencies (%) of diseased fruits of the 2 cultivars were compared using the chi-square test. The statistical analysis tests were performed using SPSS Statistics (version 11.0; IBM, NY).

Plant material utilized for proteomic analysis. The experimental design included the following fruit classes: (i) fruit of the two cultivars artificially inoculated with *M. fructicola* isolates, (ii) fruit of the two cultivars artificially inoculated with *M. laxa* isolates, (iii) fruit of the two cultivars inoculated with sterile water (control). For the proteomic analysis, samples were taken from the mesocarp of the artificially inoculated and control fruit after 6 days of incubation at 22 °C. Approximately 50–70 gr of skinless flesh of the mesocarp were carefully received from each fruit at 1 cm distance from the rotten tissue, to avoid the presence of mycelia in the proteomic analysis. Samples were cut into small pieces, placed in polyethylene bags (3 fruits per bag), frozen instantly in liquid nitrogen and stored at -80°C until further analysis. Totally, 15 fruits (3×5 fruit in each replicate) were utilized for the analysis.

Protein extraction. The extraction was performed according to a previous report⁵⁰ following phenol-based extraction protocol. After pellet complete drying the proteins were solubilized in buffer containing 4% CHAPS (3-[(3-Cholamidopropyl) dimethylammonio]-1-propanesulfonate), 7 M urea, 2 M thiourea, 20 mM DTT, 0.5% ampholyte pH 3–10, 2% Triton X-100 and bromophenol blue. Protein concentrations were measured according to Bradford⁶⁶ using bovine serum albumin (BSA; Sigma) as a standard.

Two-dimensional gel electrophoresis and protein quantification. Proteins (50 μg) were separated by 2D-PAGE as described by Minas *et al.*⁴⁴. Isoelectric focusing was run onto immobilized pH gradient gel strips (IPG strip pH 3–10 NL, 11 cm; Biorad) and then SDS–PAGE onto 12.5% polyacrylamide gels (Criterion Tris-HCl Precast Gels-Biorad). For each treatment, 2-D gels were run in triplicate and for three independent extractions. Following silver-nitrate stained 2-D gels, were scanned with a Bio-Rad GS-800 Calibrated Densitometer equipped with PDQuest Advanced 2-D Gel Analysis Software. Spots were detected, background subtracted, matched and quantitative determination of the spot volumes was performed (mode: total quantity of valid spots normalization) as reported earlier⁴⁴. Individual means were compared using Student's t-test (significance level 95%). To validate significant differences, Student's t-test was further combined by the quantitative 2-fold change of spot volume.

Protein identification by tryptic in-gel digestion, mass spectrometry and database searching. Cut silver-stained spots were destained and processed using classical tryptic-mediated in-gel digestion⁶⁷. The generated peptide mixture was solubilized in 10 μl solution A (2% acetonitrile in 0.1% formic acid) and pre-concentrated with a flow of 5 $\mu\text{l}/\text{min}$ for 10 min on a C18 trap column (Acclaim PepMap, Thermo Scientific) and then loaded onto a 50 cm long C18 column (75 μm ID, particle size 2 μm , 100 Å, Acclaim PepMap RSLC, Thermo Scientific). The binary pumps of the HPLC (Ultimate 3000, RSLCnano, Thermo Scientific) consisted of solution A (2% acetonitrile in 0.1% formic acid) and solution B (80% acetonitrile in 0.1% formic acid). The peptides were separated using a linear gradient from 4% B up to 40% in 40 min for a 1-h gradient run with a flow rate of 300 nl/min . The column was placed in an oven operating at 35 °C. The HPLC was coupled online to a LTQ Orbitrap XL Mass spectrometer (Thermo Scientific). Full scan MS spectra were acquired in the orbitrap (m/z 350–2000) in a profile mode and data-dependent acquisition with the resolution set to 60,000 at m/z 400 and automatic gain control target at 10^6 . The six most intense parental ions were sequentially isolated for collision-induced MS/MS fragmentation (CID) and their daughter fragments were detected in the linear ion trap. Dynamic exclusion was set to 1 minute and activated for 90 s. Ions with single charge states were excluded. Lock mass of m/z 445,120025 was used for internal calibration. The Xcalibur software (Thermo Scientific) was used to control the system and acquire the raw files. The raw files were analyzed with Proteome discoverer 1.4 (Thermo Scientific) using the complete Uniprot database of *Prunus persica* (3760, 28650 entries). Search parameters were strict trypsin specificity, allowing up to two missed cleavage sites. Oxidation of methionines, cysteine caramidomethylation as well as deamidation of asparagines and glutamines were set as variable modifications. The false discovery rate (FDR) was set to 5%. In case the *Prunus persica* protein identified was not yet annotated its sequence was processed through a BLAST-mediated search against current plant databases in order to find homologous and annotated proteins suggesting its potential function.

Primer name	Nucleotide sequence (5' – 3')	Amplicon size (bp)	Accession number (GenBank)	Target gene
Thaum-Fw	ATGGAAGCGTAATTGCGTGC	92	NW_006760268.1	Thaumatin
Thaum-Rev	GCACTGGGTCTTGAAGAGCT			
UDP-Fw	ACATGCACCTGATGGCGTAA	103	NW_006760201.1	UDP-glycotransferase
UDP-Rev	GCTCGATAGCTGCATTGTGG			
Major-Fw	CTGTGGCAGGAAGTGGTAGG	111	NW_006760194.1	Major latex allergen
Major-Rev	ACCACACACGAATCCAACGT			
Glutath-Fw	CGTGAACGACATGTGAGGGA	107	NW_006760268.1	Glutathione-S-transferase
Glutath-Rev	AGCAAATTACAAGGGCGGGA			
Form-Fw	GCCCAGCACGTTAGAAAGGA	95	NW_006760268.1	Formate dehydrogenase
Form-Rev	GTCTTTTCGCATCGTGACC			
Aminocycloprop-Fw	GATTGGGCTCTTGCTGAGT			
Aminocycloprop-Rev	GACAGAAAAGGCACGACCT	104 164 178	NW_006760212.1 XM_007211382.2 XM_020565692.1	1-aminocyclopropane-1-carboxylate deaminase Actin-7 NADH dehydrogenase [ubiquinone]
Actin - Fw	TCAATGTGCCTGCCATGTAT			
Actin - Rv	AGCAAGGTCCAGACGAAGAA			
NADH -Fw	GTGGATGGGACAACCTTGCTT			
NADH - Rv	GCAATTGCATCCACAATGTC			

Table 1. List of primers used in the RT-qPCR assay.

RNA preparation and quantitative RT-PCR (RT-qPCR). For some of the proteins that showed differential accumulation among treatments (peach cultivar or pathogen) a RT-qPCR was employed to study whether protein modulation profile follows gene expression pattern. Genes utilized in the RT-qPCR were thaumatin, UDP-glycotransferase, major latex allergen, glutathione S-transferase, formate dehydrogenase, 1-aminocyclopropane-1-carboxylate deaminase, all involved in disease/defense mechanisms. Gene specific primers were designed based on the respective mRNA gene sequences deposited in GenBank (GenBank accession numbers NW_006760268.1, NW_006760201.1, NW_006760194.1, NW_006760268.1, NW_006760268.1 and NW_006760212.1, respectively). Primers were designed using the online software Primer3Plus⁶⁸. All primers are listed in Table 1.

RNA was extracted from fruit samples taken from the mesocarp of the artificially inoculated and control fruit after 72 h of incubation at 22 °C. Skinless pulp samples were removed from each fruit around the inoculation point using a cork borer and immediately frozen with liquid nitrogen and stored at –80 °C until use. Total RNA was extracted using the NucleoSpin RNA Plant kit following the manufacturer's protocol (Macherey-Nagel GmbH & Co. KG, Germany) and its concentration was measured using a P330 nanophotometer (Implen GmbH). The actin and ubiquinone genes were used as reference genes.

The qRT-PCR amplification conditions were as those described by Pappi *et al.*⁶⁹. The 25 µl qRT-PCR reaction consisted of buffer 5x, 1.5 µl of EVA Green, 0.2 mM of each dNTP, 4 mM DTT, 1 U of Superscript III RNaseH–Reverse Transcriptase, 1.5 mM additional MgSO₄ (Invitrogen-Life Technologies, Groningen, The Netherlands), 3 U of HotStartTaq DNA polymerase (Qiagen, Hilden, Germany) and 1 M of each primer. The thermal cycling conditions were the following: 50 °C for 30 min, followed by 95 °C for 12 min for cDNA synthesis and 40 cycles in 3 steps: (a) 30 s at 95 °C (denaturation), (b) 30 s at 56 °C (annealing) and (c) 20 s at 72 °C (extension). The fluorescence levels were measured at the end of each cycle. The assay was performed using the Mx3005Pro Real-Time PCR detection system (Stratagen, USA). The analysis of fluorescence data was conducted using the Mx3005P Software (version 4.00 Build 367, USA). The Cq value for each gene was measured and the expression level of the genes in the different samples was calculated using the formula $2^{-\Delta\Delta Cq}$ ⁷⁰.

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Author contributions

G.T., A.M. and G.K. designed the experiments; A.P. performed the experiment; A.S. contributed to primer design and real-time PCR experiments, A.P., M.S. and G.T. performed analysis and interpretation of the data; A.P., G.T. and G.K. drafted the manuscript; A.M., G.T., M.S., and G.K. revised the M.S.; all authors revised the paper and approved the final version to be published.

Competing interests

The authors declare no competing interests.

Additional information

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"Supplementary Materials of “Proteomic analysis upon peach fruit infection with *Monilinia fructicola* and *M. laxa* identify responses contributing to brown rot resistance”, by Antonios Papavasileiou, Georgia Tanou, Anastasios Samaras, Martina Samiotaki, Athanassios Molassiotis, George Karaoglanidis"

Table S1. Identification details of differentiable proteins in the mesocarp of the Rich Lady and Royal Glory peach (*Prunus persica*) cultivars after their inoculation with *Monilinia fructicola* and *M. laxa* isolates.

Spot No ^a	Accession Number ^b	Suggested Name ^c	Description	Matching criteria ^d	Organism ^e	Subcellular localization ^f	Functional Category ^g	SEQUEST Score	% Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI	Peptide confidence	Sequence	# PSMs	Modifications	ΔCn	XCorr	Charge	MH+ [Da]	ΔM [ppm]	RT [min]
13	M5WGH9	plastid-lipid-associated protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005787mg PE=4 SV=1 - [M5WGH9_PRUPE]	97% to GI:645236410 Prunus persica, E value 0	Prunus persica	Chloroplast	11.05- Disease/Defense/Stress responses	118,83	23,20	2	9	10	61	444	48,8	6,74	High	ETESAVAVAEDDKPAEPESAETSR	8		0,0000	4,74	3	2518,14548	1,04	41,44
																	High	GDNGSVFVLIK	2		0,0000	3,35	2	1148,63054	-0,45	49,50
																	High	ALVDSFYGTDR	10		0,0000	2,90	2	1243,59587	0,39	50,33
																	High	GDnGSVFVLIK	2	N3(Deamidated)	0,0000	2,88	2	1149,61504	-0,03	51,20
																	High	vVDEDEWGPEK	3	N-Term(Acetyl)	0,0000	2,79	2	1344,59587	0,29	50,61
																	High	SLTTSVQDTASSVVK	1		0,0000	2,62	2	1534,83330	0,62	48,80
																	High	VVDEDEWGPEK	12		0,0000	2,34	2	1302,58562	0,54	50,93
																	High	LDLTVFK	5		0,0000	2,29	2	835,49254	0,14	49,22
																	High	FSISnSK	2	N5(Deamidated)	0,0000	2,26	2	783,38823	-0,14	39,90
																	Medium	TISSQPPFK	4		0,0000	1,68	2	1004,54100	-0,16	42,27
																	Medium	FSISNSK	1		0,0000	1,61	2	782,40422	-0,13	38,76
																	Medium	GTLPLVK	10		0,0000	1,30	2	727,47161	0,43	42,95
																	Medium	KALVDSFYGTD R	1		0,1517	1,23	3	1371,68955	-0,59	43,74
19	M5WVK0	major latex allergen	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa012576mg PE=4 SV=1 - [M5WVK0_PRUPE]	65% to GI:657984121 Malus domestica, E value 1e-18	Prunus persica	Cytoplasm	11.02- Disease/defense/Defense-related	122,89	82,82	1	8	8	37	163	17,0	3,87	High	TPEEPVAAAPAAVTESEAAATTEEPK	8		0,0000	5,71	3	2496,20212	1,28	45,19
																	High	TEEKTPEEPVAAAPAAVTESEAAATTEEPK	1		0,0000	4,58	3	2983,43094	1,40	42,81
																	High	AAEAEAEPPAAETEK	7		0,0000	3,84	2	1646,74028	0,62	37,09
																	High	EVTAAEPVAAVAEETK	7		0,0000	3,60	2	1614,82366	0,90	45,06
																	High	EETTESAETPAAAPVVEEKPEETT TDVPVEK	3		0,0000	3,53	3	3369,56504	1,70	42,86

																		High	AAEAEAEPPAA TETEKTEAEEPK	6		0,0000	2,93	2	2431,10381	1,73	38,48
																		Medium	ETTPVEAEAEAE APAAPEAEAPV PAEVEIK	2		0,0000	2,21	3	3033,44529	0,94	45,97
																		High	TVEVIKTEEK	3		0,0000	2,11	2	1175,65141	-0,37	36,81
20	M5X HX6	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Prunus persica GN=PRUPE_ppa010941mg PE=3 SV=1 - [M5XHX6_PRUPE]		Prunus persica	Chlorop last	01.01- Metabolism /Amino Acid	58,23	39,3 0	1	8	8	24	229	26,9	5,82		High	LDADNYETDEE LK	5		0,0000	4,09	2	1554,68205	0,90	43,95
																		High	EEVIQAWYmDD SDEDQR	2		0,0000	3,72	2	2128,88042	1,84	48,96
																		High	GYSYMDFcEVS PEK	2	C8(Carb amidom ethyl)	0,0000	3,44	2	1711,69963	1,01	47,81
																		High	LDADNYETDEE LKK	5		0,0000	3,27	2	1682,77666	0,62	39,17
																		High	GYSYmDFcEVS EK	3	M5(Oxi dation); C8(Carb amidom ethyl)	0,0000	2,74	2	1727,69536	1,48	44,51
																		High	YAVAGSGYFDV R	1		0,0000	2,60	2	1304,62737	0,26	45,55
																		High	FTLDTNNYIK	2		0,0000	2,53	2	1228,62114	0,23	46,49
																		High	LPNYEEK	2		0,0000	2,31	2	892,44042	-0,77	37,65
																		High	EEVIQAWYmDD SDEDQR	1	M9(Oxi dation)	0,0000	2,02	2	2144,87505	1,69	48,22
																		Medium	AFVHKETGDHA VDAAA	1		0,0000	1,42	3	1638,78696	-0,11	36,22
407	M5W XC0	alanine aminotransferase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003850mg PE=4 SV=1 - [M5WXC0_PRUPE]	99% to GI:645243725 Prunus mume, E value 0	Prunus mume	Chlorop last	01.01- Metabolism /Amino acid	25,68	14,1 5	1	7	7	11	544	59,6	6,15		High	VGDSESYELYcA EK	2	C10(Car bamido methyl)	0,0000	3,12	2	1562,66924	0,81	43,57
																		High	DTIAAGIEAR	2		0,0000	2,72	2	1016,53703	-0,12	42,36
																		High	GEIVTLAQR	2		0,0000	2,66	2	986,56285	-0,12	41,88
																		High	AAEAANTAPDA FYcR	2	C14(Car bamido methyl)	0,0000	2,65	2	1627,71807	0,65	42,66
																		Medium	SETQGLFSADAI ER	1		0,0000	1,84	2	1523,73393	0,15	46,87
																		Medium	IPAIVTR	1		0,0000	1,77	2	769,49352	0,55	41,34
																		Medium	cTILPQEDK	1	C1(Carb amidom ethyl)	0,0061	1,64	2	1103,54033	0,13	40,54
812	M5Y 2Q5	patellin	Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa023884mg PE=4 SV=1 - [M5Y2Q5_PRUPE]	79% to GI:470127731 Fragaria vesca subsp. vesca, E value 0	Fragaria vesca subsp. vesca	Cytopla sm	08.07- Intracellular traffic/Vesi cular	140,76	34,9 3	2	2 2	22	87	584	65,3	4,87		High	KAEEEPKAEVA AAEEPK	2		0,0000	3,20	3	1825,91690	-0,55	37,66
																		High	AEVAAAEEPK	3		0,0000	3,13	2	1014,50981	-0,46	37,28
																		High	HEFTAPPTPPPA K	5		0,0000	3,10	2	1389,71684	0,47	39,61
																		High	KVAPADEPVISN SYK	4		0,0000	3,08	2	1617,85015	1,12	39,64
																		High	EESYVVGGELPE PQK	1		0,0000	2,93	2	1603,78594	0,55	46,28
																		High	IIAQSVSFK	3		0,0000	2,79	2	992,57762	0,07	42,46
																		High	VVLTIDNQSSK	5		0,0000	2,79	2	1203,65813	0,11	43,56
																		High	VAPADEPVISNS YK	5		0,0000	2,50	2	1489,75456	0,81	41,84
																		High	mISPFLTQR	3	M1(Oxi dation)	0,0000	2,45	2	1108,58183	-0,15	45,92

																	High	ELYQNTFTDEE KR	5		0,0000	2,45	2	1672,78313	1,06	40,90
																	High	MISPFLTQR	5		0,0000	2,36	2	1092,58696	-0,11	46,91
																	High	VVFTHGVDK	6		0,0000	2,31	2	1001,54106	-0,44	38,33
																	High	SAETLFK	5		0,0000	2,27	2	795,42461	-0,15	43,79
																	High	QLIQEALNK	3		0,0000	2,25	2	1056,60430	-0,51	42,21
																	High	FVFAGPSK	5		0,0000	2,15	2	852,46117	-0,34	45,22
																	High	ELYQNTFTDEE K	4		0,0000	2,14	2	1516,68205	1,20	46,22
																	High	SDVVLLK	2		0,0000	2,13	2	773,47661	-0,21	42,63
																	High	DAFAMIK	5		0,0000	2,09	2	795,40703	0,05	48,55
																	Medium	VKDAAFAMIK	1		0,0000	2,01	3	1022,57032	-0,06	42,42
																	High	DAFAMIK	6	M5(Oxi dation)	0,0000	2,01	2	811,40166	-0,30	42,62
																	Medium	EGPPEAEAEAV AEKPVAAEK	3		0,0000	1,86	3	2080,00815	-0,02	43,36
																	Medium	IQFLEK	2		0,0000	1,84	2	777,45049	-0,08	43,59
																	Medium	VKDAAFAMIK	1	M7(Oxi dation)	0,0000	1,77	3	1038,56540	0,10	39,40
																	Medium	ALEELK	2		0,0000	1,71	2	702,40325	-0,04	41,00
																	Medium	EGEQEFTSDPV TEITVKPATK	1		0,0000	1,41	3	2407,18961	0,83	44,77
1013	M5X G10	Proteasome subunit beta type	Proteasome subunit beta type OS=Prunus persica GN=PRUPE_ppa010791mg PE=3 SV=1 - [M5XG10_PRUPE]		Prunus persica	Chlorop last	06.13- Protein destination and storage/Prot eolysis	26,50	28,3 9	2	7	7	11	236	25,4	5,21	High	TVVINSEGVTR	2		0,0000	3,13	2	1174,64275	0,06	40,45
																	High	TSTGVVYVANR	1		0,0000	2,82	2	1067,54753	-0,47	38,13
																	High	DEAEQLVVK	1		0,0000	2,81	2	1030,54119	-0,37	42,27
																	High	SGSAADSQVVS DYVR	2		0,0000	2,68	2	1540,72539	1,00	42,87
																	High	AVSLAIAR	2		0,0000	2,12	2	800,49858	-0,41	42,32
																	Medium	DEAEqLVVK	1	Q5(Dea midated)	0,0000	1,71	2	1031,51897	-6,42	43,19
																	Medium	VcANLVR	1	C2(Carb amidom ethyl)	0,0000	1,66	2	831,45036	-0,25	38,80
																	Medium	LLSYGNK	1		0,0000	1,61	2	794,44042	-0,36	39,31
1109	M5W B91	malonyl-CoA-acyl carrier protein transacylase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa007010mg PE=4 SV=1 - [M5WB91_PRUPE]	98% to GE:645215431 Prunus mume, E value 0	Prunus mume	Mitocho ndrion	01.06- Metabolism /Lipid and sterol	40,57	23,8 3	1	9	9	18	386	40,9	8,12	High	VQQLcDAANQE VDDANK	2	C5(Carb amidom ethyl)	0,0000	4,20	2	1917,86357	1,45	40,90
																	High	SAMVSVIGLDS DK	2		0,0000	3,67	2	1321,66753	0,50	47,84
																	High	GEAMQEAAADA AK	2		0,0000	3,10	2	1191,53008	-0,87	38,19
																	High	LRGEAmQEAAAD AAK	2	M6(Oxi dation)	0,0000	2,75	3	1476,71143	0,14	36,51
																	High	LRGEAMQEAAAD AAK	1		0,0000	2,57	3	1460,71534	-0,66	38,39
																	High	SYELGPGK	1		0,0000	2,28	2	850,43028	-0,30	39,02

																	High	QVTSPVQWETT VK	2		0,0000	2,23	2	1502,78545	0,30	46,09
																	High	LAATQIR	2		0,0000	2,22	2	772,46752	-0,11	37,79
																	Medium	EAQSVPAAE LYK	2		0,0000	1,62	2	1376,70659	0,66	44,34
																	Medium	VIAGIVK	2		0,0000	1,59	2	699,47637	-0,02	40,47
1119	Q436 18	1-aminocyclopropane 1- carboxylic acid oxidase	1-aminocyclopropane 1- carboxylic acid oxidase OS=Prunus persica GN=PAO1 PE=2 SV=1 - [Q43618_PRUPE]		Prunus persica	Cytopla sm	11.05- Disease/Def ense/Stress responses	175,29	58,6 2	1 0	4	20	108	319	36,1	5,30	High	SNISEVPDLEDQ YR	8		0,0000	3,81	2	1664,77788	0,96	45,36
																	High	KAFYGTnGPTFG TK	2	N7(Dea midated)	0,0000	3,55	2	1489,73076	-0,98	42,11
																	High	AFYGTNGPTFG TK	10		0,0000	3,34	2	1360,65422	0,72	45,27
																	High	AFYGTnGPTFGT K	4	N6(Dea midated)	0,0000	3,27	2	1361,63909	1,34	46,29
																	High	AHTDAGGLILF QDDK	2		0,0000	3,25	3	1713,88089	0,11	50,36
																	High	SVEHRVIAQTD GTR	1		0,0000	2,70	3	1568,81321	-0,51	35,84
																	High	FKELVASK	6		0,0000	2,66	2	921,53996	-0,52	38,21
																	High	DGQWIDVPPMR	11		0,0000	2,61	2	1313,63091	0,11	50,87
																	High	KAFYGTNGPTF GTK	4		0,0000	2,57	3	1488,74796	-0,17	40,78
																	High	ELVASKGLEAV K	1		0,0000	2,51	2	1243,72527	-0,35	40,38
																	High	VSLQLLK	3		0,0000	2,45	2	857,54564	0,14	45,91
																	High	FVFEDYMK	8		0,0000	2,41	2	1078,49138	-0,06	48,31
																	High	DGQWIDVPPmR	6	M10(Ox idation)	0,0000	2,40	2	1329,62566	-0,01	45,85
																	High	TEVNDMDWEST FYLR	1		0,0000	2,35	2	1905,83293	0,26	51,55
																	High	TEVNDmDWEST FYLR	1	M6(Oxi dation)	0,0000	2,29	2	1921,83074	1,76	50,29
																	High	VSNYPPcPNPELI K	13	C7(Carb amidom ethyl)	0,0000	2,25	2	1627,81658	1,02	44,38
																	High	NVMKEFALK	1		0,0000	2,21	2	1079,59148	-0,34	42,74
																	High	FVFEDYmK	8	M7(Oxi dation)	0,0000	2,14	2	1094,48638	0,02	48,20
																	High	mENFPINLEGL NGEGR	1	N- Term(A cetyl)	0,0000	2,02	2	1944,95281	2,22	57,01
																	Medium	AVETNISLGPIA TA	2		0,0000	1,83	2	1356,73711	0,09	51,37
																	Medium	VIAQTDGTR	2		0,0000	1,74	2	960,51103	0,11	36,17
																	Medium	NQVYPK	1		0,0000	1,52	2	748,39855	-0,38	35,74
																	Medium	LYAGLK	10		0,0000	1,10	2	664,40318	0,49	40,87
1314	M5X RM0	3-oxo-Delta(4,5)-steroid 5- beta-reductase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006780mg PE=4 SV=1 - [M5XRM0_PRUPE]	89% to GI:694311973 Pyrus x bretschneideri, E value 0	Pyrus x bretschn eideri	Chlorop last	01.06- Metabolism /Lipid and sterol	28,07	15,9 5	2	5	6	21	395	44,6	5,27	High	ANEIENcEAnGA MFR	2	C7(Carb amidom ethyl); N10(De amidate d)	0,0000	4,86	2	1726,71147	-2,65	44,94
																	High	ANEIENcEANGA MFR	1	C7(Carb amidom ethyl)	0,0000	3,29	2	1725,73430	1,32	43,46
																	High	ANEIENcEANGA mFR	3	C7(Carb amidom ethyl); M13(Ox idation)	0,0000	3,12	2	1741,72905	1,21	41,40

																	High	AHDPPFTEDLPR	1		0,0000	2,68	3	1394,66938	-0,43	43,09
																	High	LSLVEMmK	6	M7(Oxidation)	0,0000	2,39	2	966,49950	-0,43	45,27
																	High	LSLVEMMK	1		0,0000	2,24	2	950,50456	-0,46	48,85
																	Medium	VVIPVAPNLR	3		0,0000	1,96	2	1077,67778	-0,16	47,16
																	Medium	EGVWEEIVK	1		0,0000	1,56	2	1088,56243	0,10	48,48
																	Medium	LSLVEmmK	1	M6(Oxidation); M7(Oxidation)	0,0000	1,53	2	982,49443	-0,41	41,34
1319	M5VPZ0	Eukaryotic initiation factor	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006450mg PE=4 SV=1 - [M5VPZ0_PRUPE]	99% to Gt:658005180 Malus domestica, E value 0	Malus domestica	Chloroplast	05.04- Protein synthesis/Translation factors	34,44	22,38	5	4	12	22	411	46,7	5,58	High	GLDVIQQAQSG TGK	2		0,0000	4,08	2	1401,73406	0,54	42,71
																	High	ALGDYLGVR	2		0,0000	2,50	2	963,52544	-0,43	46,43
																	High	RDELTLEGIK	1		0,0000	2,35	2	1173,64824	0,68	42,93
																	High	VHAcVGGTSVR	3	C4(Carboxamidomethyl)	0,0000	2,06	2	1142,57378	0,19	35,60
																	High	VFDMLR	2		0,0000	2,06	2	780,40709	-0,30	47,24
																	High	DELTLEGIK	1		0,0000	2,03	2	1017,54637	0,05	46,74
																	Medium	ELAQQIEK	2		0,0000	1,93	2	958,52031	-0,13	38,44
																	Medium	GVAINFVTK	2		0,0000	1,70	2	948,55113	-0,22	44,97
																	Medium	KGVAINFVTK	1		0,0000	1,67	2	1076,64629	-0,02	42,02
																	Medium	MLFDIQK	1		0,0000	1,52	2	894,47472	-0,76	47,57
																	Medium	GIVPFcK	1	C6(Carboxamidomethyl)	0,0000	1,26	2	820,43877	0,19	44,67
																	Medium	VFDmLR	2	M4(Oxidation)	0,0000	1,25	2	796,40178	-0,57	46,57
																	Medium	VLITTDLLAR	2		0,0000	1,16	2	1114,68401	0,82	50,19
1321	M5WE97	UDP-glycosyltransferase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005294mg PE=3 SV=1 - [M5WE97_PRUPE]	95% to Gt:645276064 Prunus mume, E value 0	Prunus mume	Cytoplasm	11.05- Disease/Defense/Stress responses	119,88	32,05	2	14	57	468	52,1	5,43	High	IEDDKEYGVQL YK	3		0,0000	4,51	3	1599,78971	-0,27	42,93	
																	High	LEQQVVDsmSK	5	M9(Oxidation)	0,0000	3,81	2	1279,62053	0,49	38,17
																	High	VMEGETAIEMK	4		0,0000	3,63	2	1237,58135	0,79	41,95
																	High	LEQQVVDsmSK	3		0,0000	3,42	2	1263,62517	0,14	40,53
																	High	VTVANTIFISK	2		0,0000	3,39	2	1192,69328	-0,31	46,21
																	High	VMEGETAIEmK	6	M10(Oxidation)	0,0000	3,22	2	1253,57561	0,26	39,41
																	High	KVMEGETAIEMK	3		0,0000	3,00	2	1365,67571	0,27	40,51
																	High	AESIAAYLDR	4		0,0000	2,91	2	1108,56316	-0,18	47,10
																	High	EMVLNQYSNLHK	3		0,0000	2,77	2	1475,73149	0,22	41,79
																	High	VmEGETAIEmK	1	M2(Oxidation); M10(Oxidation)	0,0000	2,66	2	1269,56963	-0,45	37,53
																	High	ADFIANSFYK	2		0,0000	2,43	2	1322,64153	-0,06	51,20

																		High	LVQDVWK	1		0,0000	2,42	2	887,49870	0,15	43,43
																		High	SSGSVQFDTISD GYDEEGFAR	1		0,0000	2,39	2	2266,97734	1,66	47,85
																		High	KVMEGETAIEm K	6	M11(Ox idation)	0,0000	2,24	2	1381,67009	-0,12	37,16
																		High	QMEELALGLK	3		0,0687	2,17	2	1131,60808	0,17	49,78
																		High	TLIELITK	3		0,0000	2,06	2	930,58660	-0,49	49,47
																		Medium	EEIEScIR	2	C6(Carb amidom ethyl)	0,0000	1,95	2	1035,47734	-0,23	39,50
																		Medium	QmEELALGLK	3	M2(Oxi dation)	0,0000	1,76	2	1147,60271	-0,09	44,96
																		Medium	MLTIGPTIPYTY LDNR	1		0,0000	1,73	2	1867,96416	0,99	51,28
																		Medium	EmVLNQYSNLH K	1	M2(Oxi dation)	0,0000	1,38	3	1491,72599	-0,07	40,68
	M5W TK5	actin	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa007242mg PE=3 SV=1 - [M5WTK5_PRUPE]	100% to GE225431585 Vitis vinifera, E value 0	Vitis vinifera	Cytopla sm	09.04-Cell structure/C ytoskeleton	76,03	32,1 0	4	3	12	44	377	41,7	5,49	High	AGFAGDDAPR	3		0,0000	3,12	2	976,44798	-0,38	38,18	
																		High	GYmFTTTAER	3	M3(Oxi dation)	0,0000	2,96	2	1192,53069	0,29	41,76
																		High	GEYDESGPSIVH R	5		0,0000	2,82	2	1445,66643	0,57	40,20
																		High	GYMFTTTAER	3		0,0000	2,78	2	1176,53569	0,22	44,11
																		High	DAYVGDEAQS	2		0,0000	2,73	2	1182,52751	0,12	37,48
																		High	NYELPDGQVITI GAER	2		0,0000	2,62	2	1774,89946	1,34	49,60
																		High	HTGVmVGMGQ K	4	M5(Oxi dation)	0,0000	2,59	2	1160,55510	-0,04	36,47
																		High	VAPEEHPVLLTE APLNPK	2		0,0000	2,57	3	1954,06528	0,40	45,58
																		High	HTGVmVGMGQ K	4		0,0000	2,30	2	1144,56023	0,00	38,38
																		High	EITALAPSSmK	4	M10(Ox idation)	0,0000	2,12	2	1163,59722	-0,43	40,42
																		High	EITALAPSSMK	2		0,0000	2,08	2	1147,60295	0,13	43,91
																		Medium	DLTDALmK	1	M7(Oxi dation)	0,0000	1,86	2	922,45470	-0,40	44,31
																		Medium	DLTDALMK	2		0,0000	1,74	2	906,45970	-0,49	47,55
																		Medium	RGILTlK	1		0,0000	1,66	2	800,53496	-0,41	39,93
																		Medium	LDLAGR	2		0,0000	1,13	2	644,37285	0,32	40,60
																		Medium	GILTlK	4		0,0000	1,09	2	644,43450	0,50	43,50
1628	M5W 3N4	mediator of RNA polymerase II transcription subunit	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa024477mg PE=3 SV=1 - [M5W3N4_PRUPE]	98% to GE645220654 Prunus mume, E value 0	Prunus mume	Endopla smic reticulu m	04.05.01.04 - Transcriptio n/transcripti onal control	74,06	33,2 3	7	6	15	31	635	69,5	5,36	High	MYQQAGADGA GPVDDEAPAGA SGPGPK	1		0,0000	3,53	3	2443,08506	0,76	41,59	
																		High	FSDASVQSDMK	2		0,0000	3,28	2	1214,53655	0,58	40,15
																		High	VEIANDQGNR	3		0,0000	3,18	2	1228,62834	0,20	39,67
																		High	TTPSYVAFTDTE R	3		0,0000	3,03	2	1487,70171	0,27	44,59
																		High	NALENYAYNM R	2		0,0000	3,02	2	1358,61711	0,97	45,92
																		High	EIAEAYLGSTIK	2		0,0000	2,69	2	1294,68901	0,04	46,87

																	High	ELESLcNPllAK	3	C6(Carbamidomethyl)	0,0000	2,67	2	1386,73052	0,52	47,05
																	High	NALENYAYNmR	2	M10(Oxidation)	0,0000	2,64	2	1374,61125	0,39	43,16
																	High	NQVAMNPINTVFDAK	2		0,0000	2,60	2	1661,83574	2,46	49,01
																	High	DAGVIAGINVLRL	1		0,0000	2,44	2	1197,69499	-0,06	49,54
																	Medium	STVHDVVVLVGGSTRL	1		0,0000	2,40	3	1426,76401	-0,64	40,61
																	High	ATAGDTHLGGEFDNRL	4		0,0000	2,29	2	1675,73137	0,37	39,53
																	High	IINEPTAAAIAYGLDK	1		0,0000	2,22	2	1659,89739	1,26	48,39
																	High	NAVVTVPAYFNDSQRL	1		0,0000	2,08	2	1680,83611	1,21	47,20
																	Medium	FEELNMDLFLRL	1		0,0000	1,86	2	1313,61931	-0,16	51,23
																	Medium	NQVAMnPlnTVFDAK	1	N6(Deamidated); N9(Deamidated)	0,2634	1,79	2	1663,81243	7,66	45,85
1705	M5WY92	HSP70	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002598mg PE=3 SV=1 - [M5WY92_PRUPE]	99% to GI:645245339 Prunus mume, E value 0	Prunus mume	Endoplasmic reticulum	06.01- Protein destination and storage/Folding and stability	105,98	23,09	7	6	12	39	654	71,7	5,38	High	NQVAMNPQNTVFDAK	3		0,0000	4,04	2	1676,80852	1,41	45,78
																	High	VDEVVLVGGSTRL	3		0,0000	3,55	2	1230,66899	0,07	44,49
																	High	ATAGDTHLGGEFDNRL	2		0,0000	3,55	2	1675,73186	0,66	39,56
																	High	NQVAmNPQNTVFDAK	3	M5(Oxidation)	0,0000	3,47	2	1692,80303	1,15	41,47
																	High	VEIIANDQGNRL	3		0,0000	3,37	2	1228,62822	0,10	40,51
																	High	DAGVIAGLNVmRL	2	M11(Oxidation)	0,0000	3,35	2	1231,64592	-0,40	46,14
																	High	NSLENYAYSMRL	2		0,0000	3,35	2	1347,60051	0,52	44,81
																	High	FSDPSVQSDMK	3		0,0000	3,21	2	1240,55193	0,35	41,52
																	High	DAGVIAGLNVmRL	1		0,0000	3,17	2	1215,65166	0,13	48,92
																	High	IINEPTAAAIAYGLDK	1		0,0000	3,08	2	1659,89629	0,60	48,21
																	High	NQLAEVEEFEDK	2		0,0000	2,96	2	1450,67009	0,27	45,37
																	High	TTPSYVAFDTDETRL	4		0,0000	2,79	2	1487,70232	0,68	45,41
																	High	ELEGLcNPllAK	2	C6(Carbamidomethyl)	0,0000	2,75	2	1356,71990	0,49	47,02
																	High	NSLENYAYSmRL	1	M10(Oxidation)	0,0000	2,53	2	1363,59538	0,48	41,75
																	High	FEEMNmDLFLRL	4	M6(Oxidation)	0,0000	2,45	2	1347,57207	0,89	47,52
																	High	FSDPSVQSDmK	2	M10(Oxidation)	0,0000	2,37	2	1256,54741	0,80	38,25
																	High	FEEmNmDLFLRL	1	M4(Oxidation); M6(Oxidation)	0,0000	2,13	2	1363,56682	0,76	44,65
	M5VX34	Peptidyl-prolyl cis-trans isomerase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003471mg PE=4 SV=1 - [M5VX34_PRUPE]	99% to GI:645279361 Prunus mume, E value 0	Prunus mume	Endoplasmic reticulum	06.01- Protein destination and storage/Fol	47,52	24,30	1	16	17	34	572	63,9	5,34	High	TDEEEVIDGLDLRL	3		0,0000	3,31	2	1390,63396	0,46	46,65

							ding and stability										High	VAcNLNNAaCK	2	C3(Carb amidom ethyl); C10(Car bamido methyl)	0,0000	3,30	2	1234,56706	0,25	36,49
																	High	SDRVEFTVK	1		0,0000	2,51	3	1080,56806	-0,36	39,53
																	High	DKESWDMNTEE K	2		0,0000	2,41	2	1511,63298	0,69	39,78
																	High	DGYFcPALS K	3	C5(Carb amidom ethyl)	0,0000	2,22	2	1157,52971	0,08	46,64
																	High	ALeIDPNNR	1		0,0000	2,21	2	1041,53203	-0,36	40,92
																	High	DAEPMSVDSK	1		0,0000	2,19	2	1078,47197	-0,19	38,80
																	High	VLEIEGR	3		0,0000	2,14	2	815,46263	0,54	41,71
																	Medium	LQDGTEFLK	2		0,0000	2,00	2	1050,54619	-0,44	44,71
																	Medium	EGEGWDTPK	2		0,0000	1,99	2	1018,44762	-0,05	39,84
																	Medium	FTLGQGQVIK	3		0,0000	1,98	2	1090,62541	-0,14	44,90
																	Medium	DAEPMSVDSKA	1		0,0000	1,78	2	1149,50957	0,23	39,85
																	Medium	DKESWDmNTEE K	2	M7(Oxi dation)	0,0000	1,45	2	1527,62663	-0,15	37,29
																	Medium	GWDEGIR	1		0,0000	1,38	2	832,39598	1,37	42,10
																	Medium	EGEGFERPNEG AVVK	2		0,0000	1,37	3	1617,78586	-0,59	41,02
																	Medium	VEFTVK	1		0,0160	1,23	2	722,40825	-0,14	41,82
																	Medium	FYGNMFAK	2		0,0000	1,09	2	977,45470	-0,30	46,23
																	Medium	DAEPmSVDSK	1	M5(Oxi dation)	0,0000	1,07	2	1094,46697	-0,12	36,31
1820	M5X T23	Protein transport protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa000665mg PE=4 SV=1 - [M5XT23_PRUPE]	96% to GI:645251127 Prunus mume, E value 0	Prunus mume	Chlorop last	0799-Transporter s/Others	19,31	7,08	1	7	7	10	1045	113,0	5,38	High	DLPVVGESTSSE K	1		0,0000	3,57	2	1347,66460	0,53	42,85
																	High	SSEFEAAIQNGE K	1		0,0000	3,04	2	1409,65715	1,97	42,04
																	High	TIVLALASGQK	1		0,0000	2,65	2	1100,66716	-0,25	45,56
																	High	IALSTEPENVSK	2		0,0000	2,60	2	1287,68010	0,75	41,43
																	High	VMLEDDGTAR	2		0,0000	2,16	2	1106,51409	-0,57	39,63
																	Medium	FSASLcK	1	C6(Carb amidom ethyl)	0,0000	1,64	2	812,39665	-0,59	38,97
																	Medium	MSHSPYLK	1		0,0071	1,39	3	962,47693	0,51	36,72
																	Medium	VmLEDDGTAR	1	M2(Oxi dation)	0,0000	1,08	2	1122,51067	0,92	37,88
1821	M5W X60	HSP70	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001317mg PE=3 SV=1 - [M5WX60_PRUPE]	98% to GI:645244630 Prunus mume, E value 0	Prunus mume	Mitocho ndrion	0601-Protein destination and storage/Fol ding and stability	81,42	26,32	2	20	22	53	855	94,6	5,27	High	FIGTAGAASSLM NPK	1	M12(Ox idation)	0,0000	4,06	2	1480,74785	0,89	42,43
																	High	FIGTAGAASSLM NPK	2		0,0000	3,57	2	1464,75261	0,68	46,50
																	High	YANPVLLSADV R	2		0,0000	3,55	2	1317,71660	0,32	47,53

																		High	FEHIDISDK	4		0,0000	3,14	3	1103,53653	-0,25	41,69
																		High	YQEFVTEPER	2		0,0000	3,03	2	1297,60661	0,51	42,74
																		High	GIDVVLNDESK	1		0,0000	3,01	2	1188,61064	-0,07	44,46
																		High	EFEMALQDR	3		0,0000	2,72	2	1138,51982	0,02	45,92
																		High	ILAHSFQSLGGR	1		0,0000	2,59	3	1400,72751	-0,46	42,26
																		High	TMNASEcVAR	3	C7(Carbamidomethyl)	0,0000	2,49	2	1138,49785	-0,14	36,75
																		High	NAVEAYVYDmR	1	M10(Oxidation)	0,0000	2,47	2	1346,60503	0,34	43,57
																		High	ETPALVcFGDK	2	C7(Carbamidomethyl)	0,0000	2,35	2	1236,59233	-0,51	45,70
																		High	IDVFQNAR	3		0,0000	2,32	2	962,50554	0,09	42,96
																		High	GSGPDTQnGAVDNNQSTIVFPK	7	N8(Deamidated)	0,0000	2,25	2	2247,05449	0,89	46,85
																		High	ISTYTIGPFQSTK	2		0,0000	2,08	2	1442,75383	0,85	47,42
																		Medium	RTMNASEcVAR	2	C8(Carbamidomethyl)	0,0000	1,92	3	1294,59858	-0,43	35,38
																		Medium	QFSDPVVQR	2		0,0000	1,88	2	1075,55278	-0,32	40,91
																		Medium	VPAlIK	3		0,0000	1,69	2	640,43932	0,09	41,26
																		Medium	EFEmALQDR	1	M4(Oxidation)	0,0000	1,65	2	1154,51470	-0,02	41,72
																		Medium	METDEAPSDAAPSTNETDVNMQDAK	2		0,0000	1,57	3	2764,15940	1,17	43,07
																		Medium	nAVEAYVYDmRnK	1	N1(Deamidated); N12(Deamidated)	0,0000	1,29	2	1574,73027	9,32	41,40
																		Medium	GNPIPSIK	2		0,0000	1,04	2	825,48296	0,04	41,03
																		Medium	GSGPDTQNGAVDNNQSTIVFPK	1		0,0000	1,02	2	2246,07158	1,38	44,64
																		Medium	EAFIAR	1		0,0105	0,94	2	706,38835	0,09	39,55
2007	M5XE29	3-hydroxyisobutyrate dehydrogenase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa009081mg PE=4 SV=1 - [M5XE29_PRUPE]	98% to GE645223765 Prunus mume, E value 0	Prunus mume	Mitochondrion	01.01-Metabolism /Amino Acid	22,74	29,32	2	7	7	13	307	32,0	5,66	High	DcWTVDPAPVSGGDIGAR	1	C2(Carbamidomethyl)	0,0000	3,49	2	1775,80522	1,91	47,86	
																		High	VTYVGPAGSGQNcK	2	C13(Carbamidomethyl)	0,0000	3,05	2	1437,67998	0,58	39,08
																		High	QLFSGMVANGDGK	2		0,0000	2,62	2	1323,63689	0,49	46,23
																		High	VAVLPGAALcK	2	C10(Carbamidomethyl)	0,0000	2,60	2	1098,63396	-0,08	45,34
																		High	QLFSGMVAnGDGK	2	N9(Deamidated)	0,0000	2,04	2	1324,62187	1,22	46,39
																		Medium	LGGQGLITVIER	1		0,0000	1,94	2	1255,73845	1,21	48,16
																		Medium	DLGMGVDVVEENEGR	1		0,0000	1,49	2	1747,78252	1,19	48,51
																		Medium	EIFNAAR	2		0,0000	1,45	2	820,43114	-0,10	41,14
2104	M5XCH9	Nudix hydrolase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa007741mg PE=3 SV=1 - [M5XCH9_PRUPE]	96% to GE645247643 Prunus mume, E value 0	Prunus mume	Chloroplast	11.05-Disease/Defense/Stress responses	64,32	30,38	3	9	9	31	293	32,8	5,43	High	SDKDYAGFSPLTTSSGK	1		0,0000	3,94	3	1992,92301	0,52	44,79	

																	High	DMANIQATGDH Q	3		0,0000	3,77	2	1300,55913	0,33	42,20
																	High	DmANIQATGDH Q	4	M2(Oxidation)	0,0000	3,52	2	1316,55351	-0,08	38,19
																	High	EILVVQEInGR	2	N9(Deamidated)	0,0000	3,48	2	1270,70036	0,12	48,40
																	High	EILVVQEINGR	2		0,0000	3,12	2	1269,71623	0,03	46,78
																	High	VGIGAFVMNSER	2		0,0000	2,95	2	1279,64702	0,48	47,54
																	High	VGIGAFVmNSER	3	M8(Oxidation)	0,0000	2,36	2	1295,64250	0,91	46,10
																	High	ASMSQWK	3		0,0000	2,06	2	837,39220	-0,23	40,85
																	High	GSYLYHNNR	4		0,0000	2,01	2	1123,52776	-0,16	36,86
																	Medium	MSVSTSSSSVAK	2		0,0000	2,00	2	1257,59905	-0,09	37,18
																	Medium	DYAGFSPMLTTSSGK	1		0,0000	1,79	2	1662,77056	1,52	48,72
																	Medium	DTGFWK	3		0,0000	1,28	2	753,35655	-0,13	46,19
	M5V QF7	2-oxoglutarate-dependent dioxygenase DAO	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa009067mg PE=3 SV=1 - [M5VQF7_PRUPE]	98% to GI:646227285 Prunus mume, E value 0	Prunus mume	Chloroplast	02.10-Energy/TC A pathway	40,69	32,57	1	11	23	307	34,1	5,69	High	DVIAGSGYMAPSK	3		0,0000	3,70	2	1295,63066	0,45	43,00	
																	High	QQNKDVIAGSGYMAPSK	2		0,0000	3,26	3	1793,88626	0,63	39,54
																	High	FPDAEEYKK	3		0,0000	2,92	3	1126,54145	-0,10	39,20
																	High	LQAGEALAVLR	2		0,0000	2,90	2	1140,67302	-0,51	46,92
																	High	DVIAGSGYmAPSK	2	M9(Oxidation)	0,0000	2,89	2	1311,62480	-0,15	43,44
																	High	DQEAVEAPPEFVDSEHPR	2		0,0000	2,59	3	2051,93186	0,62	44,68
																	High	FPDAEEYK	1		0,0000	2,35	2	998,44640	-0,19	41,55
																	Medium	EASEIWGcFR	2	C8(Carbamidomethyl)	0,0000	1,59	2	1254,55730	0,04	48,01
																	Medium	IPLALMK	2		0,0000	1,42	2	785,49529	-0,16	46,57
																	Medium	GWPCQFR	1	C4(Carbamidomethyl)	0,0000	1,40	2	950,42974	-0,46	44,46
																	Medium	VSIATFLLGPK	1		0,0000	1,31	2	1145,69243	-0,44	52,10
																	Medium	IPLALmK	1	M6(Oxidation)	0,0000	1,10	2	801,49047	0,17	42,54
																	Medium	SLLDLPmEIK	1	M7(Oxidation)	0,0000	1,00	2	1174,63823	-0,53	49,67
2311	M5W 621	Aminoacylase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005858mg PE=4 SV=1 - [M5W621_PRUPE]	99% to GI:645260433 Prunus mume, E value 0	Prunus mume	Chloroplast	01.01-Metabolism /Amino acid	58,48	23,41	1	10	25	440	48,7	5,74	High	FAESDVFK	3		0,0000	2,98	2	942,45635	-0,45	44,17	
																	High	VPPTADQESLER	3		0,0000	2,91	2	1341,66472	0,13	39,87
																	High	LGKPEIFPASTDAR	3		0,0000	2,88	3	1501,80054	-0,31	41,77
																	High	IAEEWAPSSR	2		0,0000	2,87	2	1145,55876	0,12	42,59
																	High	ASQFDLVK	2		0,0000	2,75	2	907,48802	-0,42	44,18
																	High	cVGIQYLEAIR	1	C1(Carbamidomethyl)	0,0000	2,61	2	1321,69316	-0,13	48,71

																	High	AYASYVDHGR	4		0,0000	2,45	2	1138,52739	-0,20	37,92
																	High	LYDNTATENLF K	3		0,0000	2,42	2	1428,70012	-0,32	48,54
																	High	GIEIYESIIK	1		0,0000	2,30	2	1164,65154	0,37	49,13
																	High	cPMWLVIK	2	C1(Carb amidom ethyl)	0,0000	2,07	2	1046,55168	-0,89	50,23
																	Medium	LYDnTATEnLfk	1	N4(Dea midated); N9(Dea midated)	0,0102	0,97	2	1430,67803	6,58	49,93
2312	D2X 5K2	DEAD-box RNA helicase	DEAD-box RNA helicase-like protein OS=Prunus persica GN=PRUPE_ppa006399mg PE=2 SV=1 - [D2X5K2_PRUPE]	99% to GI:645265533 Prunus mume, E value 2e-146	Prunus persica	Chlorop last	11.05- Disease/Def ense/Stress responses	89,79	35,1 1	6	5	17	55	413	46,9	5,69	High	GLDVIQQAQSG TGK	4		0,0000	4,83	2	1401,73406	0,54	43,63
																	High	GVAINFVTR	2		0,0000	2,95	2	976,55736	-0,13	45,17
																	High	DELTLEGIK	3		0,0000	2,61	2	1017,54570	-0,61	47,46
																	High	DHTVSATHGDM DQNTR	3		0,0000	2,57	3	1784,76139	-0,19	35,95
																	High	VDWLTDK	2		0,0000	2,56	2	876,44585	-0,40	45,46
																	High	VLITTDLLAR	3		0,0000	2,55	2	1114,68279	-0,27	49,57
																	High	MLYDIQR	3		0,0000	2,45	2	938,47612	-0,35	44,04
																	High	ALGDYLGVK	3		0,0000	2,45	2	935,51946	-0,26	47,95
																	High	MFVLDEADEML SR	1		0,0000	2,38	2	1555,71379	0,39	52,14
																	High	mLYDIQR	2	M1(Oxi dation)	0,0000	2,31	2	954,47118	-0,20	42,18
																	High	RDELTLEGIK	2		0,0000	2,31	2	1173,64751	0,06	43,68
																	High	VFDMLR	3		0,0000	2,28	2	780,40709	-0,30	46,00
																	High	KGVAINFVTR	2		0,0000	2,14	2	1104,65141	-0,95	41,92
																	High	VHAcVGGTSVR	4	C4(Carb amidom ethyl)	0,0000	2,05	2	1142,57329	-0,23	35,42
																	Medium	QSLRPDYIK	3		0,0000	1,95	3	1119,61512	-0,54	39,86
																	Medium	DHTVSATHGDm DQNTR	4	M11(Ox idation)	0,0000	1,93	3	1800,75638	-0,14	34,01
																	Medium	ELAQQIEK	3		0,0000	1,88	2	958,51976	-0,70	40,29
																	Medium	VFDmLR	6	M4(Oxi dation)	0,0000	1,55	2	796,40251	0,35	41,76
																	Medium	GIVPFcK	1	C6(Carb amidom ethyl)	0,0000	1,52	2	820,43834	-0,33	45,48
																	Medium	QFYVNVDK	1		0,0000	0,99	2	1012,50945	-0,40	42,64
2319	M5X CC8	dihydrolipoyllsine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003847mg PE=3 SV=1 - [M5XCC8_PRUPE]	98% to GI:645244029 Prunus mume, E value 0	Prunus mume	Mitocho ndrion	02.01- Energy/Gly colysis	58,99	28,8 6	2	1 6	17	32	544	58,8	7,96	High	ADVEEYLASR	2		0,0000	3,67	2	1152,55303	-0,14	45,91
																	High	GQLNALQEASG GK	2		0,0000	3,26	2	1272,65447	0,11	41,05
																	High	FKDYTPSASGAS AAAAK	1		0,0000	3,20	3	1642,80539	-1,10	38,25
																	High	GLSSIAEEVR	2		0,0000	2,88	2	1060,56291	-0,43	44,24

																	High	VPQcNSSWTD HIR	1	C4(Carb amidom ethyl)	0,0000	2,87	3	1714,75925	-0,59	40,31
																	High	EVVEEPVTSPE K	3		0,0000	2,83	2	1439,72698	0,34	40,44
																	High	VSKPTAAAPSG DR	5		0,0000	2,79	3	1256,65921	-0,16	35,60
																	High	KEVVEEPVTSPE PK	1		0,0000	2,69	3	1567,82132	-0,09	38,58
																	High	DYTPSASGASA AAAK	1		0,0000	2,58	2	1367,64433	0,38	38,64
																	High	AAALALQK	2		0,0000	2,30	2	785,48784	-0,22	39,26
																	High	VIDGAIGAEWL K	1		0,0000	2,05	2	1271,70061	0,88	49,21
																	Medium	GYIENPESmLL	2	M9(Oxi dation)	0,0000	1,74	2	1281,60234	-0,66	50,62
																	Medium	GTGPDGSIVK	3		0,0000	1,70	2	930,48870	-0,48	37,73
																	Medium	IFASPLAR	2		0,0000	1,51	2	874,51402	-0,61	45,17
																	Medium	LSVNDLVIK	2		0,0000	1,45	2	1000,60283	-0,94	47,60
																	Medium	VPLSSIK	1		0,0208	0,94	2	743,46605	-0,20	40,05
2609	M5W 1V2	succinate dehydrogenase [ubiquinone] flavoprotein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002787mg PE=4 SV=1 - [M5W1V2_PRUPE]	99% to Gt:645273001 Prunus mume, E value 0	Prunus mume	Mitocho ndrion	02.10- Energy/TC A pathway	54,67	14,5 3	1	8	8	22	633	69,7	6,39	High	TQETLEEGSLI DK	2		0,0000	4,35	2	1590,78716	0,86	43,33
																	High	NSNGSLPTSQIR	2		0,0000	3,23	2	1273,64983	0,22	40,23
																	High	AFGGQSLDFGK	2		0,0000	3,03	2	1126,55254	-0,24	45,66
																	High	IMQNNAAVFR	3		0,0000	2,89	2	1163,59929	0,21	41,33
																	High	FQAASTITLATGG YGR	1		0,0000	2,64	2	1512,78081	0,15	46,49
																	High	DSGEQTIAWLD K	2		0,0000	2,59	2	1362,65447	0,60	48,24
																	High	NSnGSLPTSQIR	4	N3(Dea midated)	0,0000	2,43	2	1274,63432	0,59	41,68
																	High	ImQNNAAVFR	3	M2(Oxi dation)	0,0000	2,34	2	1179,59404	0,06	40,88
																	High	AWESFDNVQVK	2		0,0000	2,27	2	1322,63750	-0,08	46,73
																	Medium	SMTMEIR	1		0,0000	1,57	2	867,40605	-0,33	41,22
	M5X DI1	phosphoglucmutase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003354mg PE=3 SV=1 - [M5XDI1_PRUPE]	99% to Gt:645229375 Prunus mume, E value 0	Prunus mume	Cytopla sm	02.01- Energy/Gly colysis	46,98	24,9 1	1	1 4	14	25	582	63,3	6,07	High	STTQDEPPEFGA AADGDADR	2		0,0000	4,83	2	2049,86601	1,32	43,59
																	High	YNMEtGGPAPE SITDK	2	N5(Dea midated)	0,0000	3,78	2	1723,74285	-3,01	42,46
																	High	YNMENGGAPE SITDK	1		0,0000	3,69	2	1722,76592	1,10	42,08
																	High	YDYENVDAGA AK	1		0,0000	3,12	2	1315,58171	1,20	40,21
																	High	LSGTGSEGATIR	2		0,0000	2,98	2	1148,59062	-0,02	38,18
																	High	YLFEDGSR	3		0,0000	2,31	2	986,45745	-0,38	43,56
																	High	ESSLLNcVPK	2	C7(Carb amidom ethyl)	0,0000	2,15	2	1146,58269	0,27	44,02
																	High	LYIEQYEK	2		0,0000	2,05	2	1085,55120	-0,16	42,58

																	Medium	IFVEELGAK	1		0,0000	1,98	2	1005,56096	-0,62	45,57
																	Medium	LVSVEDIVR	1		0,0000	1,95	2	1029,59368	-0,26	46,87
																	Medium	EDFGGGHPDPN LTYAK	1		0,0000	1,90	3	1717,78012	-0,92	40,97
																	Medium	MQEFTGR	2		0,0000	1,79	2	868,39781	-0,46	39,18
																	Medium	LYIEqYEKDP SK	1	Q5(Deamidated)	0,0541	1,75	2	1513,73088	-7,42	41,52
																	Medium	mQEFTGR	1	M1(Oxidation)	0,0000	1,42	2	884,39379	0,75	36,98
																	Medium	QHWATFGR	1		0,0000	1,29	3	1002,49070	0,23	40,51
																	Medium	NMILGK	2		0,0000	1,08	2	675,38609	0,36	40,18
2615	M5VWE8	Malic enzyme	Malic enzyme OS=Prunus persica GN=PRUPE_ppa003142mg PE=3 SV=1 - [M5VWE8_PRUPE]		Prunus persica	Chloroplast	02.30-Energy/Photosynthesis	19,24	12,67	11	9	10	21	592	65,6	5,99	High	AYELGLATR	2		0,0000	3,31	2	993,53581	-0,60	42,48
																	High	TVQVIVVTDE R	1		0,0000	3,06	2	1315,72319	1,16	42,07
																	High	DSLQQFK	1		0,0047	2,14	2	865,44121	-0,27	38,67
																	High	VLEVLK	3		0,0000	2,14	2	700,46050	0,15	41,20
																	High	IWLVD SK	1		0,0000	2,02	2	860,48754	-0,16	44,71
																	Medium	GLIVSSR	3		0,0000	1,67	2	731,44109	0,05	38,25
																	Medium	GLAFTEK	2		0,0000	1,32	2	765,41423	0,08	39,76
																	Medium	LMNnIR	2	N4(Deamidated)	0,0000	1,26	2	761,39745	-0,04	37,16
																	Medium	QYQVPLQK	2		0,0000	1,23	2	1003,55669	-0,44	38,44
																	Medium	FGSIFR	3		0,0000	1,12	2	726,39342	0,07	44,51
																	Medium	LMNNIR	1		0,0208	0,94	2	760,41301	-0,59	35,84
2617	M5W741	oligopeptidase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001572mg PE=3 SV=1 - [M5W741_PRUPE]	90% to GI:694437692 Pyrus x bretschneideri, E value 0	Pyrus x bretschneideri	Cytosol	06.13-Protein destination and storage/Proteolysis	69,24	24,13	1	7	22	42	800	90,2	6,89	High	LEGDLEELER	1		0,0000	3,07	2	1202,59001	0,02	44,30
																	High	FQENVLDATK	3		0,0000	3,00	2	1164,58965	0,06	43,16
																	High	SAIEEVQPEK	2		0,0000	2,91	2	1129,57329	-0,28	38,46
																	High	QDEGLVAGIR	2		0,0000	2,72	2	1057,56365	-0,06	42,65
																	High	LLNYYNYAEV MATK	1		0,0000	2,36	2	1730,84294	0,63	46,11
																	High	AEELLEK	2		0,0000	2,28	2	831,44591	0,05	39,87
																	High	HnGLLATASA	1	N2(Deamidated)	0,0000	2,22	2	955,48406	-0,34	44,49
																	High	AGSLSLR	2		0,0000	2,09	2	703,40990	0,21	39,38
																	High	IEQELER	3		0,0000	2,05	2	916,47283	-0,72	36,77
																	High	TQVIPPLPEDR	3		0,0000	2,05	2	1264,68987	0,18	45,62
																	Medium	HNGLLATASA	2		0,0000	1,99	2	954,49999	-0,39	41,09

																	Medium	TVEPTWPK	2		0,0000	1,87	2	957,50377	-0,29	42,77
																	Medium	ASSGDMDNTHAI DSILK	1		0,0000	1,84	2	1750,85564	1,59	51,30
																	Medium	DSLELR	2		0,0000	1,74	2	732,38872	0,05	40,79
																	Medium	RIVESQIK	1		0,0000	1,74	2	972,58385	0,15	36,08
																	Medium	DTLMSIAK	3		0,0000	1,73	2	878,46514	-0,11	44,92
																	Medium	IVESQIK	1		0,0000	1,66	2	816,48241	-0,21	36,41
																	Medium	FASVDLK	2		0,0000	1,66	2	779,42974	-0,11	42,20
																	Medium	EAVLcGVSLED DK	1	C5(Carb amidom ethyl)	0,0000	1,63	2	1434,68059	1,69	45,49
																	Medium	EAVLcGVSLED DKR	1	C5(Carb amidom ethyl)	0,0000	1,57	3	1590,77982	0,34	42,31
																	Medium	DTLmSIK	1	M4(Oxi dation)	0,0000	1,42	2	894,45970	-0,50	40,54
																	Medium	LVVPLEK	3		0,0000	1,36	2	797,51305	-0,14	44,77
																	Medium	SHVLSR	1		0,0000	1,28	2	698,39452	0,14	32,72
																	Medium	AILESPDWQTLT EAR	1		0,0000	1,19	2	1729,87847	1,64	49,31
2701	M5V P31	HSP70	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001973mg PE=3 SV=1 - [M5VP31_PRUPE]	96% to GE657963243 Malus domestica, E value 0	Malus domesti ca	Mitocho ndrion	06.01- Protein destination and storage/Fol ding and stability	90,58	30,5 2	3	1 8	19	40	734	79,5	8,46	High	GSGGDSSSGGS GTEGGDQAPEA DYEEVKK	2		0,0000	5,13	3	2758,16013	1,51	38,70
																	High	SQVFSTAADNQ TQVGIK	2		0,0000	4,01	2	1793,90459	0,95	43,75
																	High	NSADTTIYSIEK	3		0,0000	3,77	2	1341,65386	0,42	42,73
																	High	QAVTNPTNTVF GTK	3		0,0000	3,62	2	1477,76592	0,90	43,83
																	High	VQEVVTQIFGK	1		0,0000	3,54	2	1247,69963	0,13	47,24
																	High	SSGGLSEDEIEK	2		0,0000	3,41	2	1250,57500	0,21	40,41
																	High	GELLVGTPAK	2		0,0000	3,25	2	984,57207	-0,42	42,82
																	High	IINEPTAAALSY GMNNK	2		0,0000	2,80	2	1806,90788	1,30	46,84
																	High	TTPSVVAFNQK	2		0,0000	2,45	2	1191,63689	0,02	42,92
																	High	TAIGGDNAEEIK	2		0,0000	2,40	2	1217,60112	0,19	40,01
																	High	EIEDAVAE LR	4		0,0000	2,36	2	1144,58464	0,11	47,33
																	High	IINEPTAAALSY GmNNK	1	M14(Ox idation)	0,0000	2,33	2	1822,90264	1,20	44,51
																	Medium	MKETAEAYLGK	1		0,0000	2,19	3	1240,62329	-0,78	39,51
																	High	DVDEVLLVGG MTR	2		0,0000	2,18	2	1403,72124	0,90	50,81
																	High	IAGLDVQR	1		0,0000	2,03	2	871,49950	-0,16	41,39
																	Medium	ETAEAYLGK	2		0,0000	1,80	2	981,48857	-0,22	41,40
																	Medium	DVDEVLLVGGm TR	1	M11(Ox idation)	0,0000	1,66	2	1419,71501	0,08	48,76
																	Medium	TEGIDLAK	1		0,0000	1,63	2	846,45671	-0,07	40,31

																	Medium	DKIPSEVAK	2		0,0000	1,61	3	986,55182	0,08	36,34
																	Medium	ALIDIR	2		0,0000	1,07	2	700,43517	-0,11	46,41
2703	M5W QS2	V-type proton ATPase subunit A	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002892mg PE=3 SV=1 - [M5WQS2_PRUPE]	99% to GI:645243457 Prunus mume, E value 0	Prunus mume	Cytopla sm	07.22- Transporter s/Transport ATPases	140,13	39,3 3	2	2 3	24	75	623	68,6	5,45	High	TTLVANTSNM PVAAR	3		0,0000	4,20	2	1545,80705	1,05	42,95
																	High	FEDPAEGEEV VGK	3		0,0000	3,81	2	1518,73345	0,74	45,76
																	High	YSNSDTVYV VGcGER	2	C12(Car bamido methyl)	0,0000	3,67	2	1705,75078	1,23	42,57
																	High	DMGYNVSM MA DSTSR	2		0,0000	3,67	2	1664,67327	1,13	46,52
																	High	LAEmPADSG YPAYLAAR	2	M4(Oxi dation)	0,0000	3,61	2	1811,86528	1,07	44,86
																	High	TTLVANTS NmPVAAR	4	M10(Ox idation)	0,0000	3,58	2	1561,80144	0,70	40,18
																	High	DALAEGDKIT LETAK	2		0,0000	3,36	2	1574,82878	0,95	42,90
																	High	YSnSDTVY VVGcGER	1	N3(Dea midated); C12(Car bamido methyl)	0,0000	3,36	2	1706,72661	-3,56	43,36
																	High	EDYLAQNA FTPYDK	2		0,0000	3,29	2	1674,76628	0,98	46,94
																	High	DMGYNVSM mA DSTSR	6	M9(Oxi dation)	0,0000	3,26	2	1680,66765	0,80	44,55
																	High	VAADTPLL TGQR	6		0,0000	3,10	2	1241,68523	0,27	43,05
																	High	ISGDVYIPR	5		0,0000	3,08	2	1019,55187	-0,19	43,55
																	High	LAEMPADSG YPAYLAAR	2		0,0000	3,07	2	1795,87041	1,10	47,77
																	High	LGDLFYR	3		0,0000	2,55	2	883,46721	-0,06	47,84
																	High	LHEDLTSG FR	3		0,0000	2,41	2	1174,58513	-0,03	40,82
																	High	ITYVAPPG QYSLK	3		0,0000	2,38	2	1436,77971	0,89	44,11
																	High	DILWEFQPK	1		0,0000	2,21	2	1175,60954	-0,04	50,74
																	High	TVISQALSK	3		0,0000	2,12	2	946,55644	-0,39	43,27
																	Medium	LITFEDSEK	2		0,0000	2,00	2	1069,50444	-0,37	40,28
																	Medium	ISYSLIK	3		0,0000	1,82	2	823,49242	0,02	43,15
																	Medium	LASFYER	2		0,0000	1,81	2	885,44634	-0,21	41,14
																	Medium	WAEALR	2		0,0000	1,76	2	745,39910	-0,13	40,58
																	Medium	ESEYGYVR	2		0,0000	1,58	2	1002,45226	-0,46	39,78
																	Medium	ITLETAK	2		0,0000	1,49	2	775,45592	-0,14	39,20
																	Medium	tTLVAnTSn MPV AAR	1	N- Term(A cetyl); N6(Dea midated); N9(Dea midated)	0,0438	1,31	2	1589,79729	8,34	40,25
																	Medium	SVWMMR	2		0,0000	1,31	2	809,37956	-0,21	45,35

																	Medium	FcPFYK	2	C2(Carbamidomethyl)	0,0000	1,18	2	861,39617	-0,27	44,18
																	Medium	DTVLELEFQGVK	1		0,0000	1,06	2	1377,71807	-5,83	50,39
2704	M5VP31	HSP70	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001973mg PE=3 SV=1 - [M5VP31_PRUPE]	96% to GE657963243 Malus domestica, E value 0	Malus domestica	Mitochondrion	06.01- Protein destination and storage/Folding and stability	273,80	36,10	3	29	112	734	79,5	8,46		High	GSGGDS SSGGS GTEGGDQAPEA DYEEVKK	3		0,0000	5,37	3	2758,15976	1,38	38,24
																	High	IINEPTAAALSYGMNNK	6		0,0000	4,90	2	1806,90788	1,30	47,61
																	High	IINEPTAAALSYGmNNK	4	M14(Oxidation)	0,0000	4,69	2	1822,90288	1,33	45,99
																	High	GVNPDEAVAMGAAIQGGILR	1		0,0000	4,30	2	1939,00884	1,10	50,49
																	High	SQVFSTAADNQ TQVGIK	7		0,0000	4,23	2	1793,90508	1,22	43,53
																	High	MKETAEAYLGK	4		0,0000	3,93	3	1240,62412	-0,12	40,02
																	High	VQEVVTQIFGK	5		0,0000	3,68	2	1247,69988	0,32	48,15
																	High	NSADTTIYSIEK	5		0,0000	3,60	2	1341,65373	0,33	43,74
																	High	GVNPDEAVAmGAAIQGGILR	2	M10(Oxidation)	0,0000	3,43	2	1955,00420	1,32	47,45
																	High	GSGGDS SSGGS GTEGGDQAPEA DYEEVK	3		0,0000	3,37	2	2630,06255	0,60	40,47
																	High	GELLVGTPAK	5		0,0000	3,23	2	984,57219	-0,29	42,82
																	High	mKETAEAYLGK	4	M1(Oxidation)	0,0000	3,17	3	1256,61847	-0,56	39,00
																	High	QAVTNPTNTVFGTK	5		0,0000	3,08	2	1477,76579	0,81	44,77
																	High	RTEGIDLAK	1		0,0000	2,86	2	1002,55766	-0,23	37,55
																	High	DVDEVLLVGGmTR	4	M11(Oxidation)	0,0000	2,81	2	1419,71550	0,43	49,49
																	High	AVITVPAYFNDAQR	3		0,0000	2,74	2	1564,81365	1,13	48,92
																	High	TAIGGDNAEEIK	3		0,0000	2,65	2	1217,60112	0,19	38,96
																	High	SSGGLSEDEIEK	3		0,0000	2,62	2	1250,57500	0,21	42,07
																	Medium	KSQVFSTAADNQ TQVGIK	1		0,0000	2,49	3	1921,99784	-0,01	40,36
																	High	TTPSVVAFNQK	3		0,0000	2,29	2	1191,63689	0,02	43,94
																	High	IAGLDVQR	5		0,0000	2,13	2	871,50035	0,82	42,34
																	High	EIEDAVAE LR	7		0,0000	2,12	2	1144,58476	0,22	48,38
																	Medium	AVITVPAYFnDAQ R	3	N10(Deamidated)	0,0000	2,10	3	1565,79416	-1,11	48,34
																	High	TEGIDLAK	1		0,0000	2,10	2	846,45659	-0,21	40,31
																	High	ETA EAYLGK	2		0,0000	2,09	2	981,48845	-0,35	41,31
																	High	DKIPSEVAK	4		0,0000	2,08	2	986,55138	-0,37	37,22
																	High	DVDEVLLVGGMTR	4		0,0000	2,08	2	1403,72063	0,46	52,45
																	Medium	TAIGGDNAEEIKAK	1		0,0000	2,02	3	1416,73294	-0,03	37,31

																	Medium	KALIDIR	2		0,0000	1,95	2	828,53020	-0,01	40,53
																	Medium	HLNITLTR	3		0,0000	1,87	2	967,56804	-0,34	41,33
																	Medium	GELLVGTPAKR	2		0,0000	1,49	3	1140,67289	-0,63	39,48
																	Medium	ALIDIR	3		0,0000	1,36	2	700,43517	-0,11	46,23
																	Medium	RQAVTNPTNTV FGTK	1		0,0074	1,34	3	1633,86509	-0,38	40,41
																	Medium	SqVFSTAADNqT QVGIK	1	Q2(Deamidated); Q11(Deamidated)	0,5145	1,17	2	1795,87029	-0,35	47,02
																	Medium	EQQITIR	1		0,0000	1,13	2	887,49462	0,08	39,16
3205	A9YTE0	Leucoanthocyanidin dioxygenase	Leucoanthocyanidin dioxygenase OS=Prunus persica GN=LDOX PE=2 SV=1 - [A9YTE0_PRUPE]		Prunus persica	Chloroplast	20.99- Secondary metabolism /Others	35,85	21,85	3	7	8	19	357	40,4	5,63	High	VELTSSSGIATIPK	3		0,0000	3,29	2	1402,77959	0,53	45,28
																	High	SQEALLNK	2		0,0000	2,69	2	902,49358	-0,70	39,11
																	High	VLSLGLGLEEG R	2		0,0000	2,53	2	1242,70635	0,84	48,65
																	High	AFFDLPIEQK	2		0,0000	2,41	2	1207,63616	0,29	50,23
																	High	STDGPQVPTIDLK	3		0,0000	2,14	2	1370,71684	0,43	46,61
																	High	TFAEHIQHK	2		0,0000	2,12	2	1110,56914	0,03	35,72
																	High	EIDSENVNR	4		0,0000	2,02	2	1204,54460	0,43	36,34
3308	M5W1Z4	Guanosine nucleotide diphosphate dissociation inhibitor	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005772mg PE=4 SV=1 - [M5W1Z4_PRUPE]	99% to GI:645272258 Prunus mume, E value 0	Prunus mume	Chloroplast	08.99- Intracellular traffic/Others	87,19	27,48	3	11	12	46	444	49,9	5,95	High	VIGVTSEGETAR	2		0,0000	3,47	2	1218,63262	0,08	38,52
																	High	AVDGSFVYNK	3		0,0000	3,26	2	1099,54167	-0,20	42,12
																	High	YLEEPALETVK	4		0,0000	3,21	2	1291,67827	0,16	44,80
																	High	FMMANGTLVR	1		0,0000	3,19	2	1139,57024	0,15	44,50
																	High	FmMAnGTLVR	4	M2(Oxidation); N5(Deamidated)	0,0000	2,86	2	1156,55107	1,79	44,60
																	High	VVcDPSYLPNK	3	C3(Carboxamidomethyl)	0,0000	2,83	2	1291,63579	0,50	41,73
																	High	FMMAnGTLVR	2	N5(Deamidated)	0,0000	2,80	2	1140,55425	0,14	47,28
																	High	DYNVDMVPK	3		0,0000	2,79	2	1080,50286	-0,20	44,81
																	High	VPATDmEALK	2	M6(Oxidation)	0,0000	2,76	2	1090,54521	0,24	41,50
																	High	VLHTDVTK	6		0,0000	2,54	2	1025,59892	-0,08	37,71
																	High	FMmANGTLVR	6	M3(Oxidation)	0,0000	2,50	2	1155,56450	-0,42	42,08
																	High	SPLMGLFEK	3		0,0000	2,30	2	1021,53844	-0,30	49,60
																	High	DYNVDmVPK	1	M6(Oxidation)	0,0000	2,29	2	1096,49700	-0,90	45,29
																	High	LYAESLAR	2		0,0000	2,19	2	922,49901	-0,30	40,31
																	High	VPATDMEALK	2		0,0000	2,05	2	1074,54985	-0,18	42,22

																	Medium	THEGMDLR	1		0,0000	1,40	3	958,44120	0,06	36,33
3311	M5V PR4	enolase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005779mg PE=3 SV=1 - [M5VPR4_PRUPE]	99% to GI:645272258 Prunus mume, E value 0	Prunus mume	Cytopla sm	02.01- Energy/Gly colysis	110,87	38,0 6	3	1 5	16	61	444	47,7	5,82	High	KYGQDATNVG DEGGFAPNIQEN K	2		0,0000	5,86	3	2452,13871	0,44	42,69
																	High	IEEELGAEAVYA GAK	2		0,0000	4,71	2	1549,77568	0,76	45,11
																	High	YGQDATNVGDE GGFAPNIQENK	3		0,0000	4,63	2	2324,04766	2,15	45,02
																	High	VNQIGSVTESIE AVR	3		0,0000	3,85	2	1601,85100	1,00	46,13
																	High	LAmQEFmILPVG ASSFK	2	M3(Oxi dation); M7(Oxi dation)	0,0000	3,58	2	1900,95745	1,37	49,95
																	High	KAGWGVMAASH R	1		0,0000	3,56	3	1199,61005	-0,20	36,97
																	High	AVNNVNSIIGPA LIGK	5		0,0000	3,48	2	1579,91802	0,83	49,52
																	High	AGWGVMAASHR	4		0,0000	3,10	3	1071,51514	-0,17	39,80
																	High	LAmQEFMILPV GASSFK	4	M3(Oxi dation)	0,0000	2,81	2	1884,96111	0,63	51,56
																	High	ScNALLLK	3	C2(Carb amidom ethyl)	0,0000	2,60	2	918,50743	-0,35	43,18
																	High	MGVEVYHHLK	6		0,0000	2,51	2	1212,61968	0,20	37,93
																	High	AGWGVmASHR	5	M6(Oxi dation)	0,0000	2,02	2	1087,50981	-0,39	37,47
																	High	FRVPVEPY	3		0,0000	2,00	2	1006,53533	-0,35	46,93
																	Medium	NLVLPVPAPNV nGGSHAGNK	5	N13(De amidate d)	0,0000	1,98	3	2119,13559	2,84	50,44
																	Medium	mGVEVYHHLK	2	M1(Oxi dation)	0,0000	1,90	2	1228,61345	-0,73	36,55
																	Medium	KIPLYK	2		0,0000	1,81	2	761,49205	0,05	38,64
																	Medium	YNQLLR	2		0,0000	1,78	2	806,45195	0,03	40,97
																	Medium	KAGWGVmASH R	2	M7(Oxi dation)	0,0000	1,78	3	1215,60459	-0,51	34,94
																	Medium	EGLELLK	3		0,0470	1,42	2	801,47154	-0,18	45,46
																	Medium	QIFDSR	2		0,0000	1,12	2	765,38890	-0,14	39,59
3314	M5X C03	protein CLP1 homolog	Protein CLP1 homolog OS=Prunus persica GN=PRUPE_ppa006062mg PE=3 SV=1 - [M5XC03_PRUPE]		Prunus mume	Chlorop last	04.22- Transcriptio n/mRNA processing	16,78	18,8 8	2	7	7	10	429	46,9	5,95	High	SALPIGAEPAAD PTR	2		0,0000	2,50	2	1465,76518	0,38	44,60
																	High	IEVGNDAPLK	1		0,0000	2,32	2	1055,57268	-0,50	41,08
																	High	TTTYLAPSAGDL PSK	1		0,0000	2,32	2	1533,81694	0,64	45,60
																	High	ELAQVIER	2		0,0000	2,05	2	957,53630	-0,12	42,79
																	Medium	ASPPEDSNSSQP QGPR	2		0,0000	1,75	2	1653,74773	0,81	36,64
																	Medium	VIVVGPTDSGK	1		0,0000	1,71	2	1071,60381	-0,66	40,67
																	Medium	LcSMLR	1	C2(Carb amidom ethyl)	0,1037	1,21	2	779,38994	-0,44	40,49
3316	M5W 621	Aminoacylase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005858mg PE=4 SV=1 - [M5W621_PRUPE]	99% to GI:645260436 Prunus mume, E value 0	Prunus mume	Chlorop last	01.01- Metabolism /Amino acid	48,43	18,1 8	1	8	8	21	440	48,7	5,74	High	LYDNTATENLF K	3		0,0000	3,48	2	1428,70085	0,19	47,44

																	High	LKKPEIFPASTD AR	2		0,0000	3,27	3	1501,80063	-0,25	42,69
																	High	VPPTADQESLER	3		0,0000	3,10	2	1341,66411	-0,33	39,81
																	High	ASQFDLVK	2		0,0000	2,73	2	907,48802	-0,42	43,09
																	High	AYASYVDHGR	4		0,0000	2,62	2	1138,52751	-0,09	37,80
																	High	IAEEWAPSSR	3		0,0000	2,55	2	1145,55864	0,02	43,70
																	High	FAESDVFK	3		0,0000	2,06	2	942,45622	-0,58	43,85
																	Medium	TFYAER	1		0,0000	1,08	2	786,37834	0,31	38,48
3518	M5X YF8	T-complex protein 1 subunit beta	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa004143mg PE=3 SV=1 - [M5XYF8_PRUPE]	99% to GI:645228826 Prunus mume, E value 0	Prunus mume	Cytopla sm	04.22- Transcriptio n/mRNA processing	80,98	31,8 8	1	1 7	17	37	527	57,1	6,05	High	VDEITcAPR	2	C7(Carb amidom ethyl)	0,0000	4,14	2	1173,59355	0,22	42,04
																	High	GASHHVLDAAE R	5		0,0000	4,00	3	1320,62885	-0,24	35,71
																	High	ILVANTAMD TDK	2		0,0000	3,50	2	1291,65691	0,47	43,00
																	High	GHAVTVTNDGA TILK	2		0,0000	3,39	2	1496,80681	0,01	40,44
																	High	GSTNLEAIQIIK	2		0,0000	2,99	2	1286,73186	0,28	47,53
																	High	SLHIDNAAAK	2		0,0000	2,84	3	1039,55298	-0,14	37,32
																	High	IIAHGINcFVNR	1	C8(Carb amidom ethyl)	0,0000	2,81	3	1413,74091	-0,79	41,87
																	High	EGcTAGIDVISG AVGDMAER	1	C3(Carb amidom ethyl)	0,0000	2,55	2	2007,91252	0,69	49,77
																	High	IAMTTLSSK	2		0,0000	2,29	2	951,51738	-0,64	40,67
																	High	IFKDEASEEK	3		0,0000	2,24	2	1195,58464	0,39	35,45
																	Medium	IFKDEASEEKGE R	4		0,0000	2,21	3	1537,74918	-0,12	34,75
																	Medium	KSHAIEAFSR	1		0,0000	2,20	3	1145,60776	1,34	35,97
																	High	VLVDISK	3		0,0000	2,16	2	773,47661	-0,21	42,84
																	High	DSFLDEGFILDK	1		0,0000	2,16	2	1398,67729	-1,09	52,68
																	High	SHAIEAFSR	4		0,0000	2,05	2	1017,51085	-0,40	38,85
																	Medium	IGLGQPK	1		0,0000	1,91	2	712,43523	-0,02	38,21
																	Medium	GISESFK	1		0,0813	1,13	2	767,39385	0,54	39,21
	M5W MW6	Pyruvate decarboxylase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003458mg PE=3 SV=1 - [M5WMW6_PRUPE]	99% to GI:645237438 Prunus mume, E value 0	Prunus mume	Cytopla sm	11.05- Disease/Def ense/Stress responses	65,52	17,9 8	1	9	11	38	573	62,0	6,13	High	VRTEEDLTEAIA K	2		0,0000	4,31	2	1474,77568	0,57	41,41
																	High	mQGFRPANSTG TLGR	3	N- Term(A cetyl)	0,0000	4,10	2	1634,80840	0,95	45,48
																	High	TEEDLTEAIAK	2		0,0000	3,28	2	1219,60515	-0,12	43,11
																	High	AVKPVIIIGPK	5		0,0000	2,55	3	1078,69837	0,01	38,72
																	High	VSAANSRPPNP Q	4		0,0000	2,49	2	1237,62895	0,42	36,26
																	High	DPVPFFLAPK	3		0,0000	2,33	2	1130,62444	-0,07	52,10

																	High	ELLEWGRS	7		0,0000	2,24	2	989,50493	-0,19	48,42
																	High	VNVLFK	3		0,0000	2,22	2	719,44518	0,15	44,28
																	High	mQGRFPAnSTGT LGR	2	N- Term(A cetyl); N8(Dea midated)	0,0000	2,06	2	1635,78850	-1,44	47,33
																	Medium	AIIVEPNR	3		0,0000	1,83	2	911,53063	-0,35	41,94
																	Medium	IFVPPGIPLK	3		0,0000	1,62	2	1080,68169	0,04	50,75
																	Medium	nSTAVENYHR	1	N1(Dea midated)	0,0224	1,31	3	1191,53885	-0,05	37,00
3616	M5V WE8	Malic enzyme	Malic enzyme OS=Prunus persica GN=PRUPE_ppa003142mg PE=3 SV=1 - [M5VWE8_PRUPE]		Prunus persica	Chlorop last	02.30- Energy/Pho tosynthesis	132,95	34,6 3	9	1 9	24	89	592	65,6	5,99	High	YAEScMYPVY R	5	C5(Carb amidom ethyl)	0,0000	3,60	2	1525,64653	0,97	43,19
																	High	TVQVIVVTDGE R	2		0,0000	3,54	2	1315,72173	0,04	43,87
																	High	AYELGLATR	3		0,0000	3,24	2	993,53606	-0,36	45,53
																	High	AIFASGSPFDPV EYNGK	1		0,0000	3,11	2	1798,86614	0,79	49,30
																	High	ASVLDFDPK	6		0,0000	3,07	2	991,50902	-0,53	45,95
																	High	YAEScmYSPVY R	4	C5(Carb amidom ethyl); M6(Oxi dation)	0,0000	2,81	2	1541,64141	0,94	43,32
																	High	YMALTELQER	4		0,0000	2,78	2	1253,62053	0,82	45,31
																	High	GLLPATcSQQL QEK	4	C8(Carb amidom ethyl)	0,0000	2,44	2	1669,85967	1,08	44,14
																	Medium	AIKPTVLIGSSG VGR	1		0,0000	2,43	3	1454,86841	-0,42	42,77
																	High	YmALTELQER	4	M2(Oxi dation)	0,0000	2,41	2	1269,61540	0,78	44,53
																	High	mESTFNELGDK	5	N- Term(A cetyl)	0,0000	2,37	2	1312,57292	0,23	51,95
																	High	IWLVDISK	2		0,0000	2,27	2	860,48747	-0,23	47,26
																	High	DSLQQFK	3		0,0000	2,15	2	865,44145	0,01	42,56
																	High	KDSLQQFK	5		0,0000	2,09	2	993,53612	-0,29	36,72
																	Medium	LmNNIR	3	M2(Oxi dation)	0,0000	1,87	2	776,40825	-0,16	36,24
																	Medium	GLIVSSR	5		0,0000	1,78	2	731,44121	0,22	41,35
																	Medium	LMNNIR	2		0,0000	1,71	2	760,41210	-1,80	37,73
																	Medium	KIWLVDISK	3		0,0000	1,69	2	988,58226	-0,38	42,22
																	Medium	FGSIFR	5		0,0000	1,69	2	726,39348	0,15	46,56
																	Medium	KLmNNIR	3	M3(Oxi dation)	0,0000	1,52	2	904,50249	-0,95	35,39
																	Medium	LVGGSLSEHK	5		0,0000	1,48	2	1026,55669	-1,16	35,89
																	Medium	GLAFTEK	2		0,0000	1,46	2	765,41442	0,32	41,63
																	Medium	AIFASGSPFDPV EYnGK	1	N15(De amidate d)	0,0000	1,37	2	1799,84770	-0,57	50,22

																	Medium	LPRPENLVK	2		0,0000	1,27	2	1065,64153	-0,03	39,98
																	Medium	VLEVLK	4		0,0000	1,13	2	700,46031	-0,11	42,10
																	Medium	QYQVPLQK	3		0,0000	0,91	2	1003,55651	-0,62	40,12
4013	M5W CS1	Ras-related protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa011297mg PE=3 SV=1 - [M5WCS1_PRUPE]		Prunus persica	Chlorop last	08.99- Intracellular traffic/Othe rs	15,53	28,2 4	1 7	6	6	10	216	23,9	6,55	High	SVSEDDGQTLA ER	2		0,0000	3,12	2	1406,64031	0,60	35,38
																	High	AQIWDTAGQER	1		0,0000	2,31	2	1274,61211	-0,27	39,39
																	Medium	NEFcLESK	1	C4(Carb amidom ethyl)	0,0000	1,93	2	1026,45598	-0,13	38,38
																	Medium	IVLIGDSGVGK	3		0,0052	1,92	2	1057,62493	-0,31	42,74
																	Medium	AIT SAYYR	2		0,0000	1,65	2	944,48369	0,07	36,62
																	Medium	STIGVEFATR	1		0,0000	1,43	2	1080,56853	0,07	40,71
4208	M1Q DP5	S-adenosylmethionine synthase	S-adenosylmethionine synthase OS=Prunus persica GN=PRUPE_ppa006841mg PE=2 SV=1 - [M1QDP5_PRUPE]		Prunus persica	Cytopla sm	01.01- Metabolism /Amino Acid	18,90	17,3 0	3	4	7	14	393	42,9	6,05	High	IPDKEILK	4		0,0000	2,56	2	955,58190	-0,43	37,43
																	High	TIGFVSDDVGLD ADNcK	1	C16(Car bamido methyl)	0,0000	2,54	2	1825,82915	0,98	45,78
																	High	TAAYGHFGR	3		0,0000	2,16	2	979,47405	-0,43	35,07
																	High	SIVASGLAR	2		0,0000	2,10	2	873,51488	-0,47	38,50
																	Medium	SGAYIVR	1		0,0000	1,91	2	765,42522	-0,23	36,64
																	Medium	EHVIKPVIEK	1		0,0000	1,72	2	1288,76335	0,73	35,97
																	Medium	GAMVPIR	2		0,0000	1,50	2	743,42339	0,10	39,44
4209	M1Q DQ3	methylthioribose kinase	5-methylthioribose kinase OS=Prunus persica GN=mrk PE=2 SV=1 - [M1QDQ3_PRUPE]		Prunus mume	Chlorop last	01.01- Metabolism /Amino Acid	10,08	11,5 1	3	6	6	7	417	47,3	6,14	High	cIGESWPMTK	1	C1(Carb amidom ethyl)	0,0000	2,62	2	1208,54375	-0,13	42,63
																	High	TMSLIGMR	1		0,0000	2,21	2	908,46916	-0,13	43,23
																	Medium	AYFEALALR	1		0,0000	1,86	2	1053,57231	-0,46	46,13
																	Medium	VLIEYIK	2		0,0000	1,67	2	877,53960	0,27	44,46
																	Medium	FDNLTIK	1		0,0000	1,43	2	850,46666	-0,32	40,62
																	Medium	LEV AELK	1		0,0000	1,38	2	801,47215	0,58	39,96
4211	M5X CU1	Delta-aminolevulinic acid dehydratase	Delta-aminolevulinic acid dehydratase OS=Prunus persica GN=PRUPE_ppa006219mg PE=3 SV=1 - [M5XCU1_PRUPE]		Prunus persica	Chlorop last	20.99- Secondary metabolism /Others	15,46	11,3 7	1	4	4	10	422	45,9	7,09	High	NSTGDEAYNDN GLVPR	1		0,0000	2,92	2	1721,77410	0,87	40,62
																	High	NSTGDEAYnDN GLVPR	4	N9(Dea midated)	0,0000	2,82	2	1722,75591	-0,41	41,54
																	High	TYQMNPANYR	2		0,0000	2,24	2	1257,56792	-0,15	39,11
																	High	AGADVVSFSDM MDGR	1		0,0000	2,21	2	1507,65410	1,62	43,01
																	Medium	EALIEAR	2		0,0000	1,61	2	801,44676	0,28	38,81
4214	M5W 463	Protein disulfide isomerase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008282mg PE=3 SV=1 - [M5W463_PRUPE]	92% to GE:645221668 Prunus mume, E value 0	Prunus mume	Chlorop last	06.01- Protein destination and storage/Fol ding and stability	14,91	10,9 5	1	5	5	10	338	37,2	8,72	High	TAEALAEFVNK	2		0,0000	4,02	2	1192,62102	0,11	44,50

																	Medium	ADEFTLK	2		0,000	2,00	2	823,41966	0,02	41,32
																	Medium	ADEFTLKK	3		0,0000	1,97	2	951,51384	-0,82	36,28
																	Medium	NILYTFASSS	1		0,0000	1,86	2	1102,54119	-0,32	49,84
																	Medium	SLAPTYEK	2		0,0000	1,43	2	908,47228	-0,14	36,25
4215	M5W9E0	1-aminocyclopropane-1-carboxylate deaminase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006016mg PE=4 SV=1 - [M5W9E0_PRUPE]	96% to GI:645270273 Prunus mume, E value 0	Prunus mume	Chloroplast	11.05- Disease/Defense/Stress responses	37,18	20,37	2	9	9	19	432	47,5	7,58	High	EIEEQLQSGTDK	2		0,0000	3,23	2	1376,65434	0,22	37,62
																	High	DIVNVQNAR	2		0,0000	2,85	2	1028,54900	0,60	38,61
																	High	VEQmAPSLGNWR	1	M4(Oxidation)	0,0000	2,79	2	1403,67449	0,57	42,30
																	High	RDDLSGMQLSGNK	1		0,0000	2,76	3	1420,68427	-0,50	38,71
																	High	VEQMAPSLGNWR	2		0,0000	2,68	2	1387,67949	0,52	44,01
																	High	DDLSGmQLSGNK	1	M6(Oxidation)	0,0000	2,35	2	1280,57854	-0,19	37,74
																	High	MDVQESVPPSDGIGK	3		0,0000	2,18	2	1558,74419	1,51	40,33
																	Medium	AVGLDFLTK	2		0,0000	1,96	2	963,55083	-0,19	47,85
																	Medium	RDDLSGmQLSGNK	1	M7(Oxidation)	0,0000	1,95	3	1436,67954	-0,25	35,08
																	Medium	AAYGMLK	2		0,0000	1,60	2	753,39647	0,08	38,73
																	Medium	FGSGLTNLLK	1		0,0165	1,19	2	1164,62529	-0,58	47,70
																	Medium	mDVQESVPPSDGIGK	1	M1(Oxidation)	0,0000	0,98	2	1574,73564	-0,71	40,57
4313	M1QDP5	S-adenosylmethionine synthase	S-adenosylmethionine synthase OS=Prunus persica GN=PRUPE_ppa006841mg PE=2 SV=1 - [M1QDP5_PRUPE]		Prunus mume	Cytoplasm	01.01- Metabolism/Amino Acid	43,16	27,74	7	10	10	21	393	42,8817	6,049316	High	TIGFVSDDVGLDADNcK	1	C16(Carbamido methyl)	0,0000	4,69	2	1825,83025	1,58	45,73
																	High	FVIGGPHGDAGLTGR	2		0,0000	4,31	2	1453,75603	0,90	39,90
																	High	TQVTVEYYNDK	2		0,0000	3,36	2	1359,64287	0,12	38,78
																	High	IPDKEILK	4		0,0000	3,05	2	955,58171	-0,63	36,47
																	High	TIFHLNPSGR	2		0,0000	2,59	2	1141,61101	-0,26	39,33
																	High	EHVIKPVIEK	4		0,0000	2,42	2	1288,76323	0,64	35,51
																	High	SIVASGLAR	2		0,0000	2,32	2	873,51476	-0,61	39,30
																	Medium	NGTcAWLRPDGK	1	C4(Carbamidomethyl)	0,0000	2,19	3	1374,65750	-0,63	38,46
																	High	TAAYGHFGR	2		0,0000	2,17	2	979,47405	-0,43	34,73
																	Medium	GAMVPIR	1		0,0000	1,56	2	743,42284	-0,64	38,24
4421	M5XCZ6	Adenosylhomocysteinase	Adenosylhomocysteinase OS=Prunus persica GN=PRUPE_ppa004934mg PE=3 SV=1 - [M5XCZ6_PRUPE]		Prunus mume	Chloroplast	01.01- Metabolism/Amino acid	12,28	12,16	2	6	6	8	485	53,3	6,19	High	VSVVcGYGDVGK	2	C5(Carbamidomethyl)	0,0000	2,15	2	1239,59807	-4,67	40,14
																	High	LVGVSEETTTGVK	2		0,0000	2,00	2	1319,70622	0,66	38,83
																	Medium	DMSQADFGFR	1		0,0000	1,79	2	1026,43083	-0,14	39,81
																	Medium	DSAAVFAWK	1		0,0000	1,71	2	994,49938	0,07	46,51

																	Medium	TEFGPSQPFK	1		0,0000	1,53	2	1137,55803	0,42	41,05
																	Medium	VYVLPK	1		0,1346	0,90	2	718,45000	0,26	39,57
4711	M5W 2A2	Receptor-like protein kinase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001265mg PE=4 SV=1 - [M5W2A2_PRUPE]	99% to GI:645262841 Prunus mume, E value 0	Prunus mume	Cell wall	10.04.04- Signal transductio n/Kinases	5,42	1,27	1	2	2	3	867	95,0	6,01	Medium	LDICIGAAR	1		0,0054	1,84	2	931,50902	6,44	37,65
																	Medium	qRLDICIGAAR	1	Q1(Dea midated)	0,0109	1,81	2	1216,65715	8,56	46,67
																	Medium	QRLDICIGAAR	1		0,0000	1,78	2	1215,66521	2,05	45,94
4726	M5X B32	Prolyl endopeptidase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001738mg PE=4 SV=1 - [M5XB32_PRUPE]	95% to GI:645228649 Prunus mume, E value 0	Prunus mume	Chlorop last	06.13- Protein destination and storage/Prot eolysis	11,90	8,55	2	8	8	10	772	87,1	6,43	High	LVAYAEDTK	1		0,0000	2,03	2	1009,52001	-0,08	36,87
																	Medium	LEDGLVVLTPR	1		0,0000	1,96	2	1211,69890	-0,48	45,85
																	Medium	TPPSVYDYDMK	1		0,0000	1,87	2	1315,59062	2,36	41,43
																	Medium	MEMFGDVR	1		0,0000	1,62	2	984,42772	-0,10	43,64
																	Medium	IKEDDISAPER	3		0,0000	1,55	2	1272,64336	0,21	35,54
																	Medium	TGISVLK	1		0,0000	1,41	2	717,45067	0,17	39,26
																	Medium	EDDISAPER	1		0,0000	1,25	2	1031,46416	0,10	36,34
																	Medium	FLFVGSESK	1		0,0538	1,23	2	1013,53111	0,83	44,27
4805	M5W QJ8	neutral alpha-glucosidase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa000927mg PE=4 SV=1 - [M5WQJ8_PRUPE]	94% to GI:645265210 Prunus mume, E value 7e-112	Prunus mume	Chlorop last	01.05- Metabolism /Sugars and polysacchar ides	16,22	6,36	1	6	7	10	959	106, 9	6,20	High	SAGCTEYNNVTE R	2	C4(Carb amidom ethyl)	0,0000	2,26	2	1515,64018	1,40	36,97
																	High	IDSSIIAR	1		0,0000	2,21	2	874,49919	-0,12	39,55
																	High	ACFIGSQR	2		0,0000	2,05	2	835,44200	-0,14	37,10
																	Medium	GGDWFK	1		0,0000	1,81	2	808,39879	-0,09	42,89
																	Medium	FDVSQVYK	2		0,0000	1,78	2	985,49901	0,06	42,38
																	Medium	VVPWIGGR	1		0,0714	1,04	2	883,51457	-0,37	43,66
4828	M5V SW8	aconitate hydratase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001138mg PE=4 SV=1 - [M5VSW8_PRUPE]	99% to GI:645273719 Prunus mume, E value 0	Prunus mume	Cytopla sm	02.10- Energy/TC A pathway	22,81	13,5 9	1	8	13	19	898	98,2	6,33	High	TGEDADTLGLT GEER	1		0,0000	3,33	2	1563,71318	-0,12	40,46
																	High	DMTMSPPGAH VK	1		0,0000	2,39	2	1327,61431	0,68	36,71
																	High	ILLESAIR	2		0,0000	2,17	2	914,56688	-0,12	41,76
																	High	GPMLLGVK	1		0,0000	2,11	2	814,48522	-0,45	41,05
																	Medium	DFNSYGSR	1		0,0000	1,98	2	945,40557	-0,58	36,42
																	Medium	MFVDYNPQVE R	1		0,0000	1,93	2	1526,69634	1,22	41,31
																	Medium	DFnSYGSR	1	N3(Dea midated)	0,0000	1,90	2	946,39012	0,00	37,41
																	Medium	IIDWENTSPK	1		0,0000	1,89	2	1202,60491	-0,27	41,23
																	Medium	GPmLLGVK	1	M3(Oxi dation)	0,0172	1,71	2	830,48082	0,39	39,18
																	Medium	GFAVPK	1		0,0000	1,70	2	618,36131	0,49	37,04

																	Medium	THIPTGEK	2		0,0000	1,59	2	995,55223	0,17	35,49
																	Medium	VTLQYLK	1		0,0000	1,52	2	864,51891	-0,05	40,08
																	Medium	GTFANIR	1		0,0000	1,48	2	778,42058	-0,09	37,13
																	Medium	SFVcTLR	1	C4(Carb amidom ethyl)	0,0000	1,47	2	882,45012	-0,13	38,99
																	Medium	TSLAPGSGVVT K	3		0,0000	1,46	2	1116,62578	-0,17	36,86
4829	M5V SW8	aconitate hydratase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001138mg PE=4 SV=1 - [M5VSW8_PRUPE]	99% to GI:645273719 Prunus mume, E value 0	Prunus mume	Chlorop last	02.10- Energy/TC A pathway	18,75	10,8 0	1	6	11	13	898	98,2	6,33	High	TGEDADTLGLT GEER	1		0,0000	3,24	2	1563,71501	1,05	40,31
																	High	ILLESAIR	1		0,0000	2,60	2	914,56688	-0,12	41,64
																	Medium	SFVcTLR	1	C4(Carb amidom ethyl)	0,0000	1,98	2	882,44988	-0,41	38,85
																	Medium	GPmLLGVK	1	M3(Oxi dation)	0,0000	1,97	2	830,48088	0,47	39,06
																	Medium	IIDWENTSPK	1		0,0000	1,92	2	1202,60600	0,64	40,50
																	Medium	DFNSYGSR	1		0,0000	1,90	2	945,40587	-0,25	36,21
																	Medium	TSLAPGSGVVT K	2		0,0000	1,84	2	1116,62602	0,05	36,63
																	Medium	GFAVPK	1		0,0000	1,66	2	618,36119	0,29	36,94
																	Medium	DFnSYGSR	1	N3(Dea midated)	0,0000	1,64	2	946,39031	0,19	37,16
																	Medium	THIPTGEK	1		0,0000	1,60	2	995,55235	0,29	35,28
																	Medium	VTLQYLK	1		0,0000	1,49	2	864,51860	-0,40	39,91
																	Medium	GTFANIR	1		0,0000	1,26	2	778,42064	-0,01	36,92
5008	M5W V03	Thaumatococin	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa010471mg PE=4 SV=1 - [M5WV03_PRUPE]	96% to GI:645246258 Prunus mume, E value 8e-172	Prunus mume	Extracel lular	11.02- Disease/def ense/Defens e-related	37,32	25,8 1	4	5	5	18	248	26,0	7,30	High	YccTPPNDKPETc PPTDYSK	3	C2(Carb amidom ethyl); C3(Carb amidom ethyl); C13(Car bamido methyl)	0,0000	3,14	3	2430,00620	0,60	36,71
																	High	SACLAFNQPK	5	C3(Carb amidom ethyl)	0,0000	3,09	2	1135,55644	-0,05	40,10
																	High	SVDAPSPWWSGR	7		0,0000	2,64	2	1158,55400	0,11	41,50
																	High	TQcPQAYSAY DDK	2	C3(Carb amidom ethyl)	0,0000	2,60	2	1709,71428	1,80	40,15
																	Medium	VcPAPLQVK	1	C2(Carb amidom ethyl)	0,0000	1,13	2	1011,56548	-0,14	39,43
5414	M4Q FX1	UDP-glucose 6- dehydrogenase	UDP-glucose 6-dehydrogenase OS=Prunus persica GN=UGD PE=2 SV=1 - [M4QFX1_PRUPE]		Prunus persica	Chlorop last	01.05- Metabolism /Sugars and polysacchar ides	22,92	15,1 5	5	8	8	11	482	53,0	6,18	High	LAANAFLAQR	1		0,0000	3,06	2	1074,60539	-0,11	42,92
																	High	VVASMFTVAK	2		0,0000	2,93	2	1166,62370	-0,14	42,47
																	High	NVVNVVDQLR	2		0,0000	2,70	2	1056,57964	-0,04	40,42
																	High	QVTVVGDAYEAA AK	1		0,0000	2,16	2	1350,68999	-0,03	40,46
																	High	AADLTYWESAA R	1		0,0000	2,11	2	1353,64348	0,05	45,43
																	Medium	IEAWNSDK	1		0,0000	1,69	2	962,45781	-0,02	37,88

																	Medium	ETPAIDVcK	2	C8(Carb amidom ethyl)	0,0000	1,63	2	1032,50298	-0,09	38,85
																	Medium	RIEAWNSDK	1		0,0000	1,25	2	1118,55876	-0,17	35,65
5509	M5W P36	delta-1-pyrroline-5- carboxylate dehydrogenase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003713mg PE=3 SV=1 - [M5WP36_PRUPE]	99% to GI:645269075 Prunus mume, E value 0	Prunus persica	Mitocho ndrion	01.01- Metabolism /Amino acid	10,55	9,75	1	6	6	7	554	61,7	7,02	High	LEDAGFDWK	1		0,0000	2,49	2	1080,50005	0,31	42,92
																	High	EIIYDVGPLPK	1		0,0000	2,39	2	1243,69316	-0,13	43,68
																	High	LLQISGSK	1		0,0000	2,10	2	845,50914	0,01	37,40
																	Medium	GAGIGTPEAIK	1		0,0000	1,82	2	1013,56236	-0,28	37,15
																	Medium	LLFGGEPLK	1		0,0000	1,75	2	973,57158	-0,18	43,47
																	Medium	LALDLK	2		0,0492	1,16	2	672,42912	0,05	40,45
																	High	mDAQSQPQVG VVK	1	N- Term(A cetyl)	0,0000	2,21	2	1556,77397	0,11	41,69
5703	M5V IK0	laccase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003580mg PE=4 SV=1 - [M5VIK0_PRUPE]	96% to GI:645264281 Prunus mume, E value 0	Prunus mume	Chlorop last	20.99- Secondary metabolism /Others	12,64	4,79	3	3	3	7	564	62,2	6,40	High	ATVYGAIILPK	1		0,0000	2,71	2	1258,77751	0,41	47,62
																	High	GDVNEIHK	2		0,0000	2,17	2	887,48326	-0,07	38,71
																	High	nGWATVR	2	N1(Dea midated)	0,0000	2,09	2	804,39977	-0,19	42,33
																	High	NGWATVR	2		0,0000	2,08	2	803,41606	0,20	37,33
5705	M5X 661	transketolase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001865mg PE=4 SV=1 - [M5X661_PRUPE]		Prunus mume	Chlorop last	02.30- Energy/Pho tosynthesis	34,38	13,8 3	1	1 0	10	23	752	80,9	6,84	High	VTTTIGFGSPNK	2		0,0000	3,37	2	1221,64775	0,26	41,58
																	High	NGNTGYDEIR	2		0,0000	3,09	2	1138,51225	-0,11	37,62
																	High	nGNTGYDEIR	6	N1(Dea midated)	0,0000	2,78	2	1139,49651	0,10	40,79
																	High	ALPTYTPENPAD ATR	2		0,0000	2,64	2	1616,79338	1,14	42,19
																	High	NPYWFNR	2		0,0000	2,02	2	996,46874	0,09	44,34
																	Medium	AVTDRPTLIK	1		0,0000	1,97	2	1113,66252	-0,15	37,23
																	Medium	ESVLPAAVTAR	2		0,0000	1,69	2	1113,62578	-0,48	41,62
																	Medium	FLAIDAVEK	1		0,0000	1,56	2	1005,56133	-0,25	44,38
																	Medium	TTETSLVEK	2		0,0000	1,49	2	1007,52538	-0,19	36,10
																	Medium	SFGDFQK	2		0,0000	1,23	2	828,38915	0,56	40,63
																	Medium	ANSYSVHGAAAL GAK	1		0,0000	1,08	2	1345,68584	-0,08	36,00
5707	M5W GM1	4-hydroxy-3-methylbut-2-en- 1-yl diphosphate synthase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002111mg PE=3 SV=1 - [M5WGM1_PRUPE]	99% to GI:645217430 Prunus mume, E value 0,00	Prunus mume	Chlorop last	20.2- Secondary metabolism /Terpenoids	30,72	19,8 6	1	1 5	15	29	715	79,6	6,55	High	NTKTEYVScPSc GR	3	C9(Carb amidom ethyl); C12(Car bamido methyl)	0,0000	2,94	3	1658,72605	-0,07	34,34
																	High	IADKGADLVR	4		0,0000	2,51	3	1057,60022	0,12	35,41
																	High	TEYVScPScGR	3	C6(Carb amidom ethyl); C9(Carb amidom ethyl)	0,0000	2,19	2	1315,54143	0,64	36,03
																	High	NTSFNLLQGcR	2	C10(Car bamido methyl)	0,0000	2,19	2	1309,63298	0,91	43,77

																		High	IMSYYGDSPR	1		0,0000	2,17	2	1188,53642	0,84	39,88
																		High	ASNPVIMVQAYR	1		0,0000	2,07	2	1348,70488	0,47	43,50
																		High	VSLTEAPEEEIDPcR	1	C14(Carbamido methyl)	0,0000	2,03	2	1744,80791	1,15	43,85
																		Medium	IDLYVGK	2		0,0000	1,91	2	807,46092	-0,23	41,52
																		Medium	WVDPPVEE	1		0,0000	1,59	2	970,45250	0,83	45,17
																		Medium	VNPGNFADR	1		0,0000	1,53	2	989,47972	-0,25	38,33
																		Medium	QLPPVDDNDSR	3		0,0000	1,52	2	1255,59160	0,17	39,08
																		Medium	DVAATVEQVmR	1	M10(Oxidation)	0,0000	1,50	2	1234,60991	0,18	41,31
																		Medium	ImSYYGDSPR	1	M2(Oxidation)	0,0000	1,40	2	1204,53008	-0,22	37,84
																		Medium	LLPEGTR	2		0,0000	1,20	2	785,45146	-0,20	37,17
																		Medium	LVVSVR	2		0,0000	1,19	2	672,44017	-0,22	38,16
																		Medium	GmVESAFEFAR	1	M2(Oxidation)	0,0000	1,06	2	1259,57207	-0,40	44,55
5712	M5VZ56	dehydrogenase/reductase SDR family	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008500mg PE=4 SV=1 - [M5VZ56_PRUPE]	99% to GE645223245 Prunus mume, E value 0	Prunus mume	Plasma membrane	11.05- Disease/Defense/Stress responses	3,81	3,65	1	1	1	2	329	35,8	9,38	High	GHFVVmSSAAGK	2	M6(Oxidation)	0,0000	2,08	2	1206,60161	6,61	40,27	
6101	M5X1U6	6-phosphogluconolactonase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008941mg PE=4 SV=1 - [M5X1U6_PRUPE]	98% to GE645257997 Prunus mume, E value 0,00	Prunus mume	Chloroplast	02.07- Energy/Pentose phosphate	18,40	15,97	1	6	6	13	313	34,1	8,75	High	FETEEEVAVR	2		0,0000	3,01	2	1208,57976	0,28	40,10	
																		High	ASAVcTALGK	3	C5(Carbamidomethyl)	0,0000	2,55	2	977,50810	-0,40	38,32
																		Medium	YTADLSAK	3		0,0000	1,73	2	868,44084	-0,30	37,10
																		Medium	LAEAPYK	2		0,0000	1,53	2	791,42955	-0,33	36,50
																		Medium	LALDGFLSK	2		0,0000	1,48	2	963,55077	-0,25	47,01
																		Medium	WVTcIK	1	C4(Carbamidomethyl)	0,0000	1,03	2	806,42345	0,61	39,96
6206	M5X0L9	Phosphoglycerate kinase	Phosphoglycerate kinase OS=Prunus persica GN=PRUPE_ppa005669mg PE=3 SV=1 - [M5X0L9_PRUPE]		Prunus persica	Cytosol	02.01- Energy/Glycolysis	156,77	36,53	2	16	16	81	449	47,5	7,03	High	AQGYSVGSSLVEEDK	1		0,0000	4,08	2	1568,74504	0,71	39,61	
																		High	GVTTIIGGDSVAAVEK	8		0,0000	3,70	2	1573,84490	1,03	42,69
																		High	ELDYLVGAVGNPK	1		0,0000	3,64	2	1374,72734	0,67	43,86
																		High	IAnDcIGEEVEK	1	N3(Deamidated); C5(Carbamidomethyl)	0,0000	3,16	2	1377,61919	-0,82	38,21
																		High	VDLNVPLDDNSK	15		0,0000	3,04	2	1328,67046	0,87	43,27
																		High	IANDcIGEEVEK	20	C5(Carbamidomethyl)	0,0000	2,99	2	1376,63603	-0,19	56,06
																		High	IANDcIGEEVEK	1		0,0000	2,60	2	1319,61589	0,80	41,18
																		High	RPFAAIVGGSK	2		0,0000	2,55	3	1102,63694	0,10	36,96
																		High	LSELLGVEVK	8		0,0000	2,43	2	1086,64031	-0,23	45,84
																		High	FAAGTEAIAK	2		0,0000	2,34	2	978,52501	-0,53	36,29

																	High	LAELSDK	1		0,0000	2,28	2	775,41948	-0,22	34,59
																	Medium	YSLKPLVPR	2		0,0000	1,99	3	1072,65140	0,02	38,57
																	Medium	KLAE SDK	1		0,0000	1,98	2	903,51445	-0,19	32,51
																	Medium	AHASTEGVAK	1		0,0000	1,75	2	970,49498	-0,31	29,99
																	Medium	AAVPTIK	13		0,0000	1,57	2	699,44005	0,08	36,44
																	Medium	vDLnVPLDnSK	1	N- Term(A cetyl); N4(Dea midated); N10(De amidate d)	0,0000	1,42	2	1372,63457	-9,71	41,88
																	Medium	EEEKNDPEFSK	1		0,0000	1,31	3	1351,60050	-0,58	31,93
																	Medium	YLQGHGAK	1		0,0000	1,17	2	873,45757	-0,21	29,96
																	Medium	SVSTLKEAELK	1		0,0000	1,06	2	1204,67961	1,01	35,48
6220	M5X E62	26S proteasome non-ATPase regulatory subunit 11 homolog	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006204mg PE=4 SV=1 - [M5XE62_PRUPE]	96% to Gt:658009294 Malus domestica, E value 0	Malus domesti ca	Nucleus	06.13- Protein destination and storage/Prot eolysis	15,28	23,2 2	2 0	9	9	9	422	47,1	6,48	High	ILENPSSSEALR	1		0,0000	2,62	2	1402,71733	0,02	37,91
																	High	AQLEEDPIVHR	1		0,0000	2,42	2	1306,67583	0,60	36,90
																	High	IMVSQADDVAG ISSK	1		0,0000	2,40	2	1633,85332	4,09	44,02
																	High	VPGTSDLQISLc K	1	C12(Car bamido methyl)	0,0000	2,24	2	1417,73967	2,87	42,46
																	High	VVDSL YVR	1		0,0000	2,02	2	950,53038	-0,22	39,09
																	Medium	AGLQYVGPELD AMK	1		0,0000	1,83	2	1491,75102	-0,17	44,37
																	Medium	LASLLMESK	1		0,0000	1,74	2	991,54924	-0,06	41,58
																	Medium	EMVQWTR	1		0,0000	1,56	2	949,45537	-0,73	39,72
																	Medium	LFETALR	1		0,0000	1,49	2	849,48290	-0,03	40,89
6413	M5W PG7	6-phosphogluconate dehydrogenase, decarboxylating	6-phosphogluconate dehydrogenase, decarboxylating OS=Prunus persica GN=PRUPE_ppa005270mg PE=3 SV=1 - [M5WPG7_PRUPE]		Prunus mume	Chlorop last	02.07- Energy/Pen tose phosphate	36,24	19,6 2	2	6	10	23	469	50,8	7,46	High	LPANLVQAQR	3		0,0000	3,08	2	1109,64214	-0,44	39,38
																	High	EVIGSVTSGIDK	3		0,0000	2,98	2	1204,64238	0,30	41,62
																	High	DDLADGFLVDK	1		0,0000	2,92	2	1207,58452	0,28	48,74
																	High	mEASPALSR	2	N- Term(A cetyl)	0,0000	2,60	2	1003,48747	-0,29	43,57
																	High	YLSGLKEER	4		0,0000	2,21	2	1094,58415	0,06	36,67
																	High	GFPISVYNR	2		0,0000	2,15	2	1052,55217	-0,21	44,53
																	Medium	SVIILVK	3		0,0000	1,93	2	771,53392	0,04	43,68
																	Medium	LIDDDR	2		0,0000	1,82	2	730,40941	-0,01	38,37
																	Medium	AVFLDR	2		0,0000	1,53	2	720,40392	-0,03	40,97
																	Medium	LAQKSGSGVGALN	1		0,0000	1,50	2	1201,65300	-0,49	36,55

6419	M5W P70	Uncharacterized aminotransferase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa004689mg PE=3 SV=1 - [M5WP70_PRUPE]	98% to GI:645221853 Prunus mume, E value 0,00	Prunus persica	Mitocho ndrion	01.06- Metabolism /Lipid and sterol	14,90	10,7 1	3	5	6	17	467	52,3	6,43	High	NHDAVVEMGK	4		0,0000	2,81	2	1099,52031	0,16	35,56
																	High	DAVNQLVR	2		0,0000	2,07	2	914,50517	-0,30	40,79
																	High	FGVEVR	2		0,0000	2,06	2	706,38854	0,35	39,89
																	Medium	NHDAVVEmGK	3	M8(Oxi dation)	0,0000	1,60	2	1115,51421	-0,75	32,72
																	Medium	DGEVGSTTGYY R	1		0,0000	1,51	2	1240,58196	1,20	38,39
																	Medium	TQVPIEPK	3		0,0000	1,48	2	911,51921	-0,54	37,94
																	Medium	IVIFcR	2	C5(Carb amidom ethyl)	0,0000	1,21	2	807,45433	-0,33	43,09
6708	M5X QJ0	Phosphoenolpyruvate carboxykinase [ATP]	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002490mg PE=3 SV=1 - [M5XQJ0_PRUPE]	99% to GI:645224569 Prunus mume, E value 0	Prunus mume	Cytopla sm	02.02- Energy/Glu coneogenes is	34,92	21,2 9	2	1 2	12	26	667	74,0	7,23	High	AAEnGGFSFTR	2	N4(Dea midated)	0,0000	3,52	2	1157,52361	1,18	40,62
																	High	AAEnGGFSFTR	1		0,0000	3,14	2	1156,53850	0,24	40,05
																	High	AAYPIEYIPnAK	2	N10(De amidate d)	0,0000	3,06	2	1350,69292	-0,83	43,53
																	High	EMVILGTQYAG EmK	1	M13(Ox idation)	0,0000	2,49	2	1585,76225	1,34	42,67
																	Medium	IQTHPEATSEVc HDDSGTPVK	2	C12(Car bamido methyl)	0,0000	2,48	3	2308,05338	0,99	34,14
																	High	YAAMLSEK	1		0,0000	2,30	2	912,44902	-0,60	37,09
																	High	AAYPIEYIPNAK	5		0,0000	2,23	2	1349,71086	0,62	43,41
																	High	IPcVGPHPK	2	C3(Carb amidom ethyl)	0,0000	2,10	2	1004,53441	-0,23	33,91
																	High	AVDYLNSLDK	1		0,0000	2,01	2	1137,57878	0,10	41,94
																	Medium	LLNASYTK	1		0,0000	1,95	2	909,50377	-0,29	36,28
																	Medium	GSFITATGALAT LSGAK	1		0,0000	1,89	2	1565,85503	1,02	46,85
																	Medium	EMVILGTQYAG EMK	1		0,0000	1,73	2	1569,76579	0,37	44,31
																	Medium	SSQPTTPInGK	1	N9(Dea midated)	0,0000	1,59	2	1130,56914	0,27	34,15
																	Medium	IIDAIHSGR	2		0,0000	1,59	2	981,54723	-0,43	34,54
																	Medium	LTEEILAAGPNF	1		0,0000	1,56	2	1274,66265	-0,09	48,76
																	Medium	EmVILGTQYAG EmK	1	M2(Oxi dation); M13(Ox idation)	0,0000	1,55	2	1601,75481	-0,15	40,12
																	Medium	YAAmLSEK	1	M4(Oxi dation)	0,0000	1,34	2	928,44396	-0,57	34,52
6709	M5X QL3	subtilisin-like protease	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001756mg PE=4 SV=1 - [M5XQL3_PRUPE]	98% to GI:645227002 Prunus mume, E value 0,00	Prunus mume	Chlorop last	06.13- Protein destination and storage/Prot eolysis	51,03	15,4 7	3	1 0	11	25	769	81,0	6,32	High	GYEALGPIDE K	3		0,0000	3,95	2	1262,62712	0,60	41,77
																	High	TLTNVGTPATY K	3		0,0000	3,58	2	1265,67400	0,29	39,28
																	High	SYDDTGLAAMP SSWK	2		0,0000	3,13	2	1596,75530	0,75	45,26
																	High	LTTHKDFTcDSS K	3	C9(Carb amidom ethyl)	0,0000	3,12	3	1539,71097	0,09	33,27
																	High	VSVSSQTPSVK	3		0,0000	2,76	2	1118,60527	0,05	36,59

																	High	SEAFLPASDK	2		0,0000	2,59	2	1064,52593	0,00	39,74
																	High	TPEFLGLGK	3		0,0000	2,38	2	961,53520	-0,16	45,23
																	Medium	LEWSDGK	3		0,0000	1,99	2	834,40044	1,42	39,53
																	Medium	SALMTTSYTTY K	1		0,0000	1,70	2	1366,65691	0,72	40,67
																	Medium	DFPAFVSLGNE K	1		0,0000	1,19	2	1323,65752	-0,37	48,45
																	Medium	GISLYR	1		0,0000	1,17	2	708,40410	0,25	39,38
7004	M5W TZ4	Glutathione S-transferase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa011337mg PE=3 SV=1 - [M5WTZ4_PRUPE]	95% to GI:645246909 Prunus mume, E value 8e-145	Prunus mume	Cytopla sm	11.06- Disease/Def ense/Detoxi fication	27,44	16,8 2	4	4	4	14	214	24,7	6,30	High	VLDIYEER	3		0,0000	2,72	2	1036,53069	-0,29	41,32
																	High	VIQESEEKLGK	2		0,0000	2,33	2	1259,68401	-0,17	34,70
																	High	VLVcLVEK	6	C4(Carb amidom ethyl)	0,0000	2,21	2	959,55876	-0,73	42,00
																	Medium	SQGTALLGK	3		0,0000	1,78	2	874,49889	-0,47	39,18
7106	M5W GS1	extradiol ring-cleavage dioxygenase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa009849mg PE=4 SV=1 - [M5WGS1_PRUPE]	97% to GI:645218731 Prunus mume, E value 0	Prunus persica	Cell wall	20.99- Secondary metabolism /Others	99,78	22,2 6	1	7	7	54	274	30,1	6,86	High	YEDVNQYEEK	18		0,0000	3,11	2	1316,56462	0,37	35,80
																	High	DATYHYNMGR	4		0,0000	2,73	2	1227,52178	0,50	36,50
																	High	YEDVnQYEEK	2	N5(Dea midated)	0,0000	2,65	2	1317,54888	0,55	35,25
																	High	YPAPGSPNLAG R	21		0,0000	2,34	2	1199,61711	0,26	50,96
																	Medium	DALLEGR	2		0,0000	1,79	2	773,41484	-0,52	37,96
																	Medium	FLQSWK	1		0,0000	1,75	2	808,43511	-0,15	39,71
																	Medium	DLLTASGFPR	1		0,0000	1,71	2	1076,57317	-0,35	45,33
																	Medium	SmYQLK	1	M2(Oxi dation)	0,1317	1,45	2	785,38616	-0,09	34,40
																	Medium	DATYHYNmGR	3	M8(Oxi dation)	0,0000	1,18	2	1243,51677	0,56	33,02
																	Medium	SMYQLK	1		0,0000	1,16	2	769,39141	0,12	36,87
7109	M5W 9G4	S-formylglutathione hydrolase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa009542mg PE=4 SV=1 - [M5W9G4_PRUPE]	99% to GI:645278527 Prunus mume, E value 0,00	Prunus mume	Chlorop last	11.06- Disease/Def ense/Detoxi fication	44,26	25,0 9	2	7	7	22	287	32,2	7,08	High	VASSEGVALIAP DTSPR	4		0,0000	3,87	2	1669,87688	0,75	43,74
																	High	mETKPSEISSK	3	N- Term(A cetyl)	0,0000	3,20	2	1365,65764	0,70	38,64
																	High	AFSNYLGGNK	2		0,0000	2,39	2	1070,52641	-0,15	41,38
																	High	LLNENFPQLDTS R	1		0,0000	2,22	2	1546,78740	0,87	45,24
																	High	mYDYVVVK	3	M1(Oxi dation)	0,0000	2,07	2	933,43907	0,45	39,90
																	Medium	MYDYVVVK	3		0,0000	1,92	2	917,44353	-0,23	40,89
																	Medium	mFGGYNK	1	M1(Oxi dation)	0,0000	1,84	2	832,36577	-0,08	35,61
																	Medium	MFGGYNK	2		0,0000	1,76	2	816,37078	-0,18	38,54
																	Medium	VPLLLR	3		0,0000	1,26	2	710,49242	0,08	44,04
7113	M5Y 9C1	Malate dehydrogenase	Malate dehydrogenase OS=Prunus persica GN=PRUPE_ppa008435mg		Prunus persica	Cytopla sm	02.10- Energy/TC A pathway	46,57	40,3 6	3	1 5	15	29	332	35,4	6,79	High	LDATADELSSEE K	3		0,0000	3,55	2	1320,61724	0,48	40,06

			PE=3 SV=1 - [M5Y9C1_PRUPE]														High	VLVVANPANTN ALILK	4		0,0000	3,31	2	1649,99700	1,24	47,06
																	High	VLVTGAAGQIG YALVPMIAR	2		0,0000	3,13	2	2000,13970	1,73	50,58
																	High	LNVQVSDVK	2		0,0000	3,02	2	1001,56212	-0,51	38,75
																	High	DVMSKNVSIYK	1		0,0000	2,64	2	1283,66789	1,12	39,08
																	High	KLDATADELSE EK	1		0,0000	2,55	2	1448,71330	1,20	37,65
																	High	mELVDAAFPLL K	2	M1(Oxi- dation)	0,0000	2,52	2	1362,73369	-0,11	49,32
																	High	MELVDAAFPLL K	2		0,0000	2,50	2	1346,73967	0,56	50,78
																	High	IVQGLSIDEFSR	2		0,0000	2,30	2	1363,72246	0,58	46,53
																	Medium	SQASALEKHAA ANcK	2	C14(Car- bamido methyl)	0,0000	2,09	3	1585,77536	0,11	33,88
																	Medium	KKLDATADELS EEK	1		0,0000	1,69	3	1576,80686	0,20	35,42
																	Medium	NITcLTR	2	C4(Carb- amidom ethyl)	0,0000	1,51	2	877,45592	-0,14	37,40
																	Medium	EFAPSIPEK	2		0,0000	1,48	2	1017,52513	-0,06	41,41
																	Medium	KDVMSKNVSIY K	1		0,0593	1,27	3	1411,76053	-0,63	35,95
																	Medium	ALAYSclS	1	C6(Carb- amidom ethyl)	0,0000	1,06	2	884,41820	-0,06	44,57
																	Medium	NVSIYK	1		0,0000	1,02	2	723,40386	0,38	36,67
7202	M5X 598	cinnamoyl-CoA reductase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006945mg PE=4 SV=1 - [M5X598_PRUPE]	99% to Gt:645245246 Prunus mume, E value 0	Prunus mume	Cytopla- sm	20.1- Secondary metabolism /Phenylprop- anoids/Phen- olics	37,53	26,4 8	4	1 1	11	23	389	43,0	7,46	High	AVAEQAAWEE AK	2		0,0000	3,46	2	1302,63323	0,53	41,95
																	High	LQDLGLEFTPV K	2		0,0000	3,10	2	1359,75286	0,69	49,85
																	High	ADLLDYESLK	2		0,0000	3,09	2	1166,59416	0,15	48,72
																	High	NVIVAAAEAK	3		0,0000	2,53	2	985,56719	-0,55	40,35
																	High	GDVVEILAK	2		0,0000	2,46	2	943,54546	-0,50	46,55
																	High	KADLLDYESLK	3		0,0000	2,29	2	1294,68926	0,23	44,17
																	High	FFPEYPIPTK	2		0,0000	2,03	2	1238,64580	0,14	48,79
																	Medium	NWYcYGK	3	C4(Carb- amidom ethyl)	0,0000	1,98	2	990,41368	-0,14	43,46
																	Medium	GHLAVPKPQED SIK	1		0,0000	1,44	3	1518,82715	-0,26	38,26
																	Medium	YLcAESVLHR	1	C3(Carb- amidom ethyl)	0,0000	1,26	2	1247,62065	0,40	42,11
																	Medium	QcLYDTVK	2	C2(Carb- amidom ethyl)	0,0000	1,15	2	1026,49224	-0,24	41,32
7212	M5W 2H9	Fructose-bisphosphate aldolase	Fructose-bisphosphate aldolase OS=Prunus persica GN=PRUPE_ppa007696mg PE=3 SV=1 - [M5W2H9_PRUPE]		Prunus persica	Cytopla- sm	02.01- Energy/Gly- colysis	70,16	38,5 5	3	1 5	17	44	358	38,4	7,36	High	KASPEVIAEYTV R	1		0,0000	3,52	3	1462,79010	0,02	40,85
																	High	FASINVENVESN R	2		0,0000	3,41	2	1478,72502	1,06	43,17
																	High	ANSEATLGTYK	2		0,0000	3,40	2	1154,56914	0,27	37,72

																	High	GILAADESTGTIGK	2		0,0000	3,24	2	1332,70134	0,55	42,67
																	High	GILAADESTGTIGKR	3		0,0000	3,17	2	1488,80303	0,87	39,55
																	High	ASPEVIAEYTVR	2		0,0000	2,96	2	1334,69573	0,46	44,95
																	High	AWAGKEENIGK	4		0,0000	2,85	2	1202,61675	0,22	36,93
																	High	IGPNEPSQLSINENAnGLAR	4	N16(Deamidate d)	0,0000	2,80	2	2095,04277	0,59	44,08
																	High	AKANSEATLGT YK	4		0,0000	2,46	2	1353,70134	0,31	35,53
																	High	AQAALLTR	2		0,0000	2,39	2	843,50475	0,03	39,41
																	High	TASGKPFVDVLK	1		0,0000	2,38	2	1261,71501	-0,09	41,51
																	High	LGEGAAESLHV K	2		0,0000	2,36	2	1210,64263	-0,05	38,68
																	Medium	AKANSEATLGT YKGDAK	1		0,0000	2,30	3	1724,88169	0,15	34,77
																	High	ANSEATLGT YKGDAK	4		0,0000	2,14	2	1525,75029	0,62	36,95
																	Medium	IGPNEPSQLSINENANGLAR	1		0,0000	1,74	2	2094,06059	1,47	43,87
																	Medium	EGGVLPGIK	5		0,0000	1,66	2	869,50890	-0,29	44,24
																	Medium	VLAAcYK	3	C5(Carbamidomethyl)	0,0000	1,57	2	824,43346	-0,07	37,91
																	Medium	FASINVENVESNRR	1		0,0000	1,51	3	1634,82401	-0,35	40,68
7301	M5X0L9	Phosphoglycerate kinase	Phosphoglycerate kinase OS=Prunus persica GN=PRUPE_ppa005669mg PE=3 SV=1 - [M5X0L9_PRUPE]		Prunus persica	Chloroplast	02.01 - Energy/Glycolysis	92,79	43,21	2	17	39	449	47,5	7,03	High	GVTTHIGGGDSVAAVEK	4		0,0000	4,85	2	1573,84490	1,03	44,79	
																	High	ELDYLVGAVGNPK	3		0,0000	3,61	2	1374,72661	0,14	46,03
																	High	FLKPSVAGFLMQK	2		0,0000	3,52	3	1465,82306	-0,40	46,17
																	High	FYKEEEKNDPEFSK	3		0,0000	3,27	3	1789,82755	-0,25	36,09
																	High	VDLNVPLDDNSKITDDTR	2		0,0000	3,03	3	2030,00443	0,33	43,64
																	High	IANDcIGEEVEK	2	C5(Carbamidomethyl)	0,0000	3,03	2	1376,63713	0,61	39,21
																	High	LVAQLPDGGVLLLENVR	1		0,0000	3,02	2	1806,05010	0,91	51,02
																	High	KLAELSDK	3		0,0000	2,86	2	903,51396	-0,73	35,87
																	High	RPFAAIVGGSK	4		0,0000	2,73	3	1102,63657	-0,23	39,01
																	High	FAAGTEAIAK	3		0,0000	2,59	2	978,52556	0,03	38,35
																	High	VDLNVPLDDNSK	2		0,0000	2,54	2	1328,66960	0,23	45,10
																	High	LAELSDK	2		0,0000	2,33	2	775,41979	0,17	37,82
																	High	VVPASAI PDGWMGLDIGPDSIK	1		0,0000	2,32	2	2238,15117	1,59	51,93
																	High	YSLKPLVPR	3		0,0000	2,14	2	1072,65129	-0,08	40,75
																	Medium	AAVPTIK	2		0,0000	1,50	2	699,43987	-0,18	37,59
																	Medium	GVSILLPTDVV1ADK	1		0,0000	1,25	2	1539,90068	0,88	50,57

																	Medium	YLQGHGAK	1		0,0000	1,03	2	873,45732	-0,49	32,10
7302	Q9M BD7	NAD-dependent sorbitol dehydrogenase	NAD-dependent sorbitol dehydrogenase OS=Prunus persica GN=PRUPE_ppa007458mg PE=2 SV=1 - [Q9MBD7_PRUPE]		Prunus persica	Cytopla sm	01.05- Metabolism /Sugars and polysacchar ides	42,97	33,7 9	4	1 2	12	24	367	39,1	6,90	High	VSTNPQDLEDE VSK	2		0,0000	3,08	2	1560,74077	1,24	44,11
																	High	IVIVDVDDER	3		0,0000	3,07	2	1172,61589	0,07	45,45
																	High	LPTVGPNDVR	2		0,0000	2,81	2	1067,58440	-0,04	42,36
																	High	VALEPGIScWR	2	C9(Carb amidom ethyl)	0,0000	2,63	2	1287,65154	0,04	47,40
																	High	TMSTALSATRP GKK	2		0,0000	2,56	2	1377,71526	-0,21	37,82
																	High	EIEEAFETSAR	3		0,0000	2,32	2	1281,59612	0,25	42,47
																	High	YNLcPDmK	1	C4(Carb amidom ethyl); M7(Oxi dation)	0,0000	2,18	2	1056,44829	-0,60	39,59
																	Medium	AVGlcGSDVHYL K	1	C5(Carb amidom ethyl)	0,0000	2,12	3	1418,70920	-0,36	41,85
																	High	SLGADDAVK	2		0,0000	2,01	2	875,44689	-0,06	37,23
																	Medium	YNLcPDMK	1	C4(Carb amidom ethyl)	0,0000	2,00	2	1040,45391	-0,10	42,07
																	Medium	FGFSQK	2		0,0000	1,35	2	713,36186	0,19	41,32
																	Medium	GGNAIKVmFnL	1	M8(Oxi dation); N10(De amidate d)	0,0000	1,30	2	1180,60320	0,05	47,22
																	Medium	NLVPGDR	2		0,0000	1,15	2	770,41551	-0,07	39,17
7308	M5W D75	Serine/threonine-protein kinase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa007019mg PE=4 SV=1 - [M5WD75_PRUPE]	99% to GI645268898 Prunus mume, E value 0	Prunus mume	Nucleus	10.04.04- Signal transductio n/Kinases	49,03	25,4 5	8	1 2	12	28	385	43,0	7,36	High	TEAEISSLR	2		0,0000	2,77	2	1005,52068	-0,48	39,72
																	High	SLDEQLER	2		0,0000	2,71	2	989,48961	-0,25	39,60
																	High	GmYDGQDVAV K	3	M2(Oxi dation)	0,0000	2,63	2	1198,54106	0,11	40,76
																	High	GMYDGQDVAV K	2		0,0000	2,55	2	1182,54631	0,25	41,34
																	High	IADFGVAR	3		0,0000	2,27	2	848,46214	-0,46	42,66
																	High	TENMLLDK	2		0,0000	2,23	2	963,48131	-0,31	42,34
																	High	GLSYLHSQK	3		0,0000	2,16	2	1032,54741	0,12	36,84
																	High	ccPSSLANVMK	1	C1(Carb amidom ethyl); C2(Carb amidom ethyl)	0,0000	2,09	2	1266,56450	0,40	42,29
																	High	cWDANPDK	1	C1(Carb amidom ethyl)	0,0000	2,08	2	1005,40935	-0,16	38,18
																	High	ADQIDLK	2		0,0000	2,03	2	802,43065	0,12	39,90
																	Medium	TENmLLDK	1	M4(Oxi dation)	0,0000	1,92	2	979,47612	-0,41	38,64
																	Medium	QDWEIDPAK	2		0,0000	1,82	2	1101,52129	0,11	44,67
																	Medium	QNLRPEIPR	2		0,0000	1,49	3	1122,63800	0,12	38,51

																	Medium	ccPSSLANVmK	1	C1(Carb amidom ethyl); C2(Carb amidom ethyl); M10(Ox idation)	0,0000	1,47	2	1282,55864	-0,21	38,95
																	Medium	RcWDANPDK	1	C2(Carb amidom ethyl)	0,0000	1,42	2	1161,51128	0,56	35,79
7511	M5X 1V1	inosine-5'-monophosphate dehydrogenase	Inosine-5'-monophosphate dehydrogenase OS=Prunus persica GN=PRUPE_ppa004597mg PE=3 SV=1 - [M5X1V1_PRUPE]		Prunus persica	Chlorop last	01.03- Metabolism /Nucleotide s	10,41	7,19	3	4	4	7	501	53,7	6,86	High	DDEVVDVVAK	2		0,0000	2,64	2	1088,54668	-0,35	43,94
																	Medium	IAQGVVGAVAD K	1		0,0000	1,85	2	1127,64189	-0,07	40,35
																	Medium	LLGYVAGR	2		0,0000	1,73	2	848,49870	-0,23	42,47
																	Medium	LEGLVK	2		0,0000	1,09	2	658,41332	-0,19	39,59
7609	M5X 7M3	dihydropyrimidinase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003789mg PE=4 SV=1 - [M5X7M3_PRUPE]	95% to Gt:645241843 Prunus mume, E value 0	Prunus mume	Chlorop last	01.01- Metabolism /Amino Acid	26,79	15,88	3	10	10	19	548	59,5	6,54	High	VGDDVTVLDA TGK	3		0,0000	4,32	2	1289,65862	0,16	43,64
																	High	IPNGVNGIEER	1		0,0000	2,92	2	1197,62187	-0,35	39,89
																	High	IPNGVnGIEER	2	N6(Dea midated)	0,0000	2,90	2	1198,60771	1,17	40,24
																	Medium	ALGIDDFR	1		0,0000	1,99	2	906,46745	-0,61	45,16
																	Medium	EmEIMVNEK	1	M2(Oxi dation)	0,0000	1,78	2	1138,51323	1,13	38,76
																	Medium	YVMSPPIR	3		0,0000	1,77	2	962,51262	-0,23	41,48
																	Medium	FFMAYK	2		0,0000	1,72	2	806,39043	-0,20	44,48
																	Medium	SDTNVFEGWR	1		0,0000	1,66	2	1210,54912	0,28	46,24
																	Medium	VVWLNDLTK	1		0,0000	1,66	2	1115,60893	-0,59	46,29
																	Medium	WDEVVSK	2		0,0000	1,52	2	862,43041	-0,17	39,02
																	Medium	YVmSPPIR	1	M3(Oxi dation)	0,1040	1,12	2	978,50749	-0,27	39,78
																	Medium	YLSSLK	1		0,0000	0,99	2	710,40843	0,14	38,02
7702	M5W GX8	peptidylprolyl isomerase domain and WD repeat-containing protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003495mg PE=4 SV=1 - [M5WGX8_PRUPE]	99% to Gt:645217828 Prunus mume, E value 0	Prunus mume	Chlorop last	06.01- Protein destination and storage/Fol ding and stability	12,47	13,51	3	8	8	11	570	64,3	7,25	High	GMDVVQAIK	1		0,0000	2,52	2	1089,56072	-0,21	43,91
																	High	AGTNEPIISR	2		0,0000	2,09	2	1057,56352	-0,17	37,84
																	Medium	KIPAAAANVNE SK	1		0,0000	2,03	3	1312,72281	0,61	35,17
																	Medium	TTVSSIEVSPDG K	2		0,0000	1,89	2	1319,66838	-0,44	40,04
																	Medium	IALYQGDR	1		0,0000	1,62	2	935,49407	-0,51	39,80
																	Medium	QFSITSPDR	1		0,0000	1,26	2	1050,52214	0,62	41,29
																	Medium	LAISDR	1		0,0000	1,15	2	674,38329	0,13	36,98
																	Medium	ILNVTVPK	2		0,0000	1,01	2	883,56096	-0,24	43,22
7704	M5W FB9	5-methyltetrahydropteroyltri glutamate-homocysteine methyltrans ferase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001783mg PE=3 SV=1 - [M5WFB9_PRUPE]	98% to Gt:645263470 Prunus mume, E value 0	Prunus persica	Chlorop last	01.01- Metabolism /Amino Acid	15,52	11,50	1	11	11	14	765	84,6	6,55	High	IPSTEEIADR	1		0,0000	2,99	2	1130,56914	0,25	40,42

																	High	GNASVPAMEMTK	2		0,0000	2,45	2	1235,57573	-0,18	42,47
																	High	YLFAGLVDGR	1		0,0000	2,39	2	1110,59490	0,56	49,92
																	High	IVEVNALAK	2		0,0000	2,06	2	956,57726	-0,32	43,05
																	Medium	GVTAYGFDLVR	1		0,0000	1,94	2	1197,62663	0,28	48,55
																	Medium	ISEEEYVK	1		0,0000	1,82	2	996,48815	-0,31	39,46
																	Medium	KISEEEYVK	1		0,0000	1,46	2	1124,58330	-0,11	37,02
																	Medium	EEISNVVK	1		0,0000	1,43	2	917,49321	-0,73	39,50
																	Medium	LLSVFR	1		0,0000	1,39	2	734,45592	-0,07	46,00
																	Medium	EVISELK	1		0,0000	1,37	2	817,46623	-0,45	41,11
																	Medium	TLDLIK	2		0,0000	1,31	2	702,43993	0,39	45,04
7707	M5XQJ0	Phosphoenolpyruvate carboxykinase [ATP]	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002490mg PE=3 SV=1 - [M5XQJ0_PRUPE]	99% to GI:645224569 Prunus mume, E value 0	Prunus mume	Cytoplasm	02.02-Energy/Gluconeogenesis	78,14	27,89	2	15	16	54	667	74,0	7,23	High	AAEnGGFSFTR	3	N4(Deamidated)	0,0000	3,47	2	1157,52434	1,82	44,14
																	High	TIDELHSLQK	2		0,0000	3,39	2	1183,63164	-0,11	39,83
																	High	SSQP TTPInGK	4	N9(Deamidated)	0,0000	3,28	2	1130,56938	0,48	37,13
																	High	EMVILGTQYAGEmK	2	M13(Oxidation)	0,0000	3,20	2	1585,76091	0,50	46,35
																	High	AAENGGSFSTR	1		0,0000	3,20	2	1156,53838	0,14	43,09
																	High	EMVILGTQYAGEMK	2		0,0000	3,04	2	1569,76641	0,76	48,57
																	High	AVDYLnSLDK	4		0,0000	3,01	2	1137,57878	0,10	46,09
																	High	DEETENELWWGK	2		0,0000	2,83	2	1535,66557	0,41	50,75
																	High	QGSFAAISEEDR	5		0,0000	2,77	2	1309,60234	0,30	43,83
																	High	IIDAHSGR	5		0,0000	2,48	2	981,54723	-0,43	38,54
																	High	LLNASYTK	2		0,0000	2,39	2	909,50365	-0,42	40,03
																	High	YAAMLSEK	2		0,0000	2,33	2	912,44902	-0,60	40,23
																	High	AAYPIEYIPNAK	3		0,0000	2,31	2	1349,71062	0,44	46,79
																	High	YAAmLSEK	3	M4(Oxidation)	0,0000	2,16	2	928,44438	-0,11	37,39
																	Medium	IQTHPEATSEVc HDDSGTPVK	3	C12(Carbamidomethyl)	0,0000	2,05	4	2308,05092	-0,08	38,16
																	Medium	AVDYLnSLDK	1	N6(Deamidated)	0,0000	1,84	2	1138,56291	0,20	44,61
																	Medium	IPcVGPHPK	3	C3(Carbamidomethyl)	0,0000	1,64	3	1004,53443	-0,22	38,91
																	Medium	DEETEnELWWGK	1	N6(Deamidated)	0,0000	1,60	2	1536,64336	-3,65	51,51
																	Medium	EVDYSEKSVTE NTR	1		0,0000	1,55	3	1656,77085	-0,21	38,21
																	Medium	LTEEILAAGPNF	2		0,0000	1,42	2	1274,66313	0,29	52,75
																	Medium	QILSLHSGcNmGK	1	C9(Carbamidomethyl);	0,0000	1,30	3	1460,69794	-0,39	38,75

																			M11(Oxidation)							
																	Medium	QILSLHSGcNMGK	2	C9(Carbamidomethyl)	0,0000	1,20	3	1444,70285	-0,51	41,11
7709	M5XQJ0	Phosphoenolpyruvate carboxykinase [ATP]	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002490mg PE=3 SV=1 - [M5XQJ0_PRUPE]	99% to GI:645224569 Prunus mume, E value 0	Prunus persica	Cytoplasm	02.02-Energy/Gluconeogenesis	137,58	40,93	3	23	82	667	74,0	7,23	High	GSFITATGALATLSGAK	3		0,0000	4,01	2	1565,85478	0,86	50,58	
																High	EMVILGTQYAGEMK	3		0,0000	3,82	2	1569,76677	0,99	48,56	
																High	DGDVALFFGLSGTGK	2		0,0000	3,52	2	1483,74394	0,76	53,37	
																High	IQTHPEATSEVcHDDSGTPVK	3	C12(Carbamidomethyl)	0,0000	3,45	3	2308,05210	0,43	45,93	
																High	EMVILGTQYAGEmK	4	M13(Oxidation)	0,0000	3,07	2	1585,76140	0,80	47,20	
																High	AVDYLnSLDK	1	N6(Deamidated)	0,0000	3,00	2	1138,56401	1,16	44,84	
																High	DEETENELWWGK	2		0,0000	2,87	2	1535,66631	0,88	50,15	
																High	YAAMLSEK	4		0,0000	2,70	2	912,44908	-0,53	40,15	
																High	AVDYLnSLDK	5		0,0000	2,53	2	1137,57866	-0,01	45,30	
																High	DKEPDIWNAIK	1		0,0000	2,46	2	1328,68437	-0,14	48,04	
																High	AAYPIEYIPNAK	4		0,0000	2,44	2	1349,71062	0,44	47,98	
																High	QGSFAAISEEDR	5		0,0000	2,40	2	1309,60234	0,30	41,74	
																High	SSQPPTPInGK	6	N9(Deamidated)	0,0000	2,38	2	1130,56828	-0,49	37,99	
																High	TIDELHSLQK	2		0,0000	2,37	2	1183,63164	-0,11	45,76	
																High	LLNASYTK	4		0,0000	2,36	2	909,50383	-0,22	37,97	
																High	QQLQSISASLASLTR	2		0,0000	2,34	2	1602,88103	0,00	48,88	
																High	YAAmLSEK	5	M4(Oxidation)	0,0000	2,23	2	928,44408	-0,44	36,64	
																Medium	NVILLAcDAFGVLPPVSK	2	C7(Carbamidomethyl)	0,0000	1,90	2	1913,05974	1,65	52,36	
																Medium	DTLLQLGGLFK	2		0,0000	1,88	2	1204,69390	0,19	52,81	
																Medium	LTEEILAAGPNF	3		0,0000	1,69	2	1274,66313	0,29	52,86	
																Medium	GSPNIEMDEHTFLVNR	1		0,0000	1,61	3	1858,87644	0,61	47,39	
																Medium	IPcVGPHPK	5	C3(Carbamidomethyl)	0,0000	1,58	3	1004,53452	-0,13	36,66	
																Medium	cIDLSK	3	C1(Carbamidomethyl)	0,0000	1,57	2	735,37047	-0,16	39,38	
																Medium	IIDAHSGR	3		0,0000	1,44	3	981,54792	0,27	36,48	
																Medium	EVDYSEK	2		0,0000	1,27	2	869,38860	-0,15	35,80	
																Medium	TTLSTDHNR	4		0,0000	1,22	3	1044,50718	0,27	42,63	
																Medium	SSQPPTPINGK	1		0,0000	0,92	2	1129,58476	-0,05	35,45	
7716	M5X5I9	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001950mg PE=3 SV=1 - [M5X5I9_PRUPE]	99% to GI:645253901 Prunus mume, E value 0	Prunus persica	Chloroplast	01.06-Metabolism/Lipid and sterol	18,85	11,80	2	9	9	13	737	82,6	7,69	High	VINEAGISGR	2		0,0000	3,22	2	1015,55284	-0,29	38,51

																	High	GPSDPITTQAIK	1		0,000	2,74	2	1356,70098	0,28	40,59
																	High	NVVTAPPELK	1		0,0000	2,12	2	1067,60942	-0,16	40,77
																	High	SANLEVVGVTK	2		0,0000	2,07	2	1116,62602	0,05	41,20
																	Medium	LNLVSR	2		0,0000	1,86	2	701,43035	-0,19	38,97
																	Medium	ELMEEVEAVK	1		0,0000	1,58	2	1176,58098	-0,65	43,80
																	Medium	SIGGFQEGIPVEPK	1		0,0000	1,32	2	1457,76360	0,03	45,12
																	Medium	TMFGLK	2		0,0000	1,20	2	696,37480	-0,21	43,13
																	Medium	HLTPIQR	1		0,0000	1,14	2	864,50493	-0,13	34,99
7727	M5V GU2	cullin	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001948mg PE=3 SV=1 - [M5VGU2_PRUPE]	99% to GI:645258714 Prunus mume, E value 0	Prunus mume	Cytopla sm	06.07- Protein destination and storage/Mo dification	43,84	17,2 1	4	1 4	14	27	738	85,8	6,90	High	LSDEAIEETLEK	2		0,0000	3,62	2	1376,68022	0,74	45,69
																	High	YAIDAAIVR	3		0,0000	3,08	2	991,55675	-0,41	45,10
																	High	DDKVEDLSR	3		0,0000	2,65	3	1076,52170	-0,19	37,24
																	High	GLEPVSSVFK	2		0,0000	2,29	2	1062,58269	-0,33	45,80
																	High	IEDLITR	1		0,0000	2,23	2	859,48833	-0,08	42,25
																	High	EAFEVFcNK	2	C7(Carb amidom ethyl)	0,0000	2,16	2	1143,51372	-0,22	46,13
																	Medium	LLHSLScAK	2	C7(Carb amidom ethyl)	0,0000	2,12	3	1028,55585	0,08	36,59
																	Medium	DKENPNMFK	2		0,0000	2,11	3	1122,52466	-0,20	37,25
																	Medium	TISPTDSFEFNsk	2		0,0000	1,98	2	1472,69145	0,70	46,14
																	Medium	VAVIGLIDK	1		0,0000	1,83	2	927,58702	-0,41	46,41
																	Medium	VIDVDKDR	4		0,0000	1,65	2	1088,55803	-0,24	35,61
																	Medium	cVEVFK	1	C1(Carb amidom ethyl)	0,0000	1,50	2	781,39122	-0,13	40,14
																	Medium	ILIKEPNTK	1		0,0000	1,15	2	1055,64726	1,22	37,89
																	Medium	MFKPDIK	1		0,1261	1,04	2	878,47978	-0,81	39,20
7812	M5W U88	Sucrose synthase	Sucrose synthase OS=Prunus persica GN=PRUPE_ppa017606mg PE=3 SV=1 - [M5WU88_PRUPE]		Prunus persica	Chlorop last	01.05- Metabolism /Sugars and polysacchar ides	11,08	7,08	2	6	7	12	833	94,7	6,99	High	cNQELEPInGTK	2	C1(Carb amidom ethyl); N9(Dea midated)	0,0000	2,02	2	1403,64873	1,10	40,30
																	Medium	TDATYWDR	1		0,0000	1,91	2	1027,44780	-0,17	40,80
																	Medium	YSNILR	1		0,0000	1,88	2	765,42522	-0,21	39,04
																	Medium	cNQELEPINGTK	1	C1(Carb amidom ethyl)	0,0000	1,75	2	1402,66399	0,59	39,23
																	Medium	WIAAQTDNR	2		0,0000	1,69	2	960,48955	-0,26	38,59
																	Medium	VVSGINVFDPK	2		0,0000	1,54	2	1174,64763	0,78	45,39
																	Medium	IADFFEK	2		0,0000	0,91	2	869,43974	-0,74	45,67
8004	M5X A69	Universal stress protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppb010253mg	98% to GI:645276352	Prunus mume	Cytopla sm	11.05- Disease/Def	45,51	49,7 1	1	7	10	30	175	18,7	7,77	High	AILGSVSNYcVQ NAK	3	C10(Car bamido methyl)	0,0000	4,23	2	1623,81731	0,82	44,64

[illegible]

																		High	YDTVHGPWK	2		0,0000	2,41	2	1102,53118	-0,43	39,01
																		High	IGInGFGR	3	N4(Deamidated)	0,0000	2,34	2	834,44786	1,18	43,75
																		High	DAPmFVVGVNEK	4	M4(Oxidation)	0,0000	2,25	2	1321,64617	0,32	45,37
																		High	IGINGFGR	1		0,0000	2,09	2	833,46074	-2,54	42,63
																		Medium	SSIFDAK	4		0,0000	1,71	2	767,39336	-0,10	43,29
																		Medium	LTGmAFR	4	M4(Oxidation)	0,0000	1,64	2	811,41295	-0,23	42,12
																		Medium	LTGMAFR	5		0,0000	1,62	2	795,41826	0,05	41,95
																		Medium	VIIISAPSK	3		0,0000	1,51	2	814,50353	0,25	40,07
8127	M5WBP7	Alpha/beta-Hydrolases superfamily protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008197mg PE=4 SV=1 - [M5WBP7_PRUPE]	96% to GI:590586968 Theobromacacao, E value 0	Prunus persica	Chloroplast	06.13- Protein destination and storage/Proteolysis	30,44	22,29	1	7	8	15	341	38,7	7,14	High	AGYGESDPYPSPR	3		0,0000	3,65	2	1298,56548	0,51	37,88	
																		High	SEAFDIQELADK	1		0,0000	3,30	2	1365,65361	0,21	46,73
																		High	LSEAPSVGQEK	2		0,0000	3,20	2	1144,58489	0,34	37,48
																		High	IcGSPGGPPVTSPR	3	C2(Carbamidomethyl)	0,0000	3,19	2	1381,69036	0,74	38,95
																		High	DILAGYAK	3		0,0000	2,01	2	850,46703	0,11	42,93
																		Medium	TDLMLKK	1		0,0000	1,50	2	963,51842	0,43	39,26
																		Medium	IIVVHGFSSK	1		0,0000	1,21	3	1201,65827	0,55	40,58
8128	M5XCW1	voltage-gated potassium channel subunit beta	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008405mg PE=4 SV=1 - [M5XCW1_PRUPE]	99% to GI:645234796 Prunus mume, E value 0	Prunus persica	Chloroplast	07.01- Transporters/Ions	20,37	16,82	1	6	6	14	333	37,0	7,39	High	AEEIMGQAIR	3		0,0000	3,12	2	1117,56706	-0,02	42,68	
																		High	AEEImGQAIR	2	M5(Oxidation)	0,0000	3,05	2	1133,56182	-0,17	38,65
																		High	AMNYVIDK	2		0,0000	2,40	2	953,47612	0,00	41,36
																		Medium	FALDNYK	2		0,0000	1,59	2	870,43602	0,46	42,03
																		Medium	SLLQTcR	2	C6(Carbamidomethyl)	0,0000	1,54	2	877,45610	0,06	39,24
																		Medium	ESQIQENMK	1		0,0000	1,51	2	1106,51457	-0,12	36,58
																		Medium	AmNYVIDK	1	M2(Oxidation)	0,0136	1,45	2	969,47106	0,02	39,54
																		Medium	AVDVIPLLPVMEK	1		0,0000	1,32	2	1595,90935	0,98	51,51
8131	M5XWJ9	mitochondrial outer membrane protein porin	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008111mg PE=4 SV=1 - [M5XWJ9_PRUPE]	99% to GI:645229903 Prunus mume, E value 0	Prunus persica	Mitochondrion	07.01- Transporters/Ions	15,46	15,12	2	6	6	8	344	37,8	8,75	High	GDLYLGDVSTQLK	2		0,0000	3,05	2	1408,73332	1,02	47,31	
																		High	TTITIDEPAPGLK	2		0,0000	2,92	2	1355,74260	0,63	43,33
																		Medium	KGDLYLGDVSTQLK	1		0,0000	2,09	3	1536,82651	-0,23	43,52
																		Medium	AIFSIVPDQR	1		0,0000	1,81	2	1292,69939	-0,33	50,28
																		Medium	ARDLLYK	1		0,0000	1,39	2	878,50841	-1,20	36,96
																		Medium	NITTDVK	1		0,0108	0,92	2	790,43047	-0,09	36,05

8305	M5WGA9	Protein DJ-1 homolog	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005820mg PE=4 SV=1 - [M5WGA9_PRUPE]	97% to GI:645240260 Prunus mume, E value 0	Prunus persica	Chlorop last	11.05- Disease/Defense/Stress responses	109,23	24,43	2	13	51	442	47,2	8,68	High	AGADVTVASVEK	4		0,0000	3,87	2	1146,60015	-0,01	38,69
																High	GPGTSMEFALGIVEK	2		0,0000	3,67	2	1535,77910	1,04	49,86
																High	NSEVLESIVK	3		0,0000	3,14	2	1117,61016	0,16	45,53
																High	ADEVSGPLVMR	7		0,0000	3,11	2	1173,59307	-0,21	45,10
																High	RAGADVTVASVEK	4		0,0000	3,09	3	1302,70081	-0,36	37,46
																High	LEADVLLDEAAK	2		0,0000	2,82	2	1286,68450	0,46	47,63
																High	EKADEVSGPLVmR	2	M12(Oxidation)	0,0000	2,81	3	1446,72553	-0,19	38,10
																High	KATAFPAMcDK	3	C9(Carbamidomethyl)	0,0000	2,80	3	1239,58554	-0,46	37,96
																High	EKADEVSGPLVMR	3		0,0000	2,68	2	1430,73198	0,77	41,25
																High	LSDKSEIENR	3		0,0000	2,52	3	1190,60108	-0,11	34,99
																High	VVVDGNLITSR	1		0,0000	2,51	2	1172,66374	0,28	42,31
																High	nSEVLESIVK	1	N1(Deamidated)	0,0000	2,36	2	1118,59404	0,04	49,39
																High	VMLFVHP	6		0,0000	2,29	2	842,45946	0,13	47,74
																High	GPGTSmEFALGIVEK	1	M6(Oxidation)	0,0000	2,02	2	1551,77324	0,53	46,29
																Medium	ATAFPAMcDK	3	C8(Carbamidomethyl)	0,0000	1,96	2	1111,49126	0,10	41,91
																Medium	LVNLLK	2		0,0000	1,74	2	699,47655	0,25	42,52
																Medium	VmLFVHP	2	M2(Oxidation)	0,0000	1,61	2	858,45415	-0,14	46,08
																Medium	ATAFPAMcDK	2	M7(Oxidation); C8(Carbamidomethyl)	0,0000	1,21	2	1127,48650	0,39	40,81
8306	M1QDN1	Phosphoserine aminotransferase	Phosphoserine aminotransferase OS=Prunus persica PE=2 SV=1 - [M1QDN1_PRUPE]		Prunus persica	Chlorop last	01.01- Metabolism /Amino Acid	202,48	34,42	3	17	113	430	47,8	8,40	High	KADLLYNAIDESK	3		0,0000	5,07	2	1479,77007	0,71	43,78
																High	VDYVVTGSGWDK	3		0,0000	3,92	2	1325,63823	0,73	46,45
																High	ADLLYNAIDESK	3		0,0000	3,70	2	1351,67461	0,42	48,01
																High	ASIYNAMPLAGVEK	8		0,0000	3,68	2	1463,75762	0,86	49,22
																High	IPAFEELEQSPDAK	8		0,0000	3,60	2	1573,77617	1,05	49,65
																High	FGIYAGAQK	4		0,0000	3,30	2	1067,58830	-0,14	45,67
																High	ASIYNAmPLAGVEK	4	M7(Oxidation)	0,0000	3,25	2	1479,75102	-0,16	47,90
																High	NVGPSGVTVVIIIR	2		0,0000	3,20	2	1310,78008	0,72	47,56
																High	ASIYNAMPLAGVEK	1	N5(Deamidated)	0,0000	3,02	2	1464,74004	-0,22	47,06
																High	SLmNVPFTLEK	5	M3(Oxidation)	0,0000	3,00	2	1294,67107	-0,11	49,84
																High	AQSELYNWR	10		0,0000	2,83	2	1166,55925	0,27	44,70
																High	GKEFLSIQK	2		0,0000	2,83	3	1162,68326	0,15	45,00

																	High	SLMNVPTLEK	5		0,0000	2,80	2	1278,67656	0,20	50,31
																	High	GSGMSVMEMSHR	5		0,0000	2,48	2	1308,55034	0,70	39,94
																	High	SELEAEFVK	8		0,0000	2,25	2	1051,53093	0,25	46,04
																	High	GSGmSVMEMSHR	14	M4(Oxidation)	0,0000	2,01	2	1324,54460	0,20	38,65
																	Medium	VIWSGKSEK	1		0,0000	1,87	3	1033,56800	0,27	36,88
																	Medium	EFLSIQK	3		0,0000	1,77	2	977,56639	-0,26	48,69
																	Medium	LVDFMK	8		0,0000	1,70	2	752,40141	0,32	45,58
																	Medium	AEADLR	1		0,0000	1,48	2	674,34679	-0,05	35,70
																	Medium	LVDFmK	10	M5(Oxidation)	0,0000	1,46	2	768,39574	-0,45	47,07
																	Medium	VIWSGK	5		0,0000	1,27	2	689,39824	0,17	40,18
8307	M5W SM4	formate dehydrogenase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006791mg PE=3 SV=1 - [M5WSM4_PRUPE]	98% to GI:645249147 Prunus mume, E value 0	Prunus mume	Mitocho ndrion	11.06- Disease/Def ense/Detoxi fication	72,20	36,8 8	4	1 4	14	36	385	42,2	7,61	High	TLASSGSSASST TFTR	3		0,0000	4,34	2	1560,75127	0,77	39,19
																	High	IDPELEQQIGAK	3		0,0000	3,35	2	1340,70635	0,49	42,86
																	High	FEEDLDAMPLK	2		0,0000	3,06	2	1307,61943	0,44	49,04
																	High	FEEDLDAmLPK	1	M8(Oxidation)	0,0000	2,96	2	1323,61443	0,49	44,50
																	High	GEDFPAQNYIV K	3		0,0000	2,95	2	1380,68010	0,46	45,01
																	High	GVLIVnNAR	2	N6(Deamidated)	0,0000	2,81	2	956,55229	-0,12	41,59
																	High	KGVLIVNNAR	3		0,0000	2,58	2	1083,66301	-0,32	36,51
																	High	cDIVIVnTPLTEK	2	C1(Carbamidomethyl)	0,0000	2,56	2	1501,79497	1,23	46,63
																	High	GVLIVNNAR	3		0,0000	2,49	2	955,56804	-0,37	40,55
																	Medium	YIVTDDKDGPDC ELDK	2	C12(Carbamidomethyl)	0,0000	2,26	3	1882,83872	0,60	39,66
																	High	GVIASAVR	3		0,0000	2,17	2	772,46764	0,03	38,30
																	Medium	HIQDLHVLISTP FHPAYVTAR	1		0,0000	2,11	4	2544,33315	-1,06	45,33
																	High	IVGVFFYK	2		0,0000	2,08	2	825,48705	0,14	43,62
																	Medium	ILILVR	3		0,0000	1,96	2	726,52367	0,01	45,57
																	Medium	DGPDcELDK	1	C5(Carbamidomethyl)	0,0000	1,84	2	1048,42534	0,11	37,22
																	Medium	DWLESQGHK	2		0,0000	1,84	2	1099,51677	0,03	39,89
8310	B2B MP9	Endo-1,4-beta-mannosidase	Endo-1,4-beta-mannosidase protein 1 OS=Prunus persica PE=2 SV=1 - [B2BMP9_PRUPE]		Prunus persica	Chlorop last	06.07- Protein destination and storage/Mo dification	15,56	7,89	2	4	4	9	431	48,7	8,60	High	ILSAFQEATK	2		0,0000	2,63	2	1107,60430	-0,19	44,32
																	High	TNSLTGVAYK	2		0,0000	2,60	2	1053,55718	-0,34	39,95
																	High	HGLSIAR	3		0,0000	2,08	2	753,43651	-0,16	36,85
																	Medium	QYVDWAR	2		0,0000	1,49	2	937,45201	-0,70	43,65

	M5V W13	glycerate dehydrogenase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006993mg PE=3 SV=1 - [M5VW13_PRUPE]	99% to GI:645260882 Prunus mume, E value 0	Prunus mume	Chlorop last	02.30- Energy/Pho tosynthesis	13,34	23,0 6	2	9	9	14	386	42,2	7,80	High	GQTVGVIGAGR	2		0,0000	2,49	2	1014,56883	-0,29	40,54
																	High	IVEADEFMR	1		0,0000	2,48	2	1109,52959	-0,05	44,82
																	High	ANGEQPVTWK	1		0,0000	2,41	2	1129,56365	-0,05	39,89
																	Medium	AASMEEVLR	1		0,0000	1,87	2	1005,50298	-0,44	42,65
																	Medium	ALGLPVSR	2		0,0000	1,81	2	812,49901	0,12	44,06
																	Medium	NAIVVPHIASAS K	1		0,0000	1,42	2	1306,74907	0,96	41,59
																	Medium	TTYHLVNK	2		0,0000	1,23	2	975,52483	-1,02	37,22
																	Medium	NAPPPAASPSIV NAK	2		0,0000	1,09	2	1433,77532	0,37	39,78
																	Medium	QNPMPFR	2		0,0000	1,09	2	792,38194	-0,27	40,26
8311	M5W G66	src substrate protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008017mg PE=4 SV=1 - [M5WG66_PRUPE]	99% to GI:645237812 Prunus mume, E value 0	Prunus persica	Chlorop last	09.04-Cell structure/C ytoskeleton	26,03	29,8 9	3	1 0	11	18	348	38,8	7,52	High	MRQEAETQAVE VSR	2		0,0000	3,25	3	1633,79569	-0,39	37,04
																	High	AMIAGAPLEDA R	2		0,0000	2,82	2	1214,61968	-0,16	43,53
																	High	QEAEATQAVEVS R	2		0,0000	2,68	2	1346,65569	0,72	37,78
																	High	AmIAGAPLEDA R	1	M2(Oxi dation)	0,0000	2,35	2	1230,61492	0,11	40,32
																	Medium	KESAPPVIPQEN SSEK	1		0,0000	2,33	3	1739,88022	-0,51	37,13
																	High	AAEVFTAIGYK	1		0,0000	2,33	2	1169,62065	0,43	45,11
																	High	LVALVEGEK	1		0,0000	2,05	2	957,56133	-0,27	41,02
																	Medium	mRQEAETQAVE VSR	1	M1(Oxi dation)	0,0000	1,73	3	1649,79251	0,77	35,77
																	Medium	YGAENTNDKIL AK	1		0,0000	1,65	3	1436,73850	0,32	36,73
																	Medium	ESAPPVIPQENS SEK	2		0,0000	1,58	2	1611,78752	0,86	40,44
																	Medium	mDALRK	2	N- Term(A cetyl)	0,0000	1,57	2	775,41319	0,08	41,03
																	Medium	VSPSGWSEGEcK	1	C11(Car bamido methyl)	0,0000	1,30	2	1322,56841	0,15	39,40
8401	M5W ZU8	V-type proton ATPase subunit H	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005592mg PE=4 SV=1 - [M5WZU8_PRUPE]	96% to GI:658016951 Malus domesti ca, E value 0	Malus domesti ca	Chlorop last	07.22- Transporte rs/Transport ATPases	14,20	19,6 9	4	1 0	10	14	452	51,3	7,42	High	SSFVQLDGVK	2		0,0000	2,32	2	1079,57268	-0,48	43,54
																	High	mDHAELTTEQV LK	1	N- Term(A cetyl)	0,0000	2,22	2	1556,76470	1,37	45,82
																	High	NALLcIQR	2	C5(Carb amidom ethyl)	0,0000	2,11	2	987,53942	-1,05	42,21
																	Medium	LFHDGTIVDK	1		0,0000	2,11	3	1144,59903	-0,63	39,07
																	Medium	IIVTDLK	2		0,0000	1,60	2	801,50792	-0,19	42,25
																	Medium	VVVLTLR	2		0,0000	1,23	2	799,54009	0,06	44,54
																	Medium	GNWFIQEK	1		0,0167	1,18	2	1021,50994	-0,26	44,48
																	Medium	LMNHENAEVTK	1		0,0000	1,02	2	1285,62212	1,20	34,29
																	Medium	LFLGAK	1		0,0211	0,93	2	648,40801	0,07	42,06

																	Medium	ITTIDDLVK	1		0,0000	0,91	2	1017,58275	0,05	45,46
8405	M5X0L8	3-oxoacyl-[acyl-carrier-protein] synthase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005228mg PE=3 SV=1 - [M5X0L8_PRUPE]	99% to GI:645237961 Prunus mume, E value 0	Prunus mume	Chloroplast	01.06-Metabolism /Lipid and sterol	52,23	11,04	1	8	8	22	471	50,0	8,31	High	ALEDADLGGDKR	5		0,0000	3,81	2	1259,62322	0,41	37,47
																	High	RLDDcLR	3	C5(Carb amidom ethyl)	0,0000	3,43	2	947,47228	-0,53	36,63
																	High	ADGLGVSTcIER	3	C9(Carb amidom ethyl)	0,0000	3,28	2	1277,61626	0,60	41,86
																	High	ALEDADLGGDK	2		0,0000	3,27	2	1103,52165	0,07	39,87
																	High	LLAGESGVGPIDR	4		0,0000	2,93	2	1283,69524	-0,18	43,44
																	Medium	KALEDADLGGDK	1		0,0000	2,42	3	1231,61597	-0,47	36,03
																	High	LDDcLR	2	C4(Carb amidom ethyl)	0,0000	2,17	2	791,37139	-0,34	38,08
																	Medium	YSIVAGK	2		0,0000	1,91	2	737,41936	0,16	38,68
8510	M5VLY6	Adenylyl cyclase-associated protein	Adenylyl cyclase-associated protein OS=Prunus persica GN=PRUPE_ppa005136mg PE=3 SV=1 - [M5VLY6_PRUPE]		Prunus persica	Chloroplast	09.04-Cell structure/Cytoskeleton	122,40	34,32	1	19	72	475	51,0	7,65		High	VLQQAFAVQK	7		0,0000	3,51	2	1131,65239	0,24	41,61
																	High	VNNITIDK	4		0,0000	3,30	2	916,50945	-0,45	38,49
																	High	DSVVQIQGK	5		0,0000	3,04	2	973,53105	-0,29	39,49
																	High	DALGASITTAk	4		0,0000	2,88	2	1047,56743	-0,66	41,59
																	High	FETTPVSHSAGG	3		0,0000	2,68	2	1189,54802	-0,35	38,06
																	High	DLVISDcDSK	5	C7(Carb amidom ethyl)	0,0000	2,36	2	1151,52483	-0,09	44,11
																	High	IGGPVLDVTK	10		0,0000	2,33	2	998,58812	-0,01	46,17
																	High	KDLVISDcDSK	4	C8(Carb amidom ethyl)	0,0000	2,31	2	1279,61907	-0,66	36,56
																	High	DLLIQVK	2		0,0000	2,20	2	828,51903	0,07	46,41
																	High	LELQMGR	2		0,0000	2,14	2	846,45000	-0,30	41,60
																	High	KWAVENQIGK	2		0,0000	2,05	2	1172,64238	0,08	38,76
																	Medium	LELQmGR	5	M5(Oxidation)	0,0000	1,78	2	862,44493	-0,27	37,29
																	Medium	SDFFNHLK	2		0,0000	1,74	2	1007,49425	-0,29	42,07
																	Medium	QSVYIFGcK	4	C8(Carb amidom ethyl)	0,0000	1,69	2	1101,53996	0,17	45,85
																	Medium	DPNHLEWAK	1		0,0000	1,66	2	1109,53703	-0,40	39,43
																	Medium	SKDPNHLEWAK	1		0,0000	1,56	3	1324,66394	-0,41	36,34
																	Medium	ADRTGIVGTQEK	1		0,0000	1,47	3	1274,67185	1,47	34,70
																	Medium	ELYLPGLR	3		0,0000	1,44	2	960,55089	-0,46	47,94
																	Medium	ILVEYK	6		0,0000	1,27	2	764,45531	0,02	43,94
																	Medium	SFYPLGPVWSSTGK	1		0,0000	1,21	2	1525,76970	0,71	49,11
8511	M5W5K0	Pyruvate kinase	Pyruvate kinase OS=Prunus persica GN=PRUPE_ppa004703mg PE=3 SV=1 - [M5W5K0_PRUPE]		Prunus mume	Chloroplast	02.01-Energy/Glycolysis	20,79	18,38	1	9	10	20	495	53,5	7,90	High	IVcTLGPASR	1	C3(Carb amidom ethyl)	0,0000	2,63	2	1073,57659	-0,61	

																		High	cENSAVLGER	2	C1(Carb amidom ethyl)	0,0000	2,52	2	1134,52031	-0,48	
																		High	NGDAVVVALHR	3		0,0000	2,27	2	1051,56438	0,01	
																		High	GSDLVEVR	2		0,0000	2,25	2	874,46263	-0,33	
																		High	nGDAVVVALHR	3	N1(Dea midated)	0,0000	2,23	2	1052,54802	-0,35	
																		Medium	GDETTlcMSYK	1	C7(Carb amidom ethyl)	0,0000	1,77	2	1304,54741	-1,80	
																		Medium	GLVPVLSAGSSR	2		0,0000	1,62	2	1142,65288	0,02	
																		Medium	GDLGMElPIEK	1		0,0000	1,58	2	1201,61272	-0,55	
																		Medium	IFLAQK	2		0,0000	1,55	2	719,44518	0,15	
																		Medium	GDETTlcmsYK	1	C7(Carb amidom ethyl); M8(Oxi dation)	0,0000	1,44	2	1320,54521	0,40	
																		Medium	WGVPNK	1		0,0274	1,42	2	700,37779	0,10	
																		Medium	NILLMSK	1		0,0303	1,28	2	818,48046	-0,03	
8520	M5V LY6	Adenylyl cyclase-associated protein	Adenylyl cyclase-associated protein OS=Prunus persica GN=PRUPE_ppa005136mg PE=3 SV=1 - [M5VLY6_PRUPE]		Prunus persica	Chlorop last	09.04-Cell structure/C ytoskeleton	54,58	19,5 8	1	1 1	11	27	475	51,0	7,65		High	DSVVQIQGK	3		0,0000	3,14	2	973,53105	-0,29	39,46
																		High	VLQQAFAVQK	3		0,0000	3,01	2	1131,65227	0,13	41,50
																		High	IGGPVLDTVTK	3		0,0000	3,00	2	998,58794	-0,19	44,06
																		High	VNNITIDK	2		0,0000	2,91	2	916,50932	-0,59	37,63
																		High	VNnITIDK	2	N3(Dea midated)	0,0000	2,87	2	917,49382	-0,06	39,37
																		High	DALGASITTAk	3		0,0000	2,54	2	1047,56780	-0,31	42,66
																		High	DLVISDcDSK	3	C7(Carb amidom ethyl)	0,0000	2,45	2	1151,52507	0,12	42,07
																		High	FETTPVSHSAGG	2		0,0000	2,39	2	1189,54827	-0,15	37,96
																		Medium	ILVEYK	2		0,0000	1,68	2	764,45537	0,10	40,68
																		Medium	LELQmGR	1	M5(Oxi dation)	0,0000	1,43	2	862,44481	-0,41	37,24
																		Medium	QSVYIFGcK	2	C8(Carb amidom ethyl)	0,0000	1,42	2	1101,53935	-0,38	44,04
																		Medium	KDLVISDcDSK	1	C8(Carb amidom ethyl)	0,0000	1,40	2	1279,62114	0,97	36,98
8521	M5W PC0	Cannabidiolic acid synthase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003798mg PE=4 SV=1 - [M5WPC0_PRUPE]	97% to GI:645238389 Prunus mume, E value 0	Prunus persica	Plasma membra ne	20.99- Secondary metabolism /Others	22,01	13,1 4	3	7	9	27	548	61,4	8,60		High	YGLGADNVIDA R	3		0,0000	3,92	2	1263,63347	0,49	44,49
																		Medium	NGILFK	3		0,0000	1,98	2	691,41393	0,23	42,92
																		Medium	nGILFK	5	N1(Dea midated)	0,0000	1,93	2	692,39787	0,13	47,00
																		Medium	DcTETSWLK	3	C2(Carb amidom ethyl)	0,0000	1,90	2	1139,50408	0,25	45,15
																		Medium	IIDVSGR	3		0,0000	1,83	2	759,43590	-0,09	39,03
																		Medium	DLDLGINKK	3		0,0000	1,60	2	1015,57817	-0,12	40,49
																		Medium	FPELGITK	2		0,0000	1,58	2	904,51354	-0,39	45,83

																	Medium	LLDVVK	1		0,0000	1,36	2	686,44481	0,10	42,64
																	Medium	QAYVNYR	2		0,0000	1,30	2	913,45232	-0,36	38,31
																	Medium	VDPDNFFR	2		0,0000	0,94	2	1009,47386	0,04	46,02
8524	M5V KY8	Serine hydroxymethyltransferase	Serine hydroxymethyltransferase OS=Prunus persica GN=PRUPE_ppa004090mg PE=3 SV=1 - [M5VKY8_PRUPE]		Prunus persica	Chlorop last	01.01- Metabolism /Amino acid	16,41	13,5 8	2	9	10	16	530	57,7	8,34	High	LIIAGASAYPR	1		0,0000	2,40	2	1131,65288	0,67	41,99
																	High	GGMIFFK	2		0,0000	2,19	2	799,41734	0,23	46,76
																	High	YAQSPEFK	2		0,0000	2,03	2	969,46794	0,30	36,83
																	Medium	LTELGYK	2		0,0000	1,99	2	823,45574	-0,35	38,43
																	Medium	SAVVPGGIR	2		0,0000	1,68	2	855,50450	-0,27	38,11
																	Medium	YSEGLPGK	1		0,0000	1,55	2	850,43053	-0,01	36,65
																	Medium	IGSPAMTTR	2		0,0000	1,53	2	933,48192	-0,39	36,18
																	Medium	LQDFMR	1		0,0779	1,42	2	809,39745	-0,04	40,55
																	Medium	DFDYPR	2		0,0000	1,28	2	812,35753	0,20	40,99
8528	M5W Y75	Catalase	Catalase OS=Prunus persica GN=PRUPE_ppa004763mg PE=3 SV=1 - [M5WY75_PRUPE]		Prunus persica	Peroxiso me	01.01- Metabolism /Amino acid	88,18	29,4 7	3	8	17	57	492	57,0	7,43	High	WVDALSDPR	4		0,0000	3,28	2	1058,52641	-0,17	42,37
																	High	DEEVNYFPSR	3		0,0000	2,93	2	1255,55950	0,39	43,46
																	High	cVIEKENNFK	3	C1(Carb amidom ethyl)	0,0000	2,80	2	1280,63066	0,20	35,42
																	High	APGVQTPVIVR	6		0,0000	2,77	2	1136,67888	0,18	42,56
																	High	IFAYSDTQR	4		0,0000	2,73	2	1100,53728	0,13	39,26
																	High	DAMKFPDAIR	5		0,0000	2,67	2	1163,58769	-0,12	42,88
																	High	SHIQUETWR	4		0,0000	2,60	2	1056,52190	-0,24	36,33
																	High	cLLEDEAIK	3	C1(Carb amidom ethyl)	0,0000	2,56	2	1090,54448	-0,43	42,66
																	High	FSTVIHER	5		0,0000	2,55	2	988,52086	-0,23	36,97
																	High	LGPNYLQLPVN APK	2		0,0000	2,45	2	1523,85832	0,15	47,00
																	High	GPVLLEDYHLV EK	1		0,0000	2,23	2	1511,81279	1,53	44,16
																	High	LNVRPSI	4		0,0000	2,21	2	798,48320	-0,06	40,76
																	High	DAmKFPDAIR	4	M3(Oxi dation)	0,0000	2,13	2	1179,58293	0,16	40,07
																	Medium	LATFDRER	3		0,0000	1,84	2	1007,52696	0,04	35,21
																	Medium	SWAPDRQER	1		0,1844	1,46	3	1144,54950	0,05	34,56
																	Medium	FPDAIR	1		0,0809	1,25	2	718,38841	0,17	40,79
																	Medium	GSPETLRDPR	2		0,0000	1,23	3	1127,58030	-0,11	35,35
																	Medium	LATFDR	2		0,0000	1,08	2	722,38317	-0,05	37,32
8529	M5X WQ3	NADH dehydrogenase [ubiquinone] flavoprotein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa004904mg	99% to GE:645230713	Prunus persica	Mitocho ndrion	02.20- Energy/Ele	17,94	8,64	1	6	6	14	486	53,2	7,93	High	ASAAYIYIR	2		0,0000	2,71	2	1027,55718	0,04	41,42

[illegible]

																	Medium	FAEPGDPEYTA PVQK	1		0,0000	1,81	2	1648,78642	0,62	41,01
8707	M5W 944	Ras-group-related LRR protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003554mg PE=4 SV=1 - [M5W944_PRUPE]		Prunus persica	Chlorop last	08.99- Intracellular traffic/Othe rs	5,80	5,12	1	3	3	5	566	62,5	7,06	High	VEENPLEVPPR	3		0,0000	2,03	2	1278,66899	0,06	40,97
																	Medium	EVKAQPAKQK	1		0,0000	1,22	2	1126,64678	-9,91	49,56
																	Medium	ALPEAVGK	1		0,0000	1,12	2	784,45653	0,19	36,88
8711	M5X QJ0	Phosphoenolpyruvate carboxykinase [ATP]	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002490mg PE=3 SV=1 - [M5XQJ0_PRUPE]	99% to GI:645224569 Prunus mume, E value 0	Prunus mume	Cytopla sm	02.02- Energy/Glu coneogenes is	15,58	14,8 4	1	7	9	11	667	74,0	7,23	High	AAEnGGFSFTR	1	N4(Dea midated)	0,0000	3,09	2	1157,52251	0,23	40,90
																	High	IIDAIHSGR	2		0,0000	2,29	2	981,54729	-0,37	34,33
																	High	YAAMLSEK	1		0,0000	2,27	2	912,44969	0,13	37,10
																	High	DEETENELWWG K	1		0,0000	2,16	2	1535,66594	0,64	46,68
																	Medium	LLNASYTK	1		0,0000	2,00	2	909,50377	-0,29	36,01
																	Medium	SSQP TTPInGK	2		0,0000	1,89	2	1130,56902	0,16	33,99
																	Medium	IQTHPEATSEVc HDDSGTPVK	1	C12(Car bamido methyl)	0,0000	1,84	4	2308,04873	-1,03	34,04
9012	M5W 0H8	CBS domain-containing protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa012574mg PE=4 SV=1 - [M5W0H8_PRUPE]	97% to GI:645221749 Prunus mume, E value 1e-107	Prunus mume	Chlorop last	11.05- Disease/Def ense/Stress responses	102,93	66,8 7	1	1 0	10	43	163	18,1	8,29	High	LVSYAPEVTAY VENGK	7		0,0000	4,67	2	1739,88652	0,82	46,83
																	High	ADELYHGDGlc QEK	2	C11(Car bamido methyl)	0,0000	4,13	2	1634,71343	1,13	38,28
																	High	TFPVSAFENEEA ANK	11		0,0000	4,08	2	1653,77739	1,10	44,98
																	High	TFPVSAFENEEA ANKDVK	3		0,0000	3,96	2	1995,96965	1,87	41,93
																	High	SKADELYHGDG lcQEK	3	C13(Car bamido methyl)	0,0000	3,14	3	1849,83945	0,47	37,01
																	High	LLTEISLPNGLLP LK	2		0,0000	3,10	2	1620,99553	1,22	50,88
																	High	DmEEcGYVK	2	M2(Oxi dation); C5(Carb amidom ethyl)	0,0000	2,43	2	1146,44426	0,02	35,97
																	High	DMEEcGYVK	3	C5(Carb amidom ethyl)	0,0000	2,39	2	1130,44988	0,49	40,00
																	High	ELLVWVSLSDIY VDDPPTGK	1		0,0000	2,16	2	2246,16411	2,19	53,53
																	Medium	TPSGLFR	4		0,0000	1,58	2	777,42571	0,39	40,56
																	Medium	ETGFVWLK	5		0,0000	1,31	2	979,52446	-0,34	46,44
9013	M5W 6L5	Peptidyl-prolyl cis-trans isomerase	Peptidyl-prolyl cis-trans isomerase OS=Prunus persica GN=PRUPE_ppa012332mg PE=3 SV=1 - [M5W6L5_PRUPE]		Prunus persica	Cytopla sm	06.01- Protein destination and storage/Fol ding and stability	22,53	39,8 8	1	6	7	13	173	18,2	8,47	High	IVMELFADTTPR	2		0,0000	2,95	2	1392,71965	0,29	47,97
																	High	VFFDMTIGGQP AGR	2		0,0000	2,47	2	1495,73760	0,87	48,53
																	High	IVmELFADTTPR	1	M3(Oxi dation)	0,0000	2,37	2	1408,71623	1,47	44,70
																	High	TSRPVVVADcG QLS	3	C10(Car bamido methyl)	0,0000	2,19	2	1488,74870	0,76	41,60
																	Medium	FADENFIKK	1		0,0000	1,98	2	1111,57781	-0,44	38,46
																	Medium	VFFDmTIGGQPA GR	1	M5(Oxi dation)	0,0000	1,97	2	1511,73003	-0,79	44,92

																	Medium	FADENFIK	1		0,0000	1,37	2	983,48296	-0,37	42,75
																	Medium	TEWLDGK	1		0,0000	1,37	2	848,41448	-0,50	40,72
9103	M5X697	thaumatin	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa010473mg PE=4 SV=1 - [M5X697_PRUPE]	100% to GI:595941380 Prunus persica, E value 6e-179	Prunus persica	Extracel lular	11.02- Disease/def ense/Defens e-related	51,23	31,0 5	6	6	7	31	248	26,0	8,06	High	YccTPPNDKPETc PPTIDYSK	2	C2(Carb amidom ethyl); C3(Carb amidom ethyl); C13(Car bamido methyl)	0,0000	3,90	3	2430,00803	1,36	37,66
																	High	SaCLAFNQPK	8	C3(Carb amidom ethyl)	0,0000	2,97	2	1135,55705	0,48	42,02
																	High	SVDAPSPWSGR	12		0,0000	2,69	2	1158,55425	0,32	41,35
																	High	SaCLAFNQPK	1		0,0000	2,14	2	1078,53325	-1,66	44,07
																	High	GSDGSVIAcK	1	C9(Carb amidom ethyl)	0,0000	2,03	2	993,46691	-0,12	35,36
																	Medium	ASTcPADINK	1	C4(Carb amidom ethyl)	0,0000	1,23	2	1076,50408	-0,06	34,57
																	Medium	ASTcPADInK	1	C4(Carb amidom ethyl); N9(Dea midated)	0,0000	1,23	2	1077,48784	-0,29	35,70
																	Medium	VcPAPLQVK	4	C2(Carb amidom ethyl)	0,0000	1,03	2	1011,56548	-0,14	40,50
9108	M5W030	Peroxidase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa008489mg PE=3 SV=1 - [M5W030_PRUPE]	97% to GI:645219989 Prunus mume, E value 0	Prunus mume	Cell wall	11.06- Disease/Def ense/Detoxi fication	14,46	17,9 3	3	5	5	5	329	35,6	7,96	High	NVDPDIAInmDP NTPR	1	M10(Ox idation)	0,0000	3,87	2	1797,84599	1,28	40,08
																	High	VScADILALATR	1	C3(Carb amidom ethyl)	0,0000	3,18	2	1289,68901	0,58	46,10
																	High	FQQTFTVPATIR	1		0,0000	2,72	2	1507,82695	0,10	43,73
																	High	AAVDAVPQcK	1	C9(Carb amidom ethyl)	0,0000	2,51	2	1058,52983	-0,13	35,11
																	High	TFDNVYFK	1		0,0000	2,18	2	1033,49895	0,00	41,87
9109	M5VZV0	ATP synthase 24 kDa	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa010675mg PE=4 SV=1 - [M5VZV0_PRUPE]	99% to GI:645218784 Prunus mume, E value 2e-167	Prunus mume	Mitocho ndrion	01.01- Metabolism /Amino acid	102,20	45,8 3	1	1 4	14	71	240	27,8	9,11	High	ITIDPEDPAAVS QYAK	1		0,0000	3,22	2	1717,86528	0,52	43,14
																	High	DALEAMETQK	14		0,0000	3,09	2	1135,53020	0,15	40,91
																	High	ADLFESQR	17		0,0000	2,76	2	1052,50212	1,29	39,50
																	High	GMALLQAEFEK	1		0,0000	2,54	2	1236,62993	0,46	44,86
																	High	DEEMVDVK	1		0,0000	2,50	2	964,42919	-0,07	37,87
																	High	YEEQLELK	1		0,0000	2,38	2	1051,53069	0,03	38,94
																	Medium	EEFKDEEMVDVK	1		0,0000	2,27	3	1497,67719	-0,44	38,57
																	High	DALEAmETQK	3	M6(Oxi dation)	0,0000	2,24	2	1151,52373	-1,06	40,38
																	High	AQLEELK	8		0,0000	2,07	2	830,46184	-0,01	36,36
																	Medium	TqDIPDAR	1	Q2(Dea midated)	0,0000	1,85	2	916,43718	0,09	35,30
																	Medium	TQDIPDAR	1		0,0000	1,60	2	915,45281	-0,30	34,35
																	Medium	NIFLDVK	8		0,0000	1,56	2	848,48802	0,42	50,19

																	Medium	GDEMLK	1		0,0000	1,55	2	692,32805	-0,51	34,33
																	Medium	IQHTIQSR	1		0,0000	1,47	3	982,54328	0,40	30,49
																	Medium	TYLLTLK	11		0,0000	1,12	2	851,52324	-0,54	51,49
																	Medium	AQLEELKK	1		0,0000	1,06	2	958,55718	0,37	33,41
9206	M5X CT3	3-hydroxyisobutyryl-CoA hydrolase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa007004mg PE=4 SV=1 - [M5XCT3_PRUPE]	96% to GI:645254927 Prunus mume, E value 0	Prunus mume	Chlorop last	01.01- Metabolism /Amino Acid	60,36	22,0 2	6	1 0	12	40	386	42,9	7,97	High	AGDEWLASTIR	1		0,0000	3,39	2	1218,61162	0,19	45,18
																	High	LDGDEELKLPQ R	4		0,0000	2,85	3	1412,73740	-0,47	41,18
																	High	VQAMDEcLVR	3	C7(Carb amidom ethyl)	0,0000	2,85	2	1220,57634	0,05	41,43
																	High	VQAmDEcLVR	5	M4(Oxi dation); C7(Carb amidom ethyl)	0,0000	2,82	2	1236,57121	0,02	40,78
																	High	AILWDKDK	4		0,0000	2,59	2	988,54607	-0,20	39,15
																	High	YGENFAQK	2		0,0000	2,53	2	956,44713	-0,13	36,45
																	High	LDGDEELK	2		0,0000	2,35	2	918,44115	-0,41	36,73
																	High	HFLEGNLK	2		0,0000	2,28	2	957,51488	-0,42	38,94
																	Medium	TLTLNRPR	6		0,0000	1,99	2	970,57897	-0,32	36,35
																	Medium	VFANAKL	1		0,0000	1,82	2	762,45091	0,03	40,05
																	Medium	LSLLEK	6		0,0000	1,66	2	702,43987	0,31	41,93
																	Medium	AILWDK	2		0,0000	1,48	2	745,42443	0,11	42,25
9211	M5Y 500	3-ketoacyl-CoA thiolase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005421mg PE=3 SV=1 - [M5Y500_PRUPE]	92% to GI:645236120 Prunus mume, E value 0	Prunus mume	peroxiso me	01.06- Metabolism /Lipid and sterol	40,79	25,4 1	3	1 0	10	19	429	45,0	8,09	High	DGSTTAGNSSQ VSDGAGAVLLM K	2		0,0000	4,27	2	2166,03765	1,49	46,89
																	High	DGSTTAGNSSQ VSDGAGAVLLm K	3	M22(Ox idation)	0,0000	3,53	2	2182,03349	1,91	43,40
																	High	DTHADDLLAPV LK	2		0,0000	3,14	2	1407,74809	0,14	45,90
																	High	GDSTDELcNAR	2	C8(Carb amidom ethyl)	0,0000	2,75	2	1237,51177	0,28	37,00
																	High	AVATLLHEMK	1		0,0000	2,69	2	1112,61406	0,68	39,93
																	High	SCEEKPVVTISVD DGR	1		0,0000	2,58	3	1701,86551	0,03	40,30
																	High	LGLDPEK	2		0,0000	2,12	2	771,42473	-0,01	39,58
																	High	FKDEIIPVATK	2		0,0000	2,11	2	1260,71953	-0,28	40,60
																	Medium	NTTLADLAK	1		0,0000	1,99	2	946,51995	-0,51	40,80
																	Medium	DEIIPVATK	1		0,0000	1,93	2	985,55614	-0,36	42,88
																	Medium	GLPILGVFR	1		0,1318	1,12	2	971,60362	-0,10	49,89
9213	M5X 171	Aspartic protease in guard cell	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005966mg PE=4 SV=1 - [M5X171_PRUPE]	98% to GI:645251460 Prunus mume, E value 0	Prunus mume	Nucleus	01.01- Metabolism /Amino acid	6,95	7,82	1	4	4	4	435	46,9	9,11	High	LVEPAYVAVR	1		0,0000	2,69	2	1116,64153	0,27	40,29
																	High	LGPVGQPIR	1		0,0000	2,13	2	936,56236	-0,23	37,81

																	High	VLIDVPNSR	1		0,0000	2,12	2	1012,57842	-0,20	39,90
																	Medium	YTPLLK	1		0,0000	0,97	2	734,44493	0,29	38,24
9214	M5X YB0	Aspartate aminotransferase	Aspartate aminotransferase OS=Prunus persica GN=PRUPE_ppa005369mg PE=3 SV=1 - [M5XYB0_PRUPE]		Prunus persica	Cytopla sm	01.01- Metabolism /Amino acid	34,61	20,0 4	1	1 1	12	27	464	50,8	8,84	High	LNLGVGAYR	8		0,0000	2,97	2	962,54155	-0,29	41,67
																	High	AENLmIER	1	M5(Oxi dation)	0,0000	2,74	2	991,48705	-0,73	36,59
																	High	AEMEMMAGR	1		0,0000	2,71	2	1025,42119	-0,18	38,06
																	High	LAAALIER	1		0,0000	2,44	2	856,52507	-0,07	39,52
																	High	IADVIQEK	2		0,0000	2,41	2	915,51445	-0,19	37,74
																	High	AENLMIER	1		0,0000	2,40	2	975,49578	3,00	38,80
																	High	NLGLYAER	4		0,0000	2,33	2	935,49443	-0,12	39,09
																	High	KAENLMIER	2		0,0000	2,14	2	1103,58757	-0,23	35,48
																	Medium	TEELQPYVLDV VK	1		0,0000	1,85	2	1532,82244	1,12	45,92
																	Medium	LYDNLTAk	2		0,0000	1,78	2	937,49877	-0,20	38,03
																	Medium	VPWSEYR	1		0,0000	1,58	2	936,45702	-0,43	39,62
																	Medium	DWSFILK	1		0,0000	1,43	2	908,48747	-0,22	49,07
																	Medium	NIFNDSR	1		0,0000	1,38	2	865,41600	-0,33	38,16
																	Medium	KAENLmIER	1	M6(Oxi dation)	0,0579	1,14	2	1119,58159	-1,02	33,77
9216	M1P YG9	Aspartate aminotransferase	Aspartate aminotransferase OS=Prunus persica GN=PRUPE_ppa005315mg PE=2 SV=1 - [M1PYG9_PRUPE]		Prunus mume	Cytopla sm	01.01- Metabolism /Amino acid	78,30	19,7 0	3	1 0	10	36	467	50,8	8,57	High	LILGADSPPIQE NR	7		0,0000	3,12	2	1522,82451	1,35	45,99
																	High	VGALSIVcK	4	C8(Carb amidom ethyl)	0,0000	3,03	2	946,53868	-0,40	41,10
																	High	LNLGVGAYR	4		0,0000	2,90	2	962,54149	-0,35	42,91
																	High	ISMAGLSSR	2		0,0000	2,86	2	921,48204	-0,26	41,09
																	High	VGGEFLAK	4		0,0000	2,60	2	820,45696	0,70	40,09
																	High	NMGLYGER	2		0,0000	2,50	2	939,43541	0,10	38,69
																	High	ISmAGLSSR	4	M3(Oxi dation)	0,0000	2,36	2	937,47740	0,22	36,26
																	High	EYHIYMTSDGR	2		0,0000	2,10	2	1371,60149	1,22	39,20
																	Medium	HQLFESLR	1		0,0000	1,91	2	1029,54692	-0,70	39,87
																	Medium	NmGLYGER	1	M2(Oxi dation)	0,0000	1,87	2	955,42998	-0,27	39,01
																	Medium	EYHIYmTSDGR	2	M6(Oxi dation)	0,0000	1,80	2	1387,59502	0,21	36,87
																	Medium	YYDPATR	2		0,0000	1,76	2	885,41020	0,09	37,15
																	Medium	AEQLLVNDR	1		0,0000	1,50	2	1057,56352	-0,17	39,78
9217	M5W TY8	sulfite oxidase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa006835mg PE=4 SV=1 - [M5WTY8_PRUPE]	99% to GE:645250254 Prunus mume, E value 0	Prunus mume	Chlorop last	01.02- Metabolism /Nitrogen and sulphur	14,78	19,3 4	1	7	7	7	393	43,4	8,27	High	SALVSSYVTPV DFFYK	1		0,0000	2,90	2	1822,93010	2,12	49,50

																	High	AVDSAANVQPE K	1		0,0000	2,88	2	1228,61687	0,00	33,80
																	High	VEDIWNLR	1		0,0000	2,84	2	1044,54692	-0,38	44,56
																	High	LADVLELVGIPK	1		0,0000	2,52	2	1266,76775	0,72	49,40
																	Medium	HVEFVSVDK	1		0,0000	1,82	2	1059,54729	0,29	36,73
																	Medium	VIVPGVIGAR	1		0,0000	1,82	2	980,62480	-0,40	41,77
																	Medium	HPSLQINAK	1		0,0000	1,12	2	1007,56291	-0,37	34,33
9308	M5W SP0	Elongation factor 1-alpha	Elongation factor 1-alpha OS=Prunus persica GN=PRUPE_ppa005717mg PE=3 SV=1 - [M5W5P0_PRUPE]		Prunus persica	Cytopla sm	05.04-Protein synthesis/Tr anslation factors	46,75	17,2 3	4	3	9	22	447	49,4	9,07	High	YYcTVIDAPGHR	4	C3(Carb amidom ethyl)	0,0000	3,51	2	1451,67436	0,50	38,57
																	High	IGGIGTVPVGR	1		0,0000	2,86	2	1025,61016	-0,11	41,52
																	High	STTTGHLIYK	5		0,0000	2,80	2	1120,59953	-0,17	36,12
																	High	LPLQDVYK	3		0,0000	2,47	2	975,55058	-0,42	42,83
																	High	ARYDEIVK	2		0,0000	2,46	2	993,53600	-0,42	36,64
																	High	STNLDWYK	2		0,0000	2,22	2	1026,48918	0,07	43,36
																	Medium	YDEIVK	2		0,0000	1,85	2	766,39800	-0,23	37,80
																	Medium	EVSSYLK	2		0,0000	1,63	2	825,43535	0,08	37,95
9701	M5W QA3	dynamain-related protein	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003029mg PE=3 SV=1 - [M5WQA3_PRUPE]	99% to GI:645267575 Prunus mume, E value 0	Prunus mume	Mitochon dion	03.22-Cell growth/divi sion/Cell cycle	29,16	18,2 0	2	1 1	12	17	610	68,1	7,97	High	VEVTNAASDSL ER	2		0,0000	3,05	2	1390,68181	0,63	40,00
																	High	GTDAAEILEGK	1		0,0000	2,69	2	1103,55803	0,06	42,56
																	High	LIESSVITIR	1		0,0000	2,38	2	1130,67803	0,02	43,80
																	High	SIVYcQVR	2	C5(Carb amidom ethyl)	0,0000	2,20	2	1024,52458	0,13	38,26
																	High	SVNETPELK	2		0,0000	2,15	2	1016,52574	-0,17	37,74
																	High	HLETVIK	2		0,0000	2,04	2	839,49846	-0,12	36,36
																	High	YNDSYLK	1		0,0000	2,00	2	930,43120	-0,41	38,19
																	Medium	EYFSTTPEYK	1		0,0000	1,78	2	1264,57414	0,72	40,72
																	Medium	QLSMENIR	2		0,0000	1,62	2	990,50377	0,03	40,21
																	Medium	IPGIQSLISK	1		0,0000	1,50	2	1055,64653	0,53	45,93
																	Medium	IDLMDK	1		0,0199	1,48	2	734,37541	0,09	40,46
																	Medium	LGKPISADAGG K	1		0,0000	0,99	2	1113,62627	-0,05	33,77
9801	M5W T60	Monocopper oxidase	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa003224mg PE=4 SV=1 - [M5WT60_PRUPE]	99% to GI:645266448 Prunus mume, E value 0	Prunus mume	Cell wall	03.01-Cell growth/divi sion/Cell growth	27,77	7,45	1	4	4	16	591	65,8	8,28	High	ASGGFGGFIINN R	2		0,0000	3,26	2	1309,66570	0,66	46,49
																	High	NKPPVVInGR	6	N8(Dea midated)	0,0000	3,14	3	1094,63230	0,52	36,13
																	High	AAGPLPEAPND EFDK	2		0,0000	2,91	2	1570,73943	0,61	42,28
																	High	NKPPVVINGR	4		0,0000	2,84	3	1093,64774	0,03	35,73

																	Medium	WDGIAR	2		0,0000	1,81	2	717,36821	0,45	39,87
9802	M5V VS9	Eukaryotic translation initiation factor	Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001554mg PE=4 SV=1 - [M5VVS9_PRUPE]	99% to GI:645275864 Prunus mume, E value 0	Prunus mume	Chlorop last	05.04- Protein synthesis/Tr anslation factors	19,58	19,0 5	2	1 2	14	15	803	87,9	8,00	High	QMTSPEQEMER	1		0,0000	2,51	2	1365,57842	0,74	36,73
																	High	FPSDEPDGK	2		0,0000	2,36	2	991,43694	0,17	34,49
																	High	QQEANQPQFAR	1		0,0000	2,28	2	1316,63420	-0,03	34,67
																	High	ELTTNPQLAPR	1		0,0000	2,28	2	1239,66973	0,40	37,84
																	High	INDLYFSR	1		0,0000	2,15	2	1027,52068	-0,07	41,27
																	High	APSNFGEVIGK	1		0,0000	2,13	2	1118,58415	0,04	39,98
																	High	NNVTGAQGNTS PGGFPNNR	1		0,0000	2,10	2	1901,88786	1,53	36,56
																	Medium	SPAYHPVVVK	1		0,0000	1,93	3	1126,58933	0,14	33,72
																	Medium	TISEIHTEAEK	1		0,0000	1,87	2	1257,63249	0,26	33,29
																	Medium	THNSSNQGGGP APALTK	1		0,0000	1,85	3	1636,80741	2,18	32,41
																	Medium	AEVPWSAR	1		0,0000	1,48	2	915,46807	-0,30	39,32
																	Medium	VFTASDIR	1		0,0000	1,35	2	908,48351	-0,16	38,39

^a*Spot N°*, protein spot number of the reference gel maps presented in Figure S1;

^b*Accession number*, UNIPROT accession number;

^c*Suggested name*; Suggested protein name according to database identification or manual blast against current databases;

^d*Matching criteria*, adopted criteria for the valuation of similarity for proteins identified after manual blast against current databases. Blank cells correspond to proteins readily identified without further blast;

^e*Organism*, organism in which the protein has been matched to by BLAST search;

^f*Subellular localization*, Sub-cellular localization of proteins was assigned based on database searches;

^g*Functional category*, proteins ontologically classified into functional categories proposed by Bevan et al., 1998;

Table S2. Quantitative data for peach protein spot volumes on 2DE-gels. Protein extracts have been analyzed by two-dimensional electrophoresis and 2D-gels were submitted to image analysis as described in Experimental procedures.

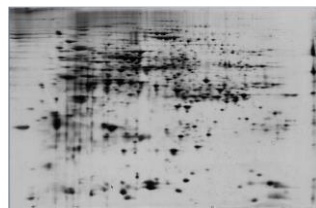
Spot N°, spot label on the reference 2DE-map presented in Figure S1;																														
RGC Mean, average of normalized spot volumes of peach cultivar "Royal Glory" Control fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RGC Coef. Var %, Coefficient of variation of normalized spot volumes of peach cultivar "Royal Glory" Control fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RGL Mean, average of normalized spot volumes of peach cultivar "Royal Glory" fruits inoculated with <i>Monilinia laxa</i> , as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RGL Coef. Var %, Coefficient of variation of normalized spot volumes of peach cultivar "Royal Glory" fruits inoculated with <i>M. laxa</i> as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RGL Mean/RGC Mean, The RGL (Mean) spot volume divided by the RGC (Mean) spot volume																														
P value RGL/RGC, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" Control fruits and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" fruits inoculated with <i>M. laxa</i> , as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RGF Mean, average of normalized spot volumes of peach cultivar "Royal Glory" fruits inoculated with <i>M. fructicola</i> as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RGF Coef. Var %, Coefficient of variation of normalized spot volumes of peach cultivar "Royal Glory" fruits inoculated with <i>M. fructicola</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RGF Mean/RGC Mean, The RGF (Mean) spot volume divided by the RGC (Mean) spot volume																														
P value RGF/RGC, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" Control fruits and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" fruits inoculated with <i>M. fructicola</i> as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RGL Mean/RGF Mean, The RGL (Mean) spot volume divided by the RGF (Mean) spot volume																														
P value RGL/RGF, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" fruits inoculated with <i>M. fructicola</i> and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" fruits inoculated with <i>M. laxa</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RLC Mean, average of normalized spot volumes of peach cultivar "Rich Lady" Control fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RLC Coef. Var %, Coefficient of variation of normalized spot volumes of peach cultivar "Rich Lady" Control fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RLC Mean/RGC Mean, The RLC (Mean) spot volume divided by the RGC (Mean) spot volume																														
P value RLC/RGC, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" Control fruits and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" Control fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RLL Mean, average of normalized spot volumes of peach cultivar "Rich Lady" fruits inoculated with <i>M. laxa</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RLL Coef. Var %, Coefficient of variation of normalized spot volumes of peach cultivar "Rich Lady" fruits inoculated with <i>M. laxa</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RLL Mean/RLC Mean, The RLL (Mean) spot volume divided by the RLC (Mean) spot volume																														
P value RLL/RLC, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" Control fruits and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" fruits inoculated with <i>M. laxa</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RLL Mean/RGL Mean, The RLL (Mean) spot volume divided by the RGL (Mean) spot volume																														
P value RLL/RGL, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" fruits inoculated with <i>M. laxa</i> fruits and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" fruits inoculated with <i>M. laxa</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RLF Mean, average of normalized spot volumes of peach cultivar "Rich Lady" fruits inoculated with <i>M. fructicola</i> fruits fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
RLF Coef. Var %, Coefficient of variation of normalized spot volumes of peach cultivar "Rich Lady" fruits inoculated with <i>M. fructicola</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RLF Mean/RLC Mean, The RLF (Mean) spot volume divided by the RLC (Mean) spot volume																														
P value RLF/RLC, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" Control fruits and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" fruits inoculated with <i>M. fructicola</i> fruits as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RLF Mean/RGF Mean, The RLF (Mean) spot volume divided by the RGF (Mean) spot volume																														
P value RLF/RGF, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Royal Glory" fruits inoculated with <i>M. fructicola</i> and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" fruits inoculated with <i>M. fructicola</i> , as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Ratio RLL Mean/RLF Mean, The RLL (Mean) spot volume divided by the RLF (Mean) spot volume																														
P value RLL/RLF, p value between normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" fruits inoculated with <i>M. fructicola</i> and normalized spot volumes of individual spots from three different gels and independent extractions of peach cultivar "Rich Lady" fruits inoculated with <i>M. laxa</i> , as obtained from densitometric analysis of individual spots from proteins in 2D gels stained with silver nitrate from three different gels and independent extractions																														
Spot N°	RGC Mean	RGC Coef. Var %	RGL Mean	RGL Coef. Var %	P value Mean/R GC	RGF Mean	RGF Coef. Var %	P value Mean/R GC	P value RGF/RG C	RGL Mean/ RGF	P value RGL/ RGF	RLC Mea n	RLC Coef. Var %	RLC Mean/ RGC	P value RLC/R GC	RLL Mean	RLL Coef. Var %	RLL Mean /RLC	P value RLL/ RLC	RLF Mean	RLF Coef. Var %	RLF Mean/R LC	P value RLF/ RLF/ RGC	Ratio RLF Mean/ RLF/ RGC	Ratio RLL Mean/ RLF/ RLC					
13	3165,2	30,1%	2786,6	15,0%	0,88	0,352	2478,7	50,0%	0,78	0,119	1,12	0,322	1471,8	17,5%	0,46	0,005	1063,1	49,5%	0,72	0,451	0,38	0,000	1668,1	15,4%	1,13	0,734	0,67	0,059	0,64	0,178
19	1790,3	38,8%	1437,3	47,1%	0,80	0,386	3315,4	1,8%	1,85	0,001	0,43	0,000	4073,8	51,2%	2,28	0,000	3188	19,7%	0,78	0,104	2,22	0,000	3390,3	35,5%	0,83	0,238	1,02	0,86	0,94	0,651
20	394,4	11,5%	667,5	33,1%	1,69	0,502	1115,4	75,8%	2,83	0,101	0,60	0,151	569,4	32,8%	1,44	0,765	1488,8	25,5%	2,61	0,092	2,23	0,017	1535,6	15,7%	2,70	0,097	1,38	0,325	0,97	0,917

407	2971,3	29,5%	1959,2	12,7%	0,66	0,014	1369,7	34,1%	0,46	0,000	1,43	0,060	2568,8	52,5%	0,86	0,493	1081,2	9,2%	0,42	0,007	0,55	0,011	932,3	84,3%	0,36	0,005	0,68	0,305	1,16	0,739
812	820,5	51,7%	1358,4	17,8%	1,66	0,187	1264,8	29,6%	1,54	0,311	1,07	0,763	867,8	37,9%	1,06	0,936	1422,7	38,5%	1,64	0,307	1,05	0,850	2057,4	22,7%	2,37	0,042	1,63	0,065	0,69	0,158
1013	406,9	55,4%	771,6	16,6%	1,90	0,370	1353,8	56,3%	3,33	0,032	0,57	0,063	1628,7	42,5%	4,00	0,039	1439,1	23,9%	0,88	0,727	1,87	0,051	1349	56,1%	0,83	0,628	1	0,991	1,07	0,840
1109	1537,7	133,2%	884,1	23,7%	0,57	0,110	548,9	30,0%	0,36	0,025	1,61	0,282	440,1	126,1%	0,29	0,063	382,4	42,4%	0,87	0,915	0,43	0,141	578,6	48,5%	1,31	0,811	1,05	0,944	0,66	0,661
1119	4389,9	30,6%	3986,7	15,5%	0,91	0,322	4107,4	19,8%	0,94	0,519	0,97	0,697	8230,5	28,4%	1,87	0,000	3452,6	9,8%	0,42	0,000	0,87	0,118	2881,1	23,1%	0,35	0,000	0,7	0,005	1,20	0,203
1314	476,4	75,1%	608,6	46,2%	1,28	0,745	438,5	16,2%	0,92	0,931	1,39	0,584	1185,8	19,3%	2,49	0,228	1120,3	23,2%	0,94	0,904	1,84	0,134	1012,6	48,1%	0,85	0,764	2,31	0,179	1,11	0,810
1319	350,1	36,4%	897,9	35,4%	2,56	0,180	699	27,1%	2,00	0,425	1,28	0,522	1656,2	15,4%	4,73	0,028	3303,5	5,9%	1,99	0,003	3,68	0,000	2627	24,2%	1,59	0,095	3,76	0	1,26	0,132
1321	459,7	25,5%	614,6	19,0%	1,34	0,703	760,6	26,4%	1,65	0,492	0,81	0,638	829	28,2%	1,80	0,529	1887,9	26,6%	2,28	0,053	3,07	0,000	1046,3	6,6%	1,26	0,707	1,38	0,503	1,80	0,062
1628	357,2	23,2%	519,3	46,6%	1,45	0,690	550,3	28,5%	1,54	0,659	0,94	0,921	951,4	38,4%	2,66	0,312	1452,6	19,1%	1,53	0,356	2,80	0,007	1050,5	18,3%	1,10	0,864	1,91	0,241	1,38	0,369
1705	313,6	25,3%	670,6	36,1%	2,14	0,381	715,8	32,1%	2,28	0,358	0,94	0,884	414,3	37,2%	1,32	0,864	285,4	37,9%	0,69	0,812	0,43	0,258	406,2	31,6%	0,98	0,989	0,57	0,468	0,70	0,787
1820	245,9	30,0%	363	32,2%	1,48	0,773	418,4	11,0%	1,70	0,693	0,87	0,859	537,1	31,4%	2,18	0,620	792,8	23,5%	1,48	0,637	2,18	0,207	729,4	12,0%	1,36	0,739	1,74	0,466	1,09	0,887
1821	84,7	26,3%	498,9	1,7%	5,89	0,309	362	46,4%	4,27	0,526	1,38	0,659	392	15,6%	4,63	0,600	572,3	25,2%	1,46	0,739	1,15	0,829	409,6	10,5%	1,04	0,976	1,13	0,911	1,40	0,716
2007	1179,2	2,7%	1009,9	49,3%	0,86	0,677	1349,2	22,3%	1,14	0,697	0,75	0,276	1983	34,2%	1,68	0,172	3588,5	17,4%	1,81	0,004	3,55	0,000	4008,5	46,4%	2,02	0,001	2,97	0	0,90	0,349
2104	2573,1	36,1%	1001,4	69,9%	0,39	0,000	1120,4	43,3%	0,44	0,001	0,89	0,701	634,6	91,3%	0,25	0,001	1535,1	107,2%	2,42	0,099	1,53	0,118	1141,4	38,0%	1,80	0,381	1,02	0,961	1,34	0,379
2311	648,3	27,1%	527,8	55,6%	0,81	0,767	570	7,1%	0,88	0,858	0,93	0,892	3202,8	36,6%	4,94	0,000	3327,1	24,9%	1,04	0,819	6,30	0,000	2861,8	25,0%	0,89	0,555	5,02	0	1,16	0,299
2312	645,1	28,5%	798	20,3%	1,24	0,707	442,3	13,4%	0,69	0,643	1,80	0,253	2556,9	28,5%	3,96	0,001	2737,2	14,1%	1,07	0,739	3,43	0,000	2509,7	2,0%	0,98	0,935	5,67	0	1,09	0,611
2319	834,6	35,2%	1197,7	14,6%	1,44	0,372	1159,1	15,1%	1,39	0,458	1,03	0,901	794,7	43,2%	0,95	0,946	1960,9	8,4%	2,47	0,033	1,64	0,026	1755,1	12,3%	2,21	0,099	1,51	0,163	1,12	0,645
2609	300,5	61,0%	560,8	25,9%	1,87	0,522	375,1	3,7%	1,25	0,864	1,50	0,550	352,4	48,5%	1,17	0,929	209	42,3%	0,59	0,791	0,37	0,301	401,3	36,5%	1,14	0,932	1,07	0,951	0,52	0,667
2617	448,6	31,1%	450,9	26,5%	1,01	0,995	346,7	29,1%	0,77	0,816	1,30	0,737	446,9	35,4%	1,00	0,998	244,6	8,3%	0,55	0,709	0,54	0,543	543,8	24,4%	1,22	0,867	1,57	0,643	0,45	0,504
2701	177,2	47,1%	501,5	26,9%	2,83	0,425	543,5	24,9%	3,07	0,403	0,92	0,892	332,6	25,9%	1,88	0,791	431,2	42,6%	1,30	0,856	0,86	0,836	568,7	64,1%	1,71	0,683	1,05	0,953	0,76	0,758
2703	424,4	43,0%	1020,8	28,8%	2,41	0,144	951,1	28,0%	2,24	0,230	1,07	0,822	751,8	5,8%	1,77	0,577	961,1	19,3%	1,28	0,699	0,94	0,860	1172,1	42,0%	1,56	0,467	1,23	0,604	0,82	0,637
2704	840,3	13,7%	1249,7	15,6%	1,49	0,315	1193,1	14,6%	1,42	0,420	1,05	0,855	716,8	34,1%	0,85	0,833	576,6	33,8%	0,80	0,796	0,46	0,049	837,1	42,1%	1,17	0,835	0,7	0,404	0,69	0,560
3205	1816,1	32,5%	870,7	50,0%	0,48	0,000	1173,1	54,5%	0,65	0,017	0,74	0,242	1564,1	20,8%	0,86	0,561	1295,4	30,0%	0,83	0,574	1,49	0,161	772,5	42,1%	0,49	0,096	0,66	0,222	1,68	0,151
3308	1302,8	29,7%	591,4	13,3%	0,45	0,002	712,9	48,2%	0,55	0,028	0,83	0,637	994,9	44,3%	0,76	0,477	901	15,0%	0,91	0,844	1,52	0,305	1071,3	31,7%	1,08	0,871	1,5	0,274	0,84	0,638
3311	782,3	27,6%	1773,5	17,4%	2,27	0,000	1477,5	47,0%	1,89	0,010	1,20	0,252	1097	71,6%	1,40	0,467	2560	22,3%	2,33	0,003	1,44	0,010	1287,3	25,2%	1,17	0,687	0,87	0,561	1,99	0,001
3314	342,1	78,1%	406,7	92,4%	1,19	0,773	209	36,5%	0,61	0,617	1,95	0,443	2512	14,9%	7,34	0,000	2145	22,5%	0,85	0,443	5,27	0,000	1666,3	22,5%	0,66	0,076	7,97	0	1,29	0,188
3316	233,6	31,7%	449,6	40,2%	1,92	0,335	326,9	27,0%	1,40	0,726	1,38	0,634	4043,4	36,3%	17,31	0,000	3057,9	8,5%	0,76	0,041	6,80	0,000	3346,9	18,3%	0,83	0,142	10,24	0	0,91	0,426
3518	742	20,8%	751,4	32,9%	1,01	0,966	521,5	31,8%	0,70	0,408	1,44	0,373	349,9	12,7%	0,47	0,366	309,5	47,9%	0,88	0,933	0,41	0,145	326,7	1,5%	0,93	0,961	0,63	0,551	0,95	0,962
3616	337,6	33,2%	644	40,6%	1,91	0,173	559,3	15,4%	1,66	0,406	1,15	0,742	1154,5	6,4%	3,42	0,061	1048,8	31,5%	0,91	0,825	1,63	0,181	858	21,6%	0,74	0,530	1,53	0,362	1,22	0,599
4208	1098,2	36,3%	422,4	58,5%	0,38	0,003	614,5	52,6%	0,56	0,071	0,69	0,456	5784,8	39,2%	5,27	0,000	5818,7	18,3%	1,01	0,944	13,78	0,000	4580,8	16,5%	0,79	0,012	7,45	0	1,27	0,001
4209	205,2	44,1%	236,5	71,5%	1,15	0,889	300,6	58,7%	1,46	0,720	0,79	0,000	5067,1	29,6%	24,69	0,000	4083,7	24,2%	0,81	0,041	17,27	0,000	2001	47,4%	0,39	0,000	6,66	0	2,04	0,000
4211	320,3	39,0%	181,4	91,8%	0,57	0,535	276,4	65,6%	0,86	0,869	0,66	0,712	884,7	46,0%	2,76	0,194	1743,9	32,0%	1,97	0,074	9,61	0,000	1147,4	50,2%	1,30	0,578	4,15	0,009	1,52	0,102

	4214	192,3	47,1%	243,7	100,1 %	1,27	0,818	359,9	79,0%	1,87	0,529	0,68	0,652	433,4	18,6%	2,25	0,578	862,4	30,3 %	1,99	0,370	3,54	0,042	631,4	42,4%	1,46	0,675	1,75	0,406	1,37	0,524
	4215	295,9	37,2%	560,3	44,3%	1,89	0,239	485,4	38,4%	1,64	0,477	1,15	0,771	611,6	54,5%	2,07	0,466	2540,9	29,7 %	4,15	0,000	4,53	0,000	881,9	114,5%	1,44	0,567	1,82	0,226	2,88	0,000
	4313	2169	5,4%	919,8	36,3%	0,42	0,000	1306,4	53,2%	0,60	0,002	0,70	0,135	2026,2	29,0%	0,93	0,741	1824,3	12,8 %	0,90	0,673	1,98	0,003	1733,6	9,5%	0,86	0,536	1,33	0,193	1,05	0,802
	4421	312,9	43,7%	453,7	5,8%	1,45	0,529	321,8	29,3%	1,03	0,973	1,41	0,609	301,1	24,4%	0,96	0,978	896,2	12,6 %	2,98	0,214	1,98	0,144	1019,3	20,4%	3,39	0,131	3,17	0,035	0,88	0,734
	4711	137,6	49,1%	232,3	34,2%	1,69	0,672	179,9	48,9%	1,31	0,874	1,29	0,839	167,5	115,3 %	1,22	0,945	36,2	59,9 %	0,22	0,783	0,16	0,516	66,7	70,9%	0,40	0,831	0,37	0,729	0,54	0,933
	4726	413	24,8%	684,6	28,6%	1,66	0,226	559,2	30,3%	1,35	0,583	1,22	0,626	460,1	33,9%	1,11	0,913	316,8	25,9 %	0,69	0,764	0,46	0,224	362,8	57,8%	0,79	0,837	0,65	0,548	0,87	0,899
	4805	159,1	49,5%	159,2	1,5%	1,00	1,000	169,4	6,0%	1,06	0,969	0,94	0,968	369,2	27,2%	2,32	0,628	402,4	39,3 %	1,09	0,945	2,53	0,420	371,6	39,5%	1,01	0,996	2,19	0,536	1,08	0,932
	4828	373,5	23,6%	990,3	43,1%	2,65	0,007	897,8	27,9%	2,40	0,051	1,10	0,719	569,6	21,5%	1,53	0,651	1181,7	23,2 %	2,07	0,202	1,19	0,526	758,4	20,5%	1,33	0,689	0,84	0,67	1,56	0,244
	4829	384,4	40,0%	1252	36,0%	3,26	0,000	1228,5	51,2%	3,20	0,000	1,02	0,927	767,8	31,4%	2,00	0,376	1586,7	47,5 %	2,07	0,089	1,27	0,268	1543,7	33,3%	2,01	0,103	1,26	0,336	1,03	0,905
	5008	3,3	88,8%	1602,3	25,9%	485,55	0,000	1686,8	52,5%	511,15	0,000	0,95	0,743	1171,3	56,8%	354,94	0,008	1941,8	26,8 %	1,66	0,109	1,21	0,261	3305,2	16,3%	2,82	0,000	1,96	0	0,59	0,000
	5414	1256,9	26,3%	630,2	32,4%	0,50	0,006	464,1	30,9%	0,37	0,004	1,36	0,519	1379,5	7,3%	1,10	0,777	984,1	10,4 %	0,71	0,408	1,56	0,242	1028,1	29,1%	0,75	0,458	2,22	0,086	0,96	0,903
	5509	944,1	25,9%	379,1	32,2%	0,40	0,013	609,8	26,9%	0,65	0,211	0,62	0,371	459,9	36,4%	0,49	0,264	464,4	29,9 %	1,01	0,993	1,23	0,777	467,7	23,1%	1,02	0,987	0,77	0,664	0,99	0,993
	5615	749,1	126,4 %	205,4	61,1%	0,27	0,017	180,3	40,8%	0,24	0,035	1,14	0,922	507,5	32,6%	0,68	0,577	442,5	43,1 %	0,87	0,892	2,15	0,432	432,7	15,0%	0,85	0,874	2,4	0,44	1,02	0,979
	5703	472,1	24,6%	728,9	37,3%	1,54	0,252	933,9	30,1%	1,98	0,085	0,78	0,427	202,8	45,2%	0,43	0,534	186,3	69,8 %	0,92	0,972	0,26	0,074	338,1	101,0%	1,67	0,775	0,36	0,07	0,55	0,675
	5705	444,2	23,5%	315,3	14,7%	0,71	0,565	282,9	24,2%	0,64	0,545	1,11	0,900	106,1	88,9%	0,24	0,435	89,2	33,1 %	0,84	0,972	0,28	0,454	84,5	93,3%	0,80	0,964	0,3	0,544	1,06	0,990
	5707	257,4	66,1%	148,5	28,7%	0,58	0,572	175,4	33,1%	0,68	0,757	0,85	0,909	119,5	99,4%	0,46	0,660	25,8	76,1 %	0,22	0,765	0,17	0,526	27,8	73,8%	0,23	0,786	0,16	0,616	0,93	0,994
	5712	4,2	60,2%	4,9	131,4 %	1,17	0,997	2,9	79,6%	0,69	0,996	1,69	0,993	200,2	98,3%	47,67	0,532	67,3	33,9 %	0,34	0,672	13,73	0,747	113,8	11,1%	0,57	0,798	39,24	0,707	0,59	0,859
	6013	480,8	11,4%	358,8	61,3%	0,75	0,527	478,8	63,2%	1,00	0,994	0,75	0,611	162,4	18,5%	0,34	0,311	165	26,2 %	1,02	0,993	0,46	0,317	155,5	15,0%	0,96	0,984	0,32	0,273	1,06	0,971
	6101	1971	32,3%	406,4	25,3%	0,21	0,000	600,6	55,8%	0,30	0,000	0,68	0,411	592,7	46,6%	0,30	0,000	334,8	57,1 %	0,56	0,412	0,82	0,711	324,4	82,4%	0,55	0,429	0,54	0,349	1,03	0,968
	6206	2375,5	31,9%	3561,9	12,7%	1,50	0,000	3073,5	34,9%	1,29	0,010	1,16	0,040	2671,8	27,1%	1,12	0,345	5358,8	17,9 %	2,01	0,000	1,50	0,000	4333,9	35,9%	1,62	0,000	1,41	0	1,24	0,000
	6220	758,3	42,7%	1755,1	8,3%	2,31	0,000	2085	52,9%	2,75	0,000	0,84	0,164	3094,9	58,9%	4,08	0,000	835	30,2 %	0,27	0,000	0,48	0,000	1112,1	7,3%	0,36	0,000	0,53	0,001	0,75	0,291
	6413	1087,3	30,2%	440	13,9%	0,40	0,001	422,8	31,5%	0,39	0,014	1,04	0,942	466,3	13,1%	0,43	0,050	202,1	33,2 %	0,43	0,400	0,46	0,220	459,3	30,5%	0,98	0,983	1,09	0,901	0,44	0,327
	6419	2018,5	30,3%	933,1	31,8%	0,46	0,000	1021,4	43,2%	0,51	0,000	0,91	0,708	793,5	34,8%	0,39	0,000	277	12,8 %	0,35	0,102	0,30	0,001	291	36,0%	0,37	0,140	0,28	0,015	0,95	0,957
	6708	363,7	26,7%	308,1	37,3%	0,85	0,773	206,5	34,3%	0,57	0,554	1,49	0,666	101,2	61,3%	0,28	0,403	32,3	38,1 %	0,32	0,826	0,10	0,156	69,7	72,0%	0,69	0,926	0,34	0,642	0,46	0,886
	6709	414,7	17,4%	127,2	22,5%	0,31	0,138	107,5	40,9%	0,26	0,248	1,18	0,934	79	62,8%	0,19	0,285	3,6	22,5 %	0,05	0,810	0,03	0,523	3	20,6%	0,04	0,822	0,03	0,723	1,20	0,998
	7004	438,2	30,9%	765,8	19,5%	1,75	0,091	1326,9	25,2%	3,03	0,001	0,58	0,019	2813,6	19,9%	6,42	0,000	2294,2	28,5 %	0,82	0,100	3,00	0,000	2601,9	12,0%	0,92	0,532	1,96	0	0,88	0,241
	7106	589,5	18,4%	581,3	33,8%	0,99	0,966	974,6	7,3%	1,65	0,148	0,60	0,097	1922,8	23,2%	3,26	0,000	1229,7	18,1 %	0,64	0,029	2,12	0,001	1316,3	20,5%	0,68	0,075	1,35	0,247	0,93	0,741
	7109	965,4	9,3%	435,3	17,6%	0,45	0,007	765,3	22,7%	0,79	0,451	0,57	0,163	609,5	32,3%	0,63	0,258	227,8	9,2%	0,37	0,225	0,52	0,284	305,2	44,8%	0,50	0,370	0,4	0,12	0,75	0,767
	7113	2068	3,4%	1890,8	13,4%	0,91	0,358	1536,6	7,7%	0,74	0,047	1,23	0,135	1035,6	32,0%	0,50	0,001	885,7	25,4 %	0,86	0,633	0,47	0,000	783,9	4,0%	0,76	0,458	0,51	0,012	1,13	0,697
	7202	525	28,6%	799,4	19,1%	1,52	0,156	689,8	33,7%	1,31	0,534	1,16	0,642	1097,3	22,3%	2,09	0,070	829,9	41,9 %	0,76	0,395	1,04	0,875	579,7	67,3%	0,53	0,128	0,84	0,708	1,43	0,340
	7212	748,4	32,4%	1040,3	44,1%	1,39	0,132	1360,2	8,3%	1,82	0,023	0,76	0,177	2014,6	32,9%	2,69	0,000	1421,7	22,2 %	0,71	0,061	1,37	0,051	934,9	25,8%	0,46	0,002	0,69	0,151	1,52	0,065
	7301	171,5	40,4%	583,8	6,8%	3,40	0,034	691,2	44,0%	4,03	0,052	0,84	0,649	1223,3	13,2%	7,13	0,001	1380,9	13,7 %	1,13	0,616	2,37	0,000	1502,6	19,4%	1,23	0,410	2,17	0,007	0,92	0,642

	7302	406,5	55,6%	1076,7	23,1%	2,65	0,001	1334,4	21,8%	3,28	0,001	0,81	0,276	1159,2	18,6%	2,85	0,018	1583,4	20,9%	1,37	0,178	1,47	0,010	1134,5	32,3%	0,98	0,942	0,85	0,497	1,40	0,088
	7308	674,6	20,0%	279,5	22,1%	0,41	0,042	424	35,1%	0,63	0,346	0,66	0,540	219,1	41,7%	0,32	0,148	168,5	50,4%	0,77	0,872	0,60	0,566	127,8	19,5%	0,58	0,787	0,3	0,315	1,32	0,876
	7511	174	38,8%	56,6	121,7%	0,33	0,543	63,6	18,0%	0,37	0,677	0,89	0,976	46,6	77,7%	0,27	0,684	9,8	62,8%	0,21	0,907	0,17	0,809	7,9	47,3%	0,17	0,909	0,12	0,85	1,24	0,994
	7609	220	34,0%	123,8	44,2%	0,56	0,618	98,8	20,3%	0,45	0,648	1,25	0,916	77,5	51,5%	0,35	0,650	19,6	14,5%	0,25	0,854	0,16	0,590	32,7	19,6%	0,42	0,895	0,33	0,822	0,60	0,960
	7702	1619,9	18,9%	921,7	0,7%	0,57	0,000	835,8	33,3%	0,52	0,004	1,10	0,715	515,9	51,5%	0,32	0,001	69,2	81,3%	0,13	0,157	0,08	0,000	68,4	80,7%	0,13	0,188	0,08	0,01	1,01	0,998
	7704	318,9	28,9%	266	16,6%	0,83	0,784	293	26,7%	0,92	0,922	0,91	0,909	85	46,9%	0,27	0,456	31,4	61,4%	0,37	0,864	0,12	0,226	58,2	69,9%	0,68	0,937	0,2	0,426	0,54	0,918
	7707	581,2	15,8%	233,5	20,1%	0,40	0,073	190,8	22,2%	0,33	0,143	1,22	0,856	175,2	55,8%	0,30	0,197	55,6	69,9%	0,32	0,703	0,24	0,358	103,1	26,2%	0,59	0,831	0,54	0,766	0,54	0,856
	7709	543,4	7,6%	164,2	8,4%	0,30	0,051	138,3	26,7%	0,25	0,129	1,19	0,913	175,4	36,4%	0,32	0,242	172,9	63,9%	0,99	0,994	1,05	0,964	146,2	10,8%	0,83	0,931	1,06	0,979	1,18	0,919
	7716	553,8	14,9%	219,8	27,7%	0,40	0,106	236,6	42,8%	0,43	0,094	0,93	0,940	157,4	29,2%	0,28	0,019	59	22,9%	0,37	0,600	0,27	0,471	80,7	52,3%	0,51	0,592	0,34	0,353	0,73	0,898
	7727	177,8	41,4%	79	46,8%	0,44	0,631	70	46,5%	0,39	0,567	1,13	0,967	58,2	28,2%	0,33	0,474	29,1	14,2%	0,50	0,877	0,37	0,823	38,3	23,7%	0,66	0,889	0,55	0,85	0,76	0,956
	7812	464,4	11,0%	457,3	30,2%	0,98	0,972	757,8	28,2%	1,63	0,121	0,60	0,177	69,1	61,0%	0,15	0,019	165,6	92,5%	2,40	0,607	0,36	0,192	94,3	71,6%	1,36	0,860	0,12	0	1,76	0,672
	8004	1575	32,0%	1072,3	72,6%	0,68	0,016	747,4	74,1%	0,47	0,000	1,43	0,145	604	14,8%	0,38	0,000	527,7	23,9%	0,87	0,684	0,49	0,016	428,8	9,1%	0,71	0,222	0,57	0,059	1,23	0,558
	8005	719,8	56,1%	979,2	64,5%	1,36	0,208	1487,3	27,4%	2,07	0,000	0,66	0,024	493	91,7%	0,68	0,176	710,1	42,8%	1,44	0,249	0,73	0,228	430,3	35,7%	0,87	0,661	0,29	0	1,65	0,099
	8006	784,1	24,7%	963,1	65,0%	1,23	0,384	1015,1	68,7%	1,29	0,221	0,95	0,814	1168,9	24,5%	1,49	0,023	536,6	21,4%	0,46	0,001	0,56	0,058	583,6	7,0%	0,50	0,000	0,57	0,011	0,92	0,780
	8122	1295,4	29,5%	1672,9	14,2%	1,29	0,068	1192,3	23,6%	0,92	0,584	1,40	0,032	494,6	15,3%	0,38	0,000	1300,7	28,7%	2,63	0,000	0,78	0,097	875,4	39,5%	1,77	0,009	0,73	0,061	1,49	0,013
	8127	290,3	42,2%	486,6	50,2%	1,68	0,340	572,5	13,8%	1,97	0,135	0,85	0,698	737,1	19,1%	2,54	0,008	1241,1	14,9%	1,68	0,008	2,55	0,001	974,4	16,0%	1,32	0,099	1,7	0,018	1,27	0,116
	8128	192,9	45,2%	310,5	57,2%	1,61	0,567	467,2	63,4%	2,42	0,147	0,66	0,480	527,2	18,2%	2,73	0,047	621,6	19,2%	1,18	0,615	2,00	0,164	485,2	24,4%	0,92	0,769	1,04	0,914	1,28	0,419
	8131	15,5	114,2%	116,4	48,2%	7,51	0,623	286,8	51,6%	18,50	0,151	0,41	0,443	204,1	39,9%	13,17	0,259	465,7	14,5%	2,28	0,165	4,00	0,119	351,1	4,2%	1,72	0,305	1,22	0,701	1,33	0,497
	8305	1139,5	14,6%	587,9	32,1%	0,52	0,008	791,7	7,5%	0,69	0,067	0,74	0,359	559,4	50,1%	0,49	0,001	455,9	24,4%	0,81	0,581	0,78	0,553	411,4	6,4%	0,74	0,302	0,52	0,025	1,11	0,792
	8306	3398,5	8,4%	2535,7	16,8%	0,75	0,000	2726,7	15,7%	0,80	0,001	0,93	0,390	1479,3	32,4%	0,44	0,000	1492,9	42,0%	1,01	0,942	0,59	0,000	1785,6	24,1%	1,21	0,034	0,65	0	0,84	0,085
	8307	222,2	17,3%	567,8	32,4%	2,56	0,094	761,6	14,6%	3,43	0,005	0,75	0,383	990,4	30,0%	4,46	0,000	995,1	48,6%	1,00	0,980	1,75	0,057	1259,9	17,9%	1,27	0,062	1,65	0,004	0,79	0,118
	8310	950,1	13,1%	413,8	17,1%	0,44	0,010	432,5	9,2%	0,46	0,007	0,96	0,933	136,5	78,5%	0,14	0,000	115,5	73,6%	0,85	0,911	0,28	0,182	130,4	24,7%	0,96	0,966	0,3	0,073	0,89	0,930
	8311	354	14,1%	295,7	26,5%	0,84	0,776	434,6	9,2%	1,23	0,668	0,68	0,531	208,8	52,7%	0,59	0,385	175,3	79,3%	0,84	0,858	0,59	0,589	94,3	45,8%	0,45	0,424	0,22	0,044	1,86	0,631
	8401	1087,7	10,2%	840,9	30,0%	0,77	0,231	949,8	21,7%	0,87	0,464	0,89	0,623	451,2	45,6%	0,41	0,000	365,9	40,3%	0,81	0,650	0,44	0,035	434,2	22,0%	0,96	0,905	0,46	0,003	0,84	0,685
	8405	810,7	3,6%	354,4	14,0%	0,44	0,028	369,2	6,6%	0,46	0,021	0,96	0,946	223,1	64,1%	0,28	0,001	146,5	50,7%	0,66	0,683	0,41	0,351	99,2	9,3%	0,44	0,387	0,27	0,109	1,48	0,779
	8510	1312,6	3,5%	888	2,3%	0,68	0,041	829	23,5%	0,63	0,011	1,07	0,790	1929,7	19,7%	1,47	0,000	1746,6	19,6%	0,91	0,330	1,97	0,000	1830,7	7,0%	0,95	0,489	2,21	0	0,95	0,618
	8511	1348,3	30,2%	898,3	21,9%	0,67	0,030	824,1	28,0%	0,61	0,006	1,09	0,738	10,6	41,8%	0,01	0,000	4	81,8%	0,38	0,972	0,00	0,000	34,6	71,0%	3,26	0,867	0,04	0	0,12	0,856
	8520	695,3	34,9%	493,5	34,9%	0,71	0,327	276,6	38,9%	0,40	0,028	1,78	0,329	6,1	62,0%	0,01	0,000	6,1	106,8%	1,00	1,000	0,01	0,030	10,5	29,4%	1,72	0,975	0,04	0,114	0,58	0,979
	8521	334,3	3,5%	132,9	85,0%	0,40	0,328	56,2	71,3%	0,17	0,141	2,36	0,730	1,7	72,1%	0,01	0,048	1,9	71,0%	1,12	0,999	0,01	0,556	0,5	57,9%	0,29	0,993	0,01	0,739	3,80	0,994
	8524	361,2	17,4%	226,1	14,9%	0,63	0,511	290	22,9%	0,80	0,705	0,78	0,773	51,7	51,3%	0,14	0,066	62,8	111,3%	1,21	0,953	0,28	0,464	28,8	54,0%	0,56	0,872	0,1	0,121	2,18	0,840
	8528	325,8	13,2%	362,9	37,8%	1,11	0,857	356,6	11,3%	1,09	0,870	1,02	0,977	784,3	11,5%	2,41	0,007	768,3	69,6%	0,98	0,932	2,12	0,071	786,7	18,2%	1,00	0,987	2,21	0,011	0,98	0,913
	8529	536	30,8%	516,7	51,9%	0,96	0,925	435,3	27,1%	0,81	0,592	1,19	0,713	285,2	64,0%	0,53	0,134	652,6	62,7%	2,29	0,052	1,26	0,542	829,7	20,9%	2,91	0,000	1,91	0,02	0,79	0,294

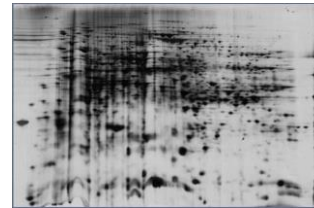
8604	492,9	25,5%	279,1	41,0%	0,57	0,299	263,1	16,0%	0,53	0,223	1,06	0,943	101,6	73,0%	0,21	0,021	71,1	77,9 %	0,70	0,871	0,25	0,351	77	19,1%	0,76	0,863	0,29	0,268	0,92	0,972
8611	61,3	23,1%	1207, 4	50,3%	19,70	0,010	927,6	47,4%	15,13	0,020	1,30	0,571	120,5	98,6%	1,97	0,864	257,7	69,9 %	2,14	0,720	0,21	0,044	1718,1	54,3%	14,26	0,002	1,85	0,12	0,15	0,003
8615	258	16,1%	139,1	67,6%	0,54	0,785	37,9	63,7%	0,15	0,548	3,67	0,838	767,2	84,2%	2,97	0,142	2,7	109,5 %	0,00	0,048	0,02	0,769	12,9	79,1%	0,02	0,126	0,34	0,96	0,21	0,983
8702	782	7,8%	200,8	6,4%	0,26	0,184	140,9	38,4%	0,18	0,083	1,43	0,903	299,4	36,9%	0,38	0,164	188,6	50,7 %	0,63	0,772	0,94	0,979	170,5	19,1%	0,57	0,792	1,21	0,953	1,11	0,970
8707	1070, 8	15,1%	374,3	37,9%	0,35	0,112	675,1	27,9%	0,63	0,281	0,55	0,543	254,6	91,0%	0,24	0,020	275	65,8 %	1,08	0,957	0,73	0,831	392,2	11,0%	1,54	0,779	0,58	0,575	0,70	0,806
8711	137,4	32,2%	153,3	29,1%	1,12	0,971	124,7	29,5%	0,91	0,972	1,23	0,954	4,1	54,7%	0,03	0,699	3,6	12,6 %	0,88	0,999	0,02	0,748	2,4	34,3%	0,59	0,047	0,02	0,809	1,50	0,998
9012	3507, 9	20,8%	3457	29,7%	0,99	0,907	3586,4	28,9%	1,02	0,830	0,96	0,793	6545, 5	6,7%	1,87	0,000	2218, 7	28,5 %	0,34	0,000	0,64	0,009	2607,1	25,4%	0,40	0,000	0,73	0,055	0,85	0,416
9013	1454, 1	15,1%	1673, 5	53,0%	1,15	0,614	2157,2	29,3%	1,48	0,057	0,78	0,328	2047, 4	29,3%	1,41	0,088	717,3	39,3 %	0,35	0,001	0,43	0,042	912,1	17,2%	0,45	0,023	0,42	0,015	0,79	0,683
9103	639,8	34,7%	3304, 7	74,9%	5,17	0,000	3232,8	42,6%	5,05	0,000	1,02	0,884	1437, 3	54,8%	2,25	0,023	3794, 4	44,9 %	2,64	0,000	1,15	0,294	5956	46,9%	4,14	0,000	1,84	0	0,64	0,000
9108	3072, 9	13,1%	2031	12,0%	0,66	0,019	2168,4	30,1%	0,71	0,015	0,94	0,781	7,9	83,4%	0,00	0,000	1,4	152,9 %	0,18	0,986	0,00	0,000	20,9	97,3%	2,65	0,979	0,01	0	0,07	0,967
9109	436,8	72,4%	460,7	35,1%	1,05	0,956	1032,1	18,8%	2,36	0,107	0,45	0,249	146,7	18,1%	0,34	0,401	244,1	18,1 %	1,66	0,799	0,53	0,642	373,1	82,9%	2,54	0,644	0,36	0,194	0,65	0,787
9206	1857, 9	23,9%	604,7	47,1%	0,33	0,005	663	37,4%	0,36	0,002	0,91	0,906	1540, 9	24,3%	0,83	0,359	699,4	26,2 %	0,45	0,030	1,16	0,839	1104	4,3%	0,72	0,373	1,67	0,383	0,63	0,397
9211	1216, 3	12,0%	834	3,1%	0,69	0,381	894,9	15,2%	0,74	0,381	0,93	0,902	574,7	32,4%	0,47	0,066	476,9	19,0 %	0,83	0,798	0,57	0,444	576,6	23,0%	1,00	0,997	0,64	0,529	0,83	0,835
9213	1243, 1	20,4%	835,2	13,7%	0,67	0,350	814,4	2,9%	0,66	0,243	1,03	0,966	609	38,2%	0,49	0,069	525,4	27,6 %	0,86	0,827	0,63	0,506	561,3	28,1%	0,92	0,922	0,69	0,616	0,94	0,940
9214	1331, 9	20,8%	724,1	3,0%	0,54	0,165	687,5	14,5%	0,52	0,081	1,05	0,941	504,5	5,0%	0,38	0,018	361,6	31,1 %	0,72	0,709	0,50	0,437	392,1	16,8%	0,78	0,819	0,57	0,559	0,92	0,949
9216	2054, 6	13,4%	1421, 5	11,3%	0,69	0,148	1875,4	23,4%	0,91	0,000	0,76	0,359	985,2	31,9%	0,48	0,003	730,5	21,6 %	0,74	0,505	0,51	0,140	763,7	12,2%	0,78	0,651	0,41	0,03	0,96	0,944
9217	1419, 3	10,6%	650	38,3%	0,46	0,080	802,7	30,1%	0,57	0,095	0,81	0,757	703	86,0%	0,50	0,040	400,2	85,0 %	0,57	0,429	0,62	0,592	527,6	48,4%	0,75	0,720	0,66	0,586	0,76	0,789
9308	2360, 6	23,1%	782,5	27,9%	0,33	0,000	1270,8	18,1%	0,54	0,004	0,62	0,324	1237, 4	52,9%	0,52	0,002	884,8	56,3 %	0,72	0,357	1,13	0,826	1196,4	8,8%	0,97	0,933	0,94	0,883	0,74	0,514
9701	1620, 1	32,2%	346,5	38,7%	0,21	0,004	173,5	25,0%	0,11	0,000	2,00	0,726	1933, 1	71,7%	1,19	0,365	316,7	70,8 %	0,16	0,000	0,91	0,949	459,9	96,4%	0,24	0,003	2,65	0,571	0,69	0,764
9801	2486, 4	25,7%	3285, 9	11,7%	1,32	0,069	3187	32,1%	1,28	0,058	1,03	0,841	40,4	59,1%	0,02	0,000	110,7	93,3 %	2,74	0,854	0,03	0,000	97,8	85,8%	2,42	0,907	0,03	0	1,13	0,978
9802	378,8	28,3%	595,2	42,5%	1,57	0,619	701,2	44,6%	1,85	0,379	0,85	0,830	13,6	77,4%	0,04	0,291	29,7	61,0 %	2,18	0,967	0,05	0,226	19,8	84,3%	1,46	0,990	0,03	0,179	1,50	0,983



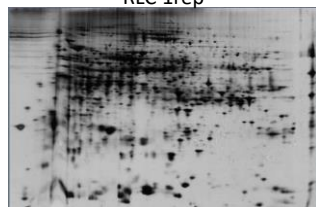
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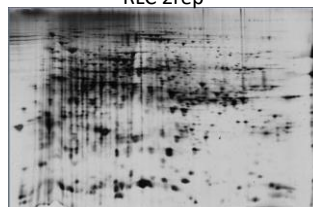
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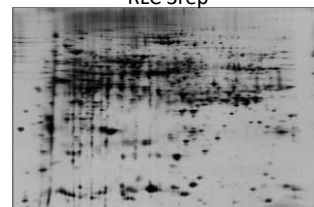
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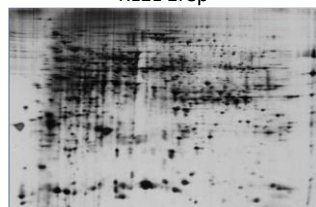
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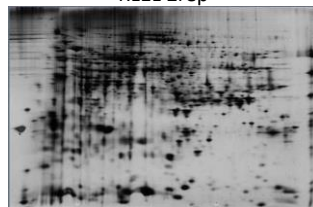
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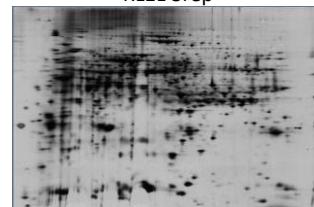
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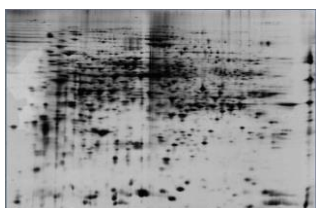
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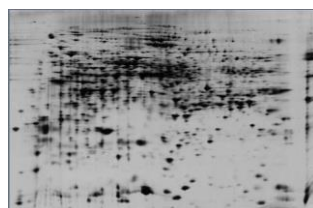
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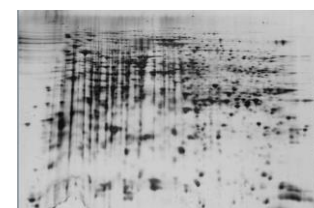
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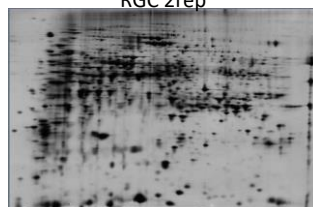
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RGC 3rep



RG1L 1rep



RG1L 2rep



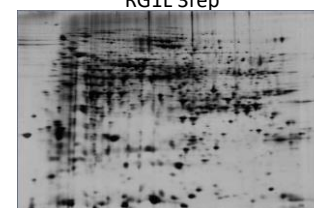
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RG101F 1rep



RG101F 1rep

Figure S2. Full-length gels of peach fruit proteins of ‘Rich Lady’ control fruits (RLC), ‘Rich Lady’ fruits inoculated with *M. laxa* (RL1L) and *M. fructicola* (RL101F), ‘Royal Glory’ control fruits (RGC), ‘Royal Glory’ fruits inoculated with *M. laxa* (RGL) and *M. fructicola* (RGF) of which zoomed in views of selected areas are presented in Figure 2.