

REVIEW

Proteomics in the fruit tree science arena: New insights into fruit defense, development, and ripening

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Fruit tree crops are agricultural commodities of high economic importance, while fruits also represent one of the most vital components of the human diet. Therefore, a great effort has been made to understand the molecular mechanisms covering fundamental biological processes in fruit tree physiology and fruit biology. Thanks to the development of cutting-edge “omics” technologies such as proteomic analysis, scientists now have powerful tools to support traditional fruit tree research. Such proteomic analyses are establishing high-density 2DE reference maps and peptide mass fingerprint databases that can lead fruit science into a new postgenomic research era. Here, an overview of the application of proteomics in key aspects of fruit tree physiology as well as in fruit biology, including defense responses to abiotic and biotic stress factors, is presented. A panoramic view of ripening-related proteins is also discussed, as an example of proteomic application in fruit science.

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1 Introduction

Perennial fruit trees are subjected to a variety of both abiotic and biotic stress conditions throughout the year [1]. In addition, the fruits of fruit trees are one of the most vital groups of plant tissues playing a key role in human nutrition [2]. Moreover, fruit tree tissues, including leaves, roots, and fruits, comprise one of the most complex fields in plant physiology. Hence, application of state-of-the-art technologies is needed in order to meet the grand challenges posed in

fruit science. The current development of high-throughput technologies for analyzing genome structure and function is starting to have an important impact on fruit research. For example, the whole genomes of two fruit crop species (peach and apple) that belong to different genera of the Rosaceae family, have been recently sequenced [3], thus allowing in-depth molecular studies in *Prunus* and *Malus* species in the so-called postgenomics era. During the last years, the technique of proteome analysis, mainly using 2D-PAGE and MS, has dramatically changed the experimental approaches by which complex biological systems can be characterized [4]. Constraints in the estimation of gene expression levels, mRNA degradation or inefficient translation, gene alternative splicing, as well as protein PTMs, processing and protein turnover, make the application of proteomics an essential tool in plant science [5], especially in the case of nonmodel plants, such as fruit trees [6]. The application of more reliable protein extraction methods for fruit tissues, combined with the

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Abbreviations: 1-MCP, 1-methylcyclopropene; ABA, abscisic acid; BABA, β -aminobutyric acid; CI, chilling injury; DiGE, difference in-gel electrophoresis; HT, heat treatment; OA, oxalic acid; PR, pathogen resistance; RNS, reactive nitrogen species; SA, salicylic acid; SOD, superoxide dismutase; TCA, tricarboxylic acid cycle

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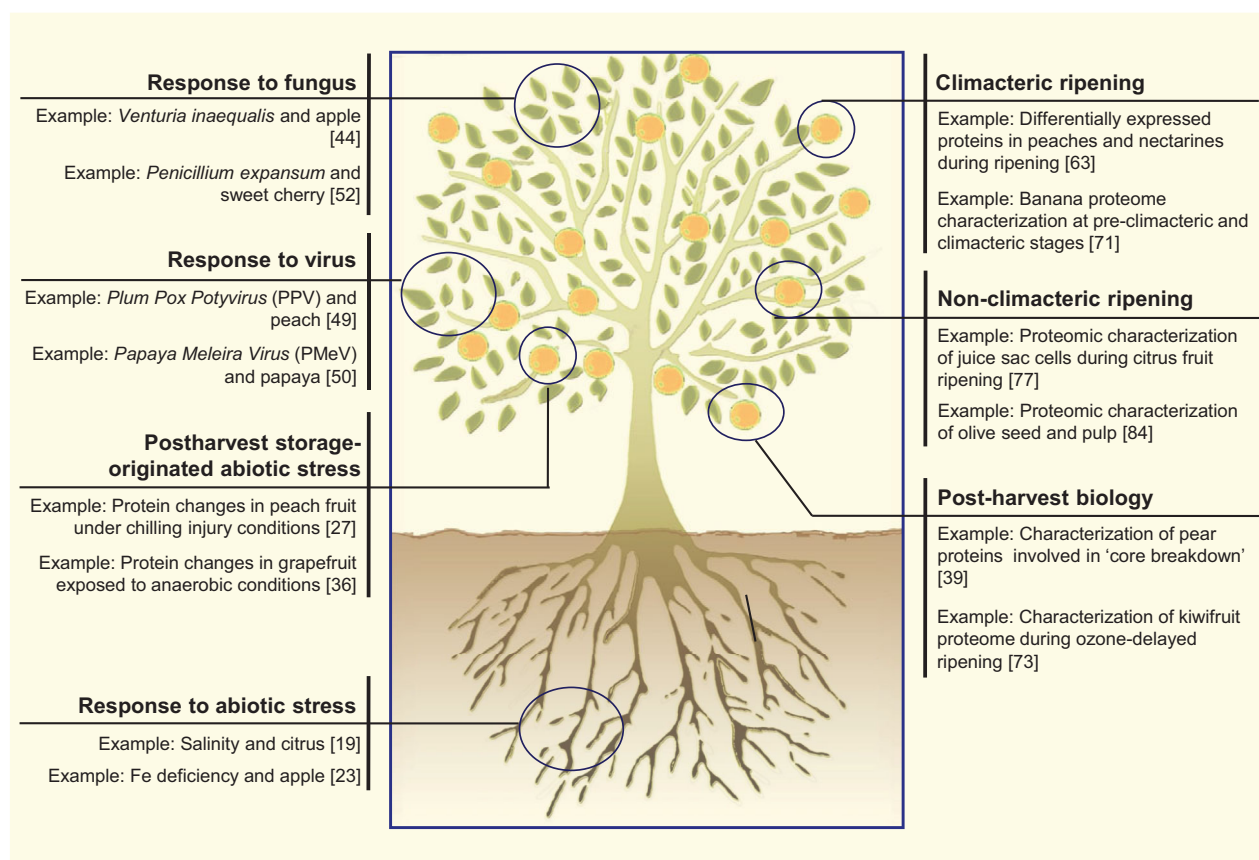


Figure 1. A brief overview of the key physiological processes examined by proteomic approaches in fruit trees, showing their respective target organs and experimental systems (discussed in greater detail in the text).

contribution of EST databases and the new revised approaches (iTRAQ, DIGE, immunoblotting, differential MS plus SC, etc.) together with the advances in MS-based proteomics and the availability of powerful search engines provide key tools for large-scale comparative proteomic analyses in fruit tree species [7]. On this basis, this review focuses on the present knowledge and future potential use of global protein analysis in fruit trees. In particular, proteome changes are discussed in fruit tree tissues (leaves, roots, and fruits) in response to (a)biotic stress factors as well as with specific changes in fruits during ripening and storage. Specific examples which will be discussed in the text are indicated in Fig. 1.

2 Proteome analysis in fruit trees exposed to abiotic stress conditions

Abiotic stresses are major factors causing extensive agricultural losses to crop production worldwide [8]. In response to stressful environmental conditions, plants adapt various molecular strategies, most of which are preceded by specific protein changes whose biological functions are linked to acclimation process [9]. In addition, postharvest treatments

of fruits, such as cold storage and anaerobic conditions, often lead to abiotic stress situations. Therefore, recent improvements in proteomics comprise an efficient approach for screening stress-related proteins or identifying proteins involved in stress acclimation [10]. Proteomic analysis has been widely used to investigate plant responses to various environmental stimuli [11]; however, proteomic approaches have emerged only recently to study abiotic stress physiology in fruit trees. An up-to-date overview of the proteomic work in leaves and roots of fruit trees during environmental challenges, as well as in fruits upon specific abiotic stress conditions and physiological disorders during storage, is presented.

2.1 Proteome changes in leaves and roots of fruit trees during abiotic stress

Salt-induced modifications in protein accumulation patterns are well documented [12], but plant acclimation to salinity is an extremely complex process that involves a network of various molecular components and signaling cascades. To evaluate the impact of salt stress on fruit tree physiology, De Abreu et al. [13] studied protein pattern in leaves and

roots of salt-stressed cashew (cashew nut and cashew apple) seedlings. In leaves, the accumulation of 75 proteins was regulated by salt stress, with 35 of them increasing in abundance, while three were apparently de novo synthesized. In comparison, abundance levels of 69 proteins were also changed by salt stress in roots, with 34 proteins showing an increase in abundance and two proteins being detected only in stressed seedlings. Moreover, citrus plants are the most extensively studied fruit trees species utilizing proteomics [14–17]. A comprehensive proteomic analysis by Tanou et al. [18] disclosed 85 leaf proteins that underwent significant quantitative variations in salt-stressed sour orange plants (*Citrus aurantium* L.), while PTMs patterns, such as oxidation (carbonylation; 40 proteins) and *S*-nitrosylation (49 proteins) of leaf proteins were specifically determined in salinity-stressed citrus plants. In addition, pretreatment of citrus plants with H₂O₂ or sodium nitroprusside, a nitric oxide donor, alleviated salinity-induced protein carbonylation and shifted the accumulation levels of leaf *S*-nitrosylated proteins to those of unstressed control plants [18]. Furthermore, latest findings by Tanou and colleagues [19] established the physiological and molecular network of H₂O₂- or sodium nitroprusside-induced acclimation to salinity stress and provided further evidence that ROS and reactive nitrogen species (RNS) mediated PTMs are a key molecular strategy for signal transduction and salinity acclimation. In addition, the specific study identified a number of potential carbonylated, nitrated, and nitrosylated proteins with distinct or overlapping signatures in roots and leaves of citrus plants.

Water stress is one of the most common abiotic factors that may limit fruit crop productivity, as fruit trees are frequently exposed to varying levels of soil water. A proteomic approach carried out by Macarasin et al. [20] regarding the responses of crabapple (*Malus pumila*) to water deficit attempted to determine the ability of β -aminobutyric acid (BABA), an elicitor of plant defense against biotic stresses [21], and abscisic acid (ABA), a phytohormone that plays a key role in regulating stomatal movements in response to water stress [22], to induce drought acclimation. In this work, difference in-gel electrophoresis (DiGE) analysis quantified changes in protein abundance in leaf tissue exposed to BABA or ABA during drought stress. Some proteins showed almost identical patterns of induction or suppression in both BABA- and ABA-treated seedlings, supporting the concept that BABA-induced abiotic stress tolerance is achieved by potentiating an ABA-regulated pathway, while others were regulated only in BABA-treated plants, indicating that BABA may also mediate drought acclimation through ABA-independent pathways. Based on the putative function of the identified proteins, changes in cell wall enzymes and a suppression of lignin biosynthesis were considered to play a specific role in BABA-derived drought acclimation [20]. Meanwhile, a few studies exist at a proteome level focusing on mineral nutrition of fruit trees, such as the report by Wang et al. [23] who attempted to identify Fe stress-responsive proteins in roots of *Malus xiaojinensis*, an Fe-efficient apple species. More than 700 protein

spots were reproducibly detected and several Fe deficiency-related proteins were identified, many of which were involved in regulation of carbohydrate and energy metabolism, defense/stress response, and membrane transport.

Overall, the employment of proteomic approaches has emerged as a useful tool to identify potential biomarkers in the tissues of fruit trees that could be used to assist conventional breeding for stress-tolerant fruit tree cultivars, while deciphering the modus operandi of abiotic stress-derived signaling pathways and suggesting novel mechanisms regulating the plant's response to environmental challenges. For example, a recent study by Tanou and colleagues [19] identified malate dehydrogenase and glutathione-*S*-transferase as common targets for ROS/RNS-based PTMs in leaves and roots of citrus plants during H₂O₂- and nitric oxide-mediated acclimation to salinity stress, thus supporting the proposed cross-talk between ROS and RNS signaling in plants [24].

2.2 Proteome changes in fruits exposed to postharvest storage-associated stressful conditions

Cold storage is one of the most frequently employed methods for extending the shelf-life of fruits; however, prolonged cold storage of fruits such as peaches can trigger a physiological disorder known as chilling injury (CI), which negatively affects fruit quality [25]. Therefore, proteomics strategies have been used to study the response of peach fruit to CI. Zhang et al. [26] compared the proteome of peach fruit cv. "Hongtao" stored at 0 and 5°C and reported that some proteins related to membrane stability and phenolic metabolism were involved in CI tolerance. In a similar study, Nilo et al. [27] screened for differentially accumulated proteins in peach fruit cv. "O'Henry" during normal softening and under CI conditions. Several proteins that are related to stress response, cellular homeostasis and organization, and carbohydrate metabolism were detected as being differentially accumulated; in addition, proteins such as endopolygalacturonase, catalase, NADP-dependent isocitrate dehydrogenase, pectin methylesterase, and dehydrins were linked to CI [27]. In a more recent study, Giraldo et al. [28] reported proteomic data on differentially accumulated proteins between non cold- and cold-storage nectarine fruits (*Prunus persica* (L.) Batsch, var. *nectarine*, cv. "Venus") and confirmed the 2DE-PAGE results with qRT-PCR analysis. Abundance of four allergen proteins (Pru du 1.06A, Pru p1.05, Pru p 2.01B, and Pru p 2.01A) increased in cold storage nectarine fruit that exhibited CI symptoms, whereas genes encoding these allergen proteins were also upregulated in cold-treated fruits.

Different postharvest treatments have been applied to peach fruits in order to tolerate CI, including exposure to sublethal high temperature heat treatment (HT) following harvest. Using 2D-DIGE analysis, Lara et al. [29] demonstrated that the induction of proteins involved in stress response, including HSPs, allergen proteins, and dehydrin, along

with the repression of polyphenol oxidase by HT (39°C for 3 days), may constitute the molecular basis for protection of peach cv. “Dixiland” fruit against CI. In search of potential targets of HT, Zhang et al. [30] focused on characterizing proteins modulated by HT (48°C for 10 min) in peach fruit cv. “Huiyulu” during ripening. This work proposed that HT activates ascorbate-glutathione cycle, lowers ROS content caused by ripening, and subsequently affects ions (Cu^{2+} and Fe^{2+}) transport, cell wall structure, defense, and HSP abundance through ROS signaling. More recently, 2DE analysis in apoplastic proteins of peach fruit (cv. “Dixiland”) during softening and following HT (39°C for 3 days) revealed a decrease in DUF642 proteins after HT and an increase in glyceraldehyde-3-phosphate dehydrogenase during ripening [31]. The presence of GAPC in the peach extracellular matrix was further confirmed by in situ immunolocalization and transient accumulation in tomato fruit. These results indicated that proteins secreted by classical and noncanonical secretion pathways are involved in cell wall changes during ripening in peach fruit [31].

Proteomics were also carried out in mitochondria of apple fruits (cv. ‘Fuji’) at young (following harvest) or senescence stages (following 30 days at room temperature), as well as in fruits exposed to low oxygen (to alleviate oxidative stress) or to high oxygen (to induce oxidative stress) [32]. This study reported that mitochondrial proteins involved in tricarboxylic acid cycle (TCA) cycle, electron transport chain, carbon metabolism, and stress response were modulated by fruit senescence. In addition, treatments with low and high oxygen concentrations demonstrated the involvement of oxidative syndromes in fruit senescence and led to further identification of high oxygen-related proteins, such as mitochondrial Mn-superoxide dismutase (SOD) [32].

The growing interest in citrus proteomics produces an increasing numbers of studies on postharvest citrus fruit biology following cold storage [25]. Indeed, Yun et al. [33] carried out a proteomic study in “Egan No.1” ponkan (*Citrus reticulata* cv. “Egan No.1”) at different postharvest time points following low temperature storage at 4°C. Results showed that 74 proteins were differentially regulated that are predicted to be involved in C-compounds and carbohydrate metabolism, amino acid metabolism, and response to cold storage. It has been also proposed that fruits resist biotic stress during postharvest storage by regulating internal oxidation potential through changes of plastid-lipid-associated family proteins, GSTs, and aldo-keto reductases. Based on digital gene expression profiling and 2DE analysis, the same group also investigated gene and protein expression changes in Hirado Buntan Pummelo (*Citrus grandis* × *C. paradisi*) fruit under storage at 8–10°C [34]. During cold storage, chitinase, cysteine synthase, cysteine protease inhibitor, allyl alcohol dehydrogenase, and mitochondrial aldehyde dehydrogenase showed increased abundance. In addition, calcineurin B-like protein–CBL interacting protein kinase complexes might also be involved in low temperature signal transduction. Perotti et al. [35] identified proteomic changes in Valencia oranges

(*Citrus sinensis* cv. ‘Valencia late’) subjected to HT (48 h at 37°C) before storage at 5°C. Twenty eight proteins were modulated by HT that classified as cell rescue, defense, and storage proteins [35]. Meanwhile, exposure of citrus fruits and especially mandarins to anaerobic conditions results in induction of anaerobic respiration and accumulation of flavor volatiles ethanol and acetaldehyde. Shi et al. [36] evaluated the impact of anaerobic conditions, induced by exposure to N_2 atmospheres for 24 h, on the proteome of flavedo and juice vesicle in “Star Ruby” grapefruit (*Citrus paradisi* Macf.) and “Murcott” mandarins (*Citrus reticulata* Blanco), which differ in their tolerance to anaerobic conditions. Anaerobic responsive proteins mainly corresponded to stress-related proteins in the peel tissue, whereas the anaerobic proteins found in juice vesicles were associated with energy, cell rescue and defense, cell cycle, and protein fate. Furthermore, anaerobic treatment had minor impact on protein signatures in grapefruit juice vesicle but remarkably affected protein accumulation in mandarins, including induction of glycolytic enzymes, alcohol dehydrogenase, HSP, and ascorbate peroxidase [36].

Pear, which is the third most important fruit produced in temperate regions, has been extensively studied by Bart Nicolai and colleagues, who carried out proteomic analyses in pear fruit (*Pyrus communis* cv. “Conference”) in order to elucidate the “core breakdown” phenomenon, a significant physiological disorder during storage that is characterized by internal browning. Initially, a proteomic approach was conducted in order to compare protein accumulation in healthy, sound (intact tissue of pears with core breakdown), and brown tissue of stored pears [37]. This report demonstrated that proteins associated with energy metabolism (e.g. triosephosphate isomerase, NAD-dependent malate dehydrogenase, and fumarase) and antioxidant system (e.g. ascorbate peroxidase, monodehydroascorbate reductase, superoxide dismutase) were involved in “core breakdown”. In a later work, Pedreschi et al. [38] studied the pear fruit proteome at different controlled atmosphere conditions and found that triosephosphate isomerase, 1-aminocyclopropane-1-carboxylic acid oxidase and major allergen Pycr 1 were highly dependent on the oxygen and carbon dioxide concentrations. These specific proteins have been proposed to be actively involved in the physiological effects of controlled atmosphere storage on pear browning. Finally, Pedreschi et al. [39] reported that short-term exposure of pear slices to anoxia increased accumulation of transketolase and polygalacturonase inhibiting protein and decreased accumulation of several isoforms of the major allergen Pycr (pathogen resistance (PR) proteins), providing evidence for the involvement of these enzymes in “core breakdown” development. Meanwhile, in order to understand the mechanism of fruit coloring in *P. communis*, the proteomic pattern of bagged and normal pear cv. “Placer” fruit skin were compared [40]. Proteins involved in photosynthesis, signal transduction, energy pathway, protein folding and assembly, carbohydrate and acidity metabolisms as well as anthocyanin-related-like and phytochrome B-like proteins increased in abundance in bagged fruit skins, indicating that

these proteins are possibly involved in pear fruit coloration and quality [40].

3 Proteome analysis in fruit trees exposed to biotic stress conditions

An understanding of how plants and pathogens recognize each other is crucial for exploring the defense mechanisms of fruit trees. Proteomics have been successfully used to study plant–pathogen interactions [41], since several pathogenic proteins (e.g. proteases, cellulases, pectate lyases) detected in bacteria, fungi, and nematodes, are crucial in plant colonization [42]. However, proteomic studies of plant–pathogen interactions face intrinsic difficulties because, by definition, the plant–pathogen interaction is a highly complex biological system [43]. To address how leaves and fruit of fruit trees react to biotic stresses, the potential contribution of proteomics in plant–pathogen interaction is presented.

3.1 Proteome changes in leaves of fruit trees during biotic stress

In order to gain information for the interaction between *Malus domestica* and the biotrophic fungus *Venturia inaequalis*, Gau et al. [44] analyzed the protein composition of the apoplastic fluid of sterile grown apple leaves prior to or after infection by the fungus *V. inaequalis*, the causal agent of apple scab. This study identified β -1,3-glucanase, chitinase, thaumatin-like protein and a cysteine-like protease in *M. domestica* leaves infected by *V. inaequalis*, whereas an immunoblotting assay further confirmed the presence of some of these proteins. Also, the decrease in abundances of the nonspecific lipid transfer protein during the first week after infection with *V. inaequalis* points to a functional role of this protein in pathogen recognition and plant defense [44].

Until now, few studies have employed proteomic approaches to identify bacterial proteins involved in pathogenicity. Mehta and Rosato [45,46] reported the proteomic analysis of pathogenic bacteria *Xanthomonas axonopodis* pv. *citri* cultivated in the presence of host *C. sinensis* leaf extract. In another proteomic study, it was shown that *Xylella fastidiosa* (a causal agent of chlorosis) did not induce significant changes in HSP level when compared with *X. axonopodis* pv. *citri* [47], but constitutively expressed several stress-inducible proteins, such as HspA and the system GroEL/GroES, which were induced in *X. citri* under stress conditions. Therefore, the constitutive accumulation of these proteins may help *X. fastidiosa* to cope with sudden stressful conditions [42]. Moreover, proteomic study of *Pseudomonas savastanoi* pv. *Savastanoi*-infected olive trees (*Olea europaea*, cvs. “Galega” and “Cordovil de Serpa”) provided valuable information on the biotic-stress related host proteome, thus contributing to disease control [48]. Protein patterns between inoculated and noninoculated tissues uncovered differentially accumulated infection-related proteins.

In *O. europaea*, protein orthologs of enolase and calcium-dependent protein kinase were found to be differentially accumulated whereas outer membrane porin F (OprF), aconitate hydratase 2, unknown protein yt1R, and tellurium resistance (TerE) protein were putatively identified as bacterial proteins [48].

Regarding plant virus infection resistance mechanisms, Diaz-Vivancos et al. [49] investigated proteome changes within the leaf apoplast of *P. persica* cv. “GS305” on plum pox potyvirus infection. This experimental approach showed an induction of thaumatin-like protein as well as a decrease of mandelonitrile lyase in peach apoplast due to plum pox potyvirus infection. It is noted that most of the polypeptides were not identified in database searches, indicating that most of the functions of the apoplastic space remain unknown, at least in *Prunus* [49]. On the other hand, papaya (*Carica papaya* L.) hosts the only described laticifer-infecting virus (papaya meleira virus, PMeV), which is the causal agent of papaya sticky disease. Papaya was the first tropical fruit tree that had its genome sequenced and Rodrigues et al. [50] annotated the first 2DE reference map of papaya proteins to study the interaction between plants and papaya meleira virus. The authors conducted both 2DE/MALDI-TOF-MS/MS and DIGE/LC-IonTrap-MS/MS approaches in leaf samples from healthy and diseased papaya plants (cv “Golden”) grown under field conditions. The results indicated that defense proteins were stimulated and that proteins related to metabolism were induced in the diseased plant. Three proteins (calreticulin, the proteasome subunits and the 26S proteasome AAA-ATPase subunit RPT5a) were shown to increase in abundance during infection by both 2DE and DIGE analyses, indicating that these proteins could represent the first candidate markers for papaya sticky disease [50].

3.2 Proteome changes in fruits of fruit trees during biotic stress

Comparative analysis of sweet cherry (*Prunus avium* L. cv. “Hongdeng”) fruit proteome induced by SA, a phenolic phytohormone involved in plant defense against pathogens [51], at different maturity stages revealed that younger fruits exhibited stronger resistance against blue mold rot caused by *Penicillium expansum* after SA treatment [52]. Following SA treatment, 13 and 28 proteins were identified at earlier maturity stage (defined as yellow skin stage) and later maturity stage (defined as pale red skin stage), respectively. At both maturity stages, seven antioxidant enzymes and three pathogenesis related-proteins were identified, while five HSPs and four dehydrogenases were only detected at later maturity stage. Finally, several SA-responsive proteins were functionally characterized at later maturity stage as enzymes involved in glycolysis and tricarboxylic acid cycle (TCA).

Proteomic approaches have also been employed to study defense response in fruits treated with antagonistic yeast strains and chemical compounds, such as oxalic acid (OA),

which plays diverse roles, especially in PR [53], and SA. Tian et al. [54] found that antioxidant and PR proteins as well as enzymes associated with sugar metabolism, were involved in resistance of peach fruit induced by yeast antagonist *Pichia membranefaciens* and SA. Furthermore, induced resistance on peach fruit against blue mold rot caused by *P. expansum* and proteins induced by *P. membranefaciens* and SA were analyzed using a proteomics approach by Chan et al. [55]. This analysis documented that both antioxidant proteins and PR proteins are regulated by *P. membranefaciens* and SA. In addition, treatments with antagonist yeast and SA alter the metabolisms of glycolysis and TCA cycle [55]. Moreover, the mechanism by which OA increases jujube fruit resistance against blue mold caused by *P. expansum* was investigated using proteomics detecting increases in proteins related with defense/stress response by OA, thus contributing to the establishment of systemic resistance of jujube fruits against fungal pathogens [54].

From these observations, it is clear that proteomic techniques are and will be continuously employed to study plant–pathogen interaction networks and to characterize potential molecular markers of diseases. For example, proteomic analyses are being applied effectively for the identification of novel protein biomarkers of diseases such as brittle leaf disease in date palm trees, accomplishing high temporal resolution and even differentiating markers between stages of disease development [56]. Consequently, a deeper understanding of the mechanisms by which fruit trees resist pathogen infection or mount a successful defense response is vital in order to develop successful strategies aiming to minimize the negative effects of fruit tree diseases.

4 Proteomic analysis in fruit development, ripening, and postharvest life

Fruit ripening is a highly coordinated, genetically programmed, irreversible phenomenon involving a series of physiological and molecular changes that finally lead to the development of a soft edible ripe fruit with desirable quality attributes [57]. Fruits can be divided into two groups with contrasting ripening programs through a mechanism mainly related to the hormonal function of ethylene [58]. Climacteric fruit (e.g. apple, pear, peach, banana, kiwi), in which ripening is accompanied by a concomitant burst of ethylene and a peak in respiration, and nonclimacteric fruit (e.g. citrus, cherry, olive, strawberry) in which respiration shows no dramatic change and ethylene production remains at a very low level [59]. Fruit development and ripening are processes unique to plant species and, therefore, represent an opportunity for novel insights regarding plant developmental regulatory mechanisms [60]. It is only relatively recently that several proteomic approaches have been conducted in the ripening of woody fruit crops. Herein (and due to the large number of studies), we categorize proteomic analyses that

have been applied in climacteric and nonclimacteric fruit tree species. The differentially or commonly accumulated proteins during ripening in climacteric and nonclimacteric fruits and the corresponded functional categories will be also highlighted.

4.1 Proteomic analysis in fruits undergoing climacteric ripening

A number of proteomic studies on ripening have been recently conducted on fruit tree crops mainly using peach fruit as a climacteric model system. To get a global understanding in the role of ethylene in peach fruit ripening, Zhang et al. [61] identified differentially accumulated proteins in melting peach fruit (cv. “Huiyulu”) treated with 1-methylcyclopropene (1-MCP, a potent inhibitor of ethylene action) or 2-chloroethylphosphonic acid (ethephon, an ethylene-generating compound). It was shown that 1-MCP inhibits starch degradation and glycolytic pathway, 1-aminocyclopropane-1-carboxylic acid oxidase (a key regulatory enzyme involved in ethylene biosynthesis) and ABA stress ripening-like protein, while inducing chaperonin 60 and HSP, whereas ethephon induces ACO and ABA stress ripening-like protein and several cell structure-related proteins, such as tubulin and actin [61]. Meanwhile, mesocarp softening is an important event during ripening in peach melting varieties. In an effort to identify proteins regulated by ripening in peach, Prinsi et al. [62] studied the ripening mechanism of mesocarp from a nonmelting flesh (NMF; “Oro A”) and a melting flesh (MF; “Bolero”) peach cultivar, at “unripe” versus “ripe” stages, following the establishment of a suitable protein extraction procedure for peach mesocarp. The addition of phenol to the aqueous buffer combined with the use of freeze-dried powder significantly increased the protein yield and the quality of 2DE gels from peach mesocarp (eg. higher number of spots in the pI range between 3 and 6 and in the M_r range between 25 and 50 kDa). On the basis of these results, the subsequent proteomic analyses identified several enzymes associated with the primary metabolism and ethylene biosynthesis together with the identification of proteins involved in secondary metabolism and stress responses [62]. Interestingly, this study characterized differences in the ripening process between NMF and MF peach fruit. Few proteins involved in the maintenance of cellular integrity and functionality, such as HSPs, dehydrin, cinnamyl alcohol dehydrogenase, and putative histidine-containing phosphotransfer protein 3, were less abundant at “ripe” stage in MF than in NMF fruit [62]. To further understand peach fruit softening, the mesocarp of several melting type peaches (“Angelus”, “Elegant Lady”, “O’Henry”) and nectarines (“July Red” and “Spring Red”) were assessed during ripening [63]. Among the identified proteins, only 14 proteins changed in all the varieties analyzed, possibly indicating that *P. persica* commercial varieties have a narrow genetic background. These commonly

accumulated proteins are involved in carbohydrate and cell wall metabolism as well as in fruit senescence, and could be considered as potential molecular markers to discriminate between mature and soft *P. persica* fruit [63].

Together with mesocarp ripening, the peach endocarp development (e.g. degree of lignifications) plays a predominant role in the early stage of peach fruit development. To study protein changes in peach endocarp and mesocarp during early fruit development, Hu et al. [64] conducted a proteomic study using peach fruit tissues (endocarp and mesocarp) following different times after flowering. Sixty eight proteins with different patterns were identified in both the endocarp and mesocarp involved in primary or secondary metabolism, whereas the strong increase in abundance of pyruvate dehydrogenase was positively correlated with the exponentially growing lignin content in endocarp. The authors also showed that there is competition between lignin and flavonoid pathways when comparing endocarp and mesocarp tissues and observed an endocarp-specific oxidative stress that is linked with lignification and programmed cell death in endocarp [64]. On the other hand, ROS- and RNS-associated PTMs are gaining increasing recognition as regulators in a wide range of biological processes in the plant cell, affecting protein properties such as activity, structure stability, and localization [24, 65]. Although PTMs have been widely studied in various plant and mammalian systems, only a limited amount of data on PTMs in fruit research is available. A study by Qin et al. [66] served as first example to demonstrate how redox proteomics contributes to the characterization of fruit proteins targeted by oxidation (carbonylation). Using 2,4-dinitrophenylhydrazine antibodies in purified mitochondria of peach fruit at commercial harvest (defined as young) or exposed to room temperature for 12 days (defined as senescent), Qin et al. [66] identified several mitochondrial proteins, including outer membrane transporter (voltage-dependent anion-selective channel, VDAC), TCA cycle enzymes (malate dehydrogenase and aconitase), and antioxidant proteins (manganese superoxide dismutase–MnSOD) as oxidation targets. Oxidation of these proteins was paralleled by the loss of catalytic activity of antioxidant proteins and TCA enzymes, as well as alteration of VDAC function. These observations, together with treatments of peach fruit with low temperature storage (to retard senescence) or H_2O_2 (to induce senescence) demonstrated that oxidative damage of mitochondrial proteins may be responsible for impairment of mitochondrial function, leading to fruit senescence [66].

Apple (*M. domestica* Borkh) is one of the most widely consumed fleshy fruits; however, little work is available on apple fruit ripening at proteome level. The first systematic annotation of the apple fruit proteome was carried out in the pseudocarp of three accessions of cv. “Annurca”, an apple variety that is cultivated in southern Italy [67]. The identification of 44 protein spots from the reference apple map allowed the detection of the major accumulated proteins in “Annurca” at ripening stages that belong to carbon and nitrogen metabolism or energy production, stress/ripening, and

allergens. Moreover, it is generally accepted that fruit firmness constitutes an important textural property and is one of the crucial parameters for estimating apple fruit ripening. Therefore, Marondedze and Thomas [68] monitored protein profile in high and low firmness phenotypes from apple hypanthia of a “Golden Delicious” × “Dietrich” population. As expected, this study showed a lower accumulation of proteins involved in ethylene biosynthesis in the high firmness phenotype compared with low firmness phenotype. In addition, cytoskeleton-related proteins were induced in the high firmness phenotype, thus highlighting an important role for cytoskeleton in maintaining cell structure and, hence, fruit firmness. Furthermore, several proteins involved in ROS detoxification were identified in fruit hypanthium, confirming that ripening is tightly linked with oxidative stress conditions [68].

Papayas (*C. papaya* L.) are a commercially relevant crop, but their green life is very short, as a consequence of their rapid ethylene-associated pulp softening. Two comprehensive examples of proteomic analyses in papaya fruits undergoing ripening are the recent studies by Nogueira et al. [69] and Huerta-Ocampo et al. [70]. In the first study, comparative proteomic analysis in climacteric and preclimacteric stages of papaya fruit (cv. “Golden”) identified 27 proteins that were classified into carbohydrate metabolism, secondary metabolism, energy, stress responses, and storage proteins [69]. In the second study by Huerta-Ocampo et al. [70], papaya fruits (cv. “Maradol”) were harvested at a green-ripen maturity stage, treated with 1-MCP, and then allowed to ripen at room temperature. Twenty seven protein spots demonstrated differences in abundance during ripening whereas various proteins, such as cytochrome b5 (cytb5) and proteins related to ion channels regulation and cell turgor were regulated by 1-MCP application [70].

Banana (*Musa* spp.) is one of the most important food commodities after rice, wheat, and maize (FAO, <http://faostat.fao.org/>). Despite its importance, both as a food source and as a commercial crop, the proteome of banana was only recently characterized. Toledo et al. [71] identified banana proteins at preclimacteric and climacteric stages and showed that chitinases were the most abundant types of proteins in unripe bananas whereas pectate lyase, malate dehydrogenase, and starch phosphorylase were accumulated during ripening. Meanwhile, mango (*Mangifera indica* L.) is another highly perishable tropical fruit of notable economic and nutritional relevance. The characterization of mango fruit proteome during ripening was also recently reported by Andrade et al. [72]. The authors compare the proteomic changes between the preclimacteric and climacteric mango fruits (cv. “Keitt”) and found that the majority of mango proteins related to carbohydrate and energy metabolism and stress responses, including antioxidant enzymes. Interestingly, several other proteins related to fruit quality were also identified, such as proteins involved in color development (e.g. ripening-associated HSP and fibrillin) and pulp softening (e.g. chitinase, 14-3-3 protein) [72].

Kiwifruit is an economically important crop worldwide and also represents an attractive model for postharvest ripening, as it displays nonclimacteric behavior during cold storage and climacteric behavior during shelf-life ripening following cold storage [73]. The first draft of the kiwifruit (*Actinidia deliciosa* cv. “Hayward”) proteome during ozone-delayed ripening was recently reported by Minas et al. [73]. A number of proteins that are related to energy, protein metabolism, defense, cell structure, and amino acid or sugar/polysaccharide metabolism were identified. In addition, this report also revealed a set of candidate kiwifruit proteins that are sensitive to carbonylation with the use of oxy-blot analysis [73].

4.2 Proteomic analysis in fruits undergoing nonclimacteric ripening

Most of the available data on nonclimacteric fruit ripening in trees come from studies on citrus, a very important evergreen fruit crop in world trade. Eduardo Blumwald's group has been investigating the citrus fruit metabolism during ripening by using various proteomic approaches. Katz et al. [74] analyzed soluble and enriched membrane fractions of mature Navel orange (*C. sinensis* cv. “Washington”) to identify biosynthetic pathways acting in the last phase of citrus fruit development. It was shown that citric acid in ripen fruits can be utilized for the synthesis of amino acids and sugars. Interestingly, the presence of all of the enzymes associated with the glycolytic pathway suggests the capacity of the juice sac cell for energy production whereas the identification of a large number of proteins associated with protein trafficking suggests an extensive vesicle transport in mature juice sac cells. In a second paper by Katz et al. [75], broader analysis of citrus proteins has been tackled by label-free LC-MS/MS-based shot-gun proteomics workflow along with differential MS or spectral counting approaches. To overcome the bioinformatics limitations, due to the lack of orange databases, the authors created the iCitrus specific database (<http://citrus.bioinformatics.ucdavis.edu>) by merging three major sources of sequences (HarvEST:citrus, NCBI/citrus/unigenes, NCBI/citrus/proteins). Using this approach, Katz et al. [75] identified approximately 1500 citrus protein accessions recognized in fruits and quantified their accumulation changes at Stage I (cell division stage), Stage II (cell expansion stage), and Stage III (ripening or maturation stage). Such work on protein sequence databases of citrus has been complemented by adding next-generation sequencing transcriptome data in orange [76]. Finally, the use of label-free LC-MS/MS-based shot-gun proteomic and metabolic analysis has revealed that sucrose is also being synthesized in citrus juice sac cells during the later stage of fruit development [77].

Fruit color is an important factor influencing citrus quality and therefore several studies underlying the molecular mechanism of color development in citrus fruit have been

conducted. Muccilli et al. [78] investigated the differentially accumulated proteins of a pigmented sweet orange (*C. sinensis*, cv. “Moro”) in comparison with a common cultivar (cv. “Cadenera”) at ripening stage. Most of the proteins related to sugar metabolism were overaccumulated in “Moro”, while those related to stress responses were overaccumulated in “Cadenera”. The authors also noted that the abundance of secondary metabolism and oxidative stress-related proteins substantiated the important role of these proteins in anthocyanin biosynthesis in “Moro” [78]. Furthermore, Pan et al. [79] characterized protein changes in the sweet orange mutant cv. “Hong Anliu” with the striking phenotype of lycopene accumulation versus its wild-type at four maturing stages. Several antioxidant enzymes were affected by the mutation, linking the oxidative stress with the phenotype of lycopene accumulation [79]. In a complementary investigation by Pan et al. [80], a combined transcriptomic and proteomic analysis was performed to identify differential genes/proteins of a red-flesh sweet orange cv. “Cara Cara” in comparison with the common cultivar “Newhall” at ripening stages. Interpretation of the transcriptomic and proteomic data uncovered a number of candidate genes/proteins that were possibly involved in red flesh trait formation that could eventually facilitate genetic improvement of fruit quality in the future [80]. Moreover, to get a comprehensive understanding of fruit color development in citrus, more extensive mapping of proteins at the organelles level is essential. To this goal, Zeng et al. [81] applied a GeLC-MS/MS shotgun approach in chromoplasts purified from sweet orange. Following *in silico* sequence homology and functional analyses, 418 putative chromoplast proteins were identified participating in metabolism of carbohydrates, lipids, carotenoids and amino acids, protein regulation and transport, amino acid/protein synthesis, and secondary metabolism. In particular, hydroxymethylbutenyl 4-diphosphate synthase, plastid-lipid-associated protein, and plastid small heat shock proteins involved in synthesis/storage of carotenoid and in stress response were the most abundant proteins identified [81].

Olive (*O. europaea* L.) is an emblematic tree species and one of the most widespread and economically important fruit trees in the Mediterranean basin. However, extraction of proteins from the olive pulp is problematic because of its high content in interfering compounds (lipids and phenolic compounds) and due to the low amount of proteins. Thus, technical work aimed to improve protein extraction procedure in olive fruit has recently been developed greatly facilitating proteomic studies. Esteve et al. [82] proposed an ultra HPLC analytical methodology enabling the extraction of pulp proteins without interferences. Eight different methods were designed for the extraction of pulp proteins and evaluated by Esteve et al. [82]. The optimized extraction procedure consisted of a precleaning step followed by Tris/SDS/DTT extraction, protein precipitation with acetone, and final protein solubilization in a Tris-HCl buffer. Due to the lack of available olive protein sequences in databases for proteomic analysis, the same group used different protein database search

engines, such as SEQUEST and MASCOT, to assign fragmentation spectra and to characterize olive pulp proteins present in the only band appearing by 1DE-SDS-PAGE [83]. Thaumatin-like protein was the major protein present in this band whereas other low-abundant proteins, such as drought-induced protein SDi-6-like, acyl carrier protein, Cu/Zn and MnSOD, small HSP, and ATP-dependent protease subunit were identified [83]. More recently, Esteve et al. [84] established a method for protein isolation in olive fruit via combinatorial peptide ligand libraries and wide-characterized olive pulp and seed proteome. Thaumatin-like protein was detected as the most abundant protein in pulp, whereas seed storage proteins, oleosins, and histones were identified as the most abundant proteins in olive seed.

4.3 Commonly and differentially regulated proteins in fruits undergoing climacteric and nonclimacteric ripening

Based on the above-mentioned proteomic data concerning ripening, a global view of differentially regulated proteins in various climacteric and nonclimacteric fruit trees undergoing ripening is shown in Supporting Information Table 1. These ripening-related proteins were subsequently classified into functional categories, using gene classification resources proposed by Bevan et al. [85] and are presented in Fig. 2A. This analysis revealed that ripening-related proteins in climacteric fruits were mainly classified into the general categories of metabolism (23.3%), disease/defense (18.4%), energy (14.8%), and protein destination/storage (10.3%) (Fig. 2A, Supporting Information Table 1). An overrepresentation of proteins specifically involved in metabolism (23.6%), energy (11.3%), protein destination/storage (11.2%), and transporters (11.2%) was recorded in the nonclimacteric fruits experiencing ripening.

The Venn diagrams in Fig. 2B summarize the functional classification and the number of proteins that are targeted by climacteric and nonclimacteric type of ripening. Among the 223 proteins identified in climacteric fruit, 91 proteins were exclusively detected in this type of ripening. Furthermore, among the group of 636 proteins that targeted in nonclimacteric ripening fruits, 504 proteins were exclusively identified in nonclimacteric ripening fruits (Fig. 2B). Notably, this analysis also disclosed that a large number of proteins (132 proteins) were identified in both climacteric and nonclimacteric fruit species, suggesting that these types of ripening programs share commonly regulated pathways. The functional classification of the unique or overlapping set of proteins present in Fig. 2B was further examined (Fig. 2C). The largest categories of the specifically regulated proteins by climacteric ripening belong to metabolism (25.3%), followed by disease/defense (19.8%), energy (11.0%), and cell structure (11.0%). The group of proteins exclusively targeted by nonclimacteric ripening was largely represented by proteins involved in metabolism (24.0%), transporters (12.7%), energy

(9.7%), and protein destination/storage (9.7%). The common targets of the two programs of ripening included proteins involved in metabolism (22.0%), disease/defense (17.4%), and energy (17.4%) (Fig. 2C).

5 Future prospects: Fruitomics

Fruits serve as an important source of fiber, minerals, vitamins, and other beneficial compounds such as antioxidants of the human diet and therefore modern fruit research focuses on promoting nutritional and health-related compounds [2]. Thus, large-scale application of proteomics in combination with phenotypical and physiological data is a particularly promising approach for characterizing fruit quality traits and linking traits to specific protein hallmarks, thereby allowing the identification of biomarkers for future marker-assisted selection breeding programs aiming to ameliorate fruit quality. New mass spectrometric techniques are being deployed as analytical platforms for the assessment of health, sensory, quality, and safety aspects of food, including fruits [86]. Although proteomic strategies were successfully established for allergen detection, identification, and characterization in fruits [87], more detailed and comprehensive characterization of specific peptides with antioxidant properties and high-quality nutritious proteins in fruits is needed. Since numerous fruits are essential as food resources, there is also a great need for proteomic characterization in other fruit species.

Another aspect that should be taken into account is the application of proteomic-based fruit science knowledge on industry and medicine. For example, cysteine proteinases present in pineapple plant (*Ananas comosus* (L.) Merr.), including bromelain, ananain, comosain, are phytotherapeutic agents with anti-edematous, anti-inflammatory, anti-thrombotic, and fibrinolytic activities and Larocca et al. [88] identified proteolytic activities in pineapple fruit by means of direct MALDI-ToF MS analysis of the zymographic spots without the need for purification. An additional necessary and informative step in fruit science is the application of data gained from proteomic analyses to the practical setting of fruit tree cultivation strategies. For instance, a major challenge in the global proteomic view of plant–pathogen interactions is the development of new biomarkers for diagnosis and early detection of fruit disease as well as the development of new therapeutic options against various pathogens.

An important application of proteomics is the ability to study PTMs, which can affect the activity and binding of a protein and alter its role within the cell [89]. Accumulating evidence suggests that redox-based PTMs, such as S-nitrosylation and carbonylation, and possibly the crosstalk between them [65], regulate proteome remodeling during various physiological processes in fruits [17–19, 32, 66, 73]. Therefore, in order to get a comprehensive understanding of the physiological basis of PTMs in fruit science, more extensive proteome research in specific protein modifications

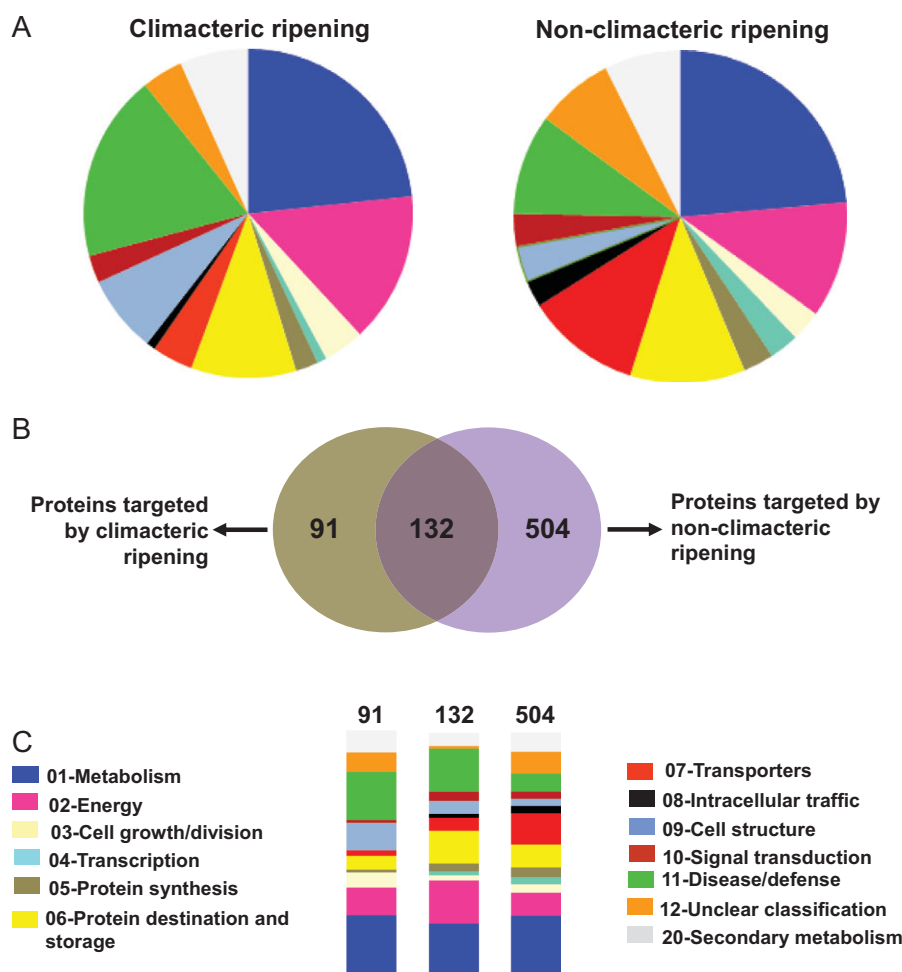


Figure 2. (A) Functional categories of the identified proteins that are differentially regulated in climacteric and nonclimacteric fruit trees during various ripening programs, as analytically presented in Supporting Information Table 1. The identified ripening-related proteins were classified into functional categories according to Bevan et al. [85]. The area for each category indicates the relative percentage (%) of proteins in that category. (B) Venn diagram analysis of the proteins identified in fruits undergoing climacteric and nonclimacteric type of ripening. The overlap as well as the specific proteins identified in the climacteric versus nonclimacteric fruits is shown. (C) Graphical representation of functional categories in each group of proteins is presented in Fig. 2B.

is required. Although 2DE has been widely used for fruit proteome analysis, it is now clear that fruit-derived proteomic analyses have to be further expanded by other gel-based or gel-free studies using alternative quantitative approaches (DIGE or iTRAQ, TMT, ICAT, etc. [90]), or integrated with complementary proteomic investigations describing PTMs mentioned above.

Finally, it should be emphasized that our understanding in fruit science can be greatly improved by the interconnection of proteomics with other -omics approaches, including metabolomics, transcriptomics, and genomics. Systems biology in fruit science, constructing a complex network of -omics data (FRUITOMICS), is expected to provide novel knowledge in understanding fruit biology. Although these high-throughput approaches have been widely studied in model plants, such as *Arabidopsis* [91] and tomato [92], the application of proteomics in combination with two or more of the “omics” concepts remains a challenge in fruit trees [93]. Given this lack of wide application of systems approaches in fruit research and the comparatively low number of fruit crops with their genomes completely sequenced, the em-

ployment of global scale -omics analysis is the key tool to understand the dynamic nature of fruit systems as a whole level.

6 Concluding remarks

Proteomics is emerging as an invaluable tool for deciphering a multitude of physiological and developmental functions in fruit trees, as well as for the identification of novel protein biomarkers involved. Ever improving proteomic technologies, along with the combined application of genomics and metabolomics, provide the means to increase our knowledge on fruit tree physiology. Thus, one of the major challenges in fruit science is posed by the interpretation of state-of-the-art studies in combination with phenotypic/physiological data, along with the conversion of large datasets into functional information, ultimately leading to the acquisition of new scientific fruit biology knowledge. Therefore, the employment of proteomics approaches in the study of fruit tree physiology

represents a very exciting and promising area of fundamental and applied research for several years to come.

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7 References

- [1] Wisniewski, M. E., Arora, R., in: Jain, M., Minocha, S. (Eds.), *Molecular Biology of Woody Plants*, Kluwer, Dordrecht 2000, Vol. 2, pp. 419–438.
- [2] Chong, M. F.-F., MacDonald, R., Lovegrove, J. A., Fruit polyphenols and CVD risk: a review of human intervention studies. *Br. J. Nutr.* 2010, 104, S28–S39.
- [3] Jung, S., Cestaro, A., Troggio, M., Main, D. et al., Whole genome comparisons of *Fragaria*, *Prunus* and *Malus* reveal different modes of evolution between Rosaceous subfamilies. *BMC Genom.* 2012, 13, 129.
- [4] Agrawal, G. K., Job, D., Zivy, M., Agrawal, V. P. et al., Time to articulate a vision for the future of plant proteomics—a global perspective: an initiative for establishing the international plant proteomics organization (INPPO). *Proteomics* 2011, 11, 1559–1568.
- [5] Renaut, J., Hausman, J.-F., Bassett, C., Artlip, T. et al., Quantitative proteomic analysis of short photoperiod and low-temperature responses in bark tissues of peach (*Prunus persica* L. Batsch). *Tree Genet. Genom.* 2008, 4, 589–600.
- [6] Carpentier, S. C., Panis, B., Vertommen, A., Swennen, R. et al., Proteome analysis of nonmodel plants: a challenging but powerful approach. *Mass Spectrom. Rev.* 2008, 27, 354–377.
- [7] Palma, J. M., Corpas, F. J., del Río, L. A., Proteomics as an approach to the understanding of the molecular physiology of fruit development and ripening. *J. Proteomics* 2011, 74, 1230–1243.
- [8] dos Reis, S. P., Lima, A. M., de Souza, C. R. B., Recent molecular advances on downstream plant responses to abiotic stress. *Int. J. Mol. Sci.* 2012, 13, 8628–8647.
- [9] Ndimba, B. K., Chivasa, S., Simon, W. J., Slabas, A. R., Identification of *Arabidopsis* salt and osmotic stress responsive proteins using two-dimensional difference gel electrophoresis and mass spectrometry. *Proteomics* 2005, 5, 4185–4196.
- [10] Marques, K., Sarazin, B., Chane-Favre, L., Zivy, M., Tiellmen, H., Comparative proteomics to establish genetic relationships in the *Brassicaceae* family. *Proteomics* 2001, 1, 1457–1462.
- [11] Kosová, K., Vítámvás, P., Prášil, I. T., Renaut, J., Plant proteome changes under abiotic stress—contribution of proteomics studies to understanding plant stress response. *J. Proteomics* 2011, 74, 1301–1322.
- [12] Sobhanian, H., Aghaei, K., Komatsu, S., Changes in the plant proteome resulting from salt stress: toward the creation of salt-tolerant crops? *J. Proteomics* 2011, 74, 1323–1337.
- [13] De Abreu, C. E. B., Prisco, J. T., Nogueira, A. R. C., Bezerra, M. A. et al., Physiological and biochemical changes occurring in dwarf-cashew seedlings subjected to salt stress. *Braz. J. Plant Physiol* 2008, 20, 105–118.
- [14] Maserti, B. E., Della Croce, C. M., Luro, F., Morillon, R. et al., A general method for the extraction of citrus leaf proteins and separation by 2D electrophoresis: a follow up. *J. Chromatogr. B Analyt. Technol. Biomed. Life Sci.* 2007, 849, 351–356.
- [15] Alos, E., Roca, M., Iglesias, D. J., Minguez-Mosquera, M. I. et al., An evaluation of the basis and consequences of a stay-green mutation in the navel negra citrus mutant using transcriptomic and proteomic profiling and metabolite analysis. *Plant Physiol* 2008, 147, 1300–1315.
- [16] Lliso, I., Tadeo, F. R., Phinney, B. S., Wilkerson, C. G. et al., Protein changes in the albedo of citrus fruits on postharvesting storage. *Phytochem. Anal.* 2008, 19, 104–115.
- [17] Tanou, G., Job, C., Belghazi, M., Molassiotis, A. et al., Proteomic signatures uncover hydrogen peroxide and nitric oxide cross-talk signaling network in citrus plants. *J. Proteome Res.* 2010, 9, 5994–6006.
- [18] Tanou, G., Job, C., Rajjou, L., Arc, E. et al., Proteomics reveals the overlapping roles of hydrogen peroxide and nitric oxide in the acclimation of citrus plants to salinity. *Plant J.* 2009, 60, 795–804.
- [19] Tanou, G., Filippou, P., Belghazi, M., Job, D. et al., Oxidative and nitrosative-based signaling and associated post-translational modifications orchestrate the acclimation of citrus plants to salinity stress. *Plant J.* 2012, 72, 585–599.
- [20] Macarasin, D., Wisniewski, M. E., Bassett, C., Thannhauser, T., Proteomic analysis of β -aminobutyric acid priming and abscisic acid—induction of drought resistance in crabapple (*Malus pumila*): effect on general metabolism, the phenylpropanoid pathway and cell wall enzymes. *Plant Cell Environ.* 2009, 32, 1612–1631.
- [21] Koehler, G., Wilson, R. C., Goodpaster, J. V., Sønsteby, A. et al., Proteomic study of low temperature responses in strawberry cultivars (*Fragaria x ananassa* Duchesne) that differ in cold tolerance. *Plant Physiol.* 2012, 159, 1787–1805.
- [22] Zimmerli, C., Ribot, C., Vavasseur, A., Bauer, H. et al., PHO1 expression in guard cells mediates the stomatal response to abscisic acid in *Arabidopsis*. *Plant J.* 2012, 72, 199–211.
- [23] Wang, J.-Y., Ruan, S.-L., Wu, W.-H., Xu, X.-F. et al., Proteomics approach to identify differentially expressed proteins induced by iron deficiency in roots of *Malus*. *Pak. J. Bot.* 2010, 42, 3055–3064.
- [24] Molassiotis, A., Fotopoulos, V., Oxidative and nitrosative signaling in plants: two branches in the same tree? *Plant Signal. Behav.* 2011, 6, 210–214.
- [25] Hertog, M. L. A. T. M., Rudell, D. R., Pedreschi, R., Schaffer, R. J. et al., Where systems biology meets postharvest. *Postharvest Biol. Tec.* 2011, 62, 223–237.
- [26] Zhang, C., Ding, Z., Xu, X., Wang, Q. et al., Crucial roles of membrane stability and its related proteins in the

- tolerance of peach fruit to chilling injury. *Amino Acids* 2010, 39, 181–194.
- [27] Nilo, R., Saffie, C., Lilley, K., Baeza-Yates, R. et al., Proteomic analysis of peach fruit mesocarp softening and chilling injury using difference gel electrophoresis (DIGE). *BMC Genom.* 2010, 11, 43.
- [28] Giraldo, E., Diaz, A., Corral, J. M., Garcia, A., Applicability of 2-DE to assess differences in the protein profile between cold storage and not cold storage in nectarine fruits. *J. Proteomics* 2012, 75, 5774–5782.
- [29] Lara, M. V., Borsani, J., Budde, C. O., Lauxmann, M. A. et al., Biochemical and proteomic analysis of “Dixiland” peach fruit (*Prunus persica*) upon heat treatment. *J. Exp. Bot.* 2009, 60, 4315–4333.
- [30] Zhang, L., Yu, Z., Jiang, L., Jiang, J. et al., Effect of post-harvest heat treatment on proteome change of peach fruit during ripening. *J. Proteomics* 2011, 74, 1135–1149.
- [31] Bustamante, C. A., Budde, C. O., Borsani, J., Lombardo, V. A. et al., Heat treatment of peach fruit: modifications in the extracellular compartment and identification of novel extracellular proteins. *Plant Physiol. Biochem* 2012, 60, 35–45.
- [32] Qin, G., Wang, Q., Liu, J., Li, B., Tian, S., Proteomic analysis of changes in mitochondrial protein expression during fruit senescence. *Proteomics* 2009, 9, 4241–4253.
- [33] Yun, Z., Li, W., Pan, Z., Xu, J. et al., Comparative proteomics analysis of differentially accumulated proteins in juice sacs of ponkan (*Citrus reticulata*) fruit during postharvest cold storage. *Postharvest Biol. Tec.* 2010, 56, 189–201.
- [34] Yun, Z., Jin, S., Ding, Y., Wang, Z. et al., Comparative transcriptomics and proteomics analysis of citrus fruit, to improve understanding of the effect of low temperature on maintaining fruit quality during lengthy post-harvest storage. *J. Exp. Bot.* 2012, 63, 2873–2893.
- [35] Perotti, V. E., Del Vecchio, H. A., Sansevich, A., Meier, G. et al., Proteomic, metabolomic, and biochemical analysis of heat treated Valencia oranges during storage. *Postharvest Biol. Tec.* 2011, 62, 97–114.
- [36] Shi, J. X., Chen, S., Gollop, N., Goren, R. et al., Effects of anaerobic stress on the proteome of citrus fruit. *Plant Sci.* 2008, 175, 478–486.
- [37] Pedreschi, R., Vanstreels, E., Carpentier, S., Hertog, M. et al., Proteomic analysis of core breakdown disorder in conference pears (*Pyrus communis* L.). *Proteomics* 2007, 7, 2083–2099.
- [38] Pedreschi, R., Hertog, M., Robben, J., Nobben, J. P., Nicolai, B., Proteomics to unravel the physiological implications of controlled atmosphere storage on conference pears (*Pyrus communis* L.). *Postharvest Biol. Technol.* 2008, 50, 110–116.
- [39] Pedreschi, R., Hertog, M., Robben, J., Lilley, K. et al., Gel-based proteomics approach to the study of metabolic changes in pear tissue during storage. *J. Agr. Food Chem.* 2009, 57, 6997–7004.
- [40] Feng, S., Chen, X., Zhang, Y., Wang, Y. et al., Differential expression of proteins in red pear following fruit bagging treatment. *Protein J.* 2011, 30, 194–200.
- [41] Rampitsch, C., Bykova, N. V., Proteomics and plant disease: advances in combating a major threat to the global food supply. *Proteomics* 2012, 12, 673–690.
- [42] Mehta, A., Brasileiro, A. C. M., Souza, D. S. L., Romano, E. et al., Plant-pathogen interactions: what is proteomics telling us? *FEBS J.* 2008, 275, 3731–3746.
- [43] Quirino, B. F., Candido, E. S., Campos, P. F., Franco, O. L. et al., Proteomic approaches to study plant–pathogen interactions. *Phytochemistry* 2010, 71, 351–362.
- [44] Gau, A. E., Koutb, M., Piotrowski, M., Kloppstech, K., Accumulation of pathogenesis-related proteins in the apoplast of a susceptible cultivar of apple (*Malus domestica* cv. Elstar) after infection by *Venturia inaequalis* and constitutive expression of PR genes in the resistant cultivar Remo. *Eur. J. Plant Pathol.* 2004, 110, 703–711.
- [45] Mehta, A., Rosato, Y. B., Differentially expressed proteins in the interaction of *Xanthomonas axonopodis* pv. *citri* with leaf extract of the host plant. *Proteomics* 2001, 1, 1111–1118.
- [46] Mehta, A., Rosato, Y. B., A simple method for in vivo expression studies of *Xanthomonas axonopodis* pv. *citri*. *Curr. Microbiol.* 2003, 47, 400–403.
- [47] Martins, D., Astua-Monge, G., Coletta-Filho, H. D., Winck, F. V. et al., Absence of classical heat shock response in the citrus pathogen *Xylella fastidiosa*. *Curr. Microbiol.* 2007, 54, 119–123.
- [48] Campos, A., da Costa, G., Coelho, A. V., Fevereiro, P., Identification of bacterial protein markers and enolase as a plant response protein in the infection of *Olea europaea* subsp. *europaea* by *Pseudomonas savastanoi* pv. *savastanoi*. *Eur. J. Plant Pathol.* 2009, 125, 603–616.
- [49] Diaz-Vivancos, P., Rubio, M., Mesonero, V., Periago, P. M. et al., The apoplastic antioxidant system in *Prunus*: response to long-term plum pox virus infection. *J. Exp. Bot.* 2006, 57, 3813–3824.
- [50] Rodrigues, S. P., Ventura, J. A., Aguilar, C., Nakayasu, E. S. et al., Proteomic analysis of papaya (*Carica papaya* L.) displaying typical sticky disease symptoms. *Proteomics* 2011, 11, 2592–2602.
- [51] Choi, S.-M., Song, H.-R., Han, S.-K., Han, M. et al., HDA19 is required for the repression of salicylic acid biosynthesis and salicylic acid-mediated defense responses in Arabidopsis. *Plant J.* 2012, 71, 135–146.
- [52] Chan, Z., Wang, Q., Xu, X., Meng, X. et al., Functions of defense-related proteins and dehydrogenases in resistance response induced by salicylic acid in sweet cherry fruits at different maturity stages. *Proteomics* 2008, 8, 4791–4807.
- [53] Liang Y., Strelkov S. E., Kav N. N. V., Oxalic acid-mediated stress responses in *Brassica napus* L. *Proteomics* 2009, 9, 3156–3173.
- [54] Tian, S., Qin, G., Chan, Z., Li, B. et al., Defense responses of different fruits induced by biotic and abiotic factors based on proteomic approach. *Abstracts Book of 6th International Postharvest symposium*, 8–12 April 2009, Antalya, Turkey, 123–132.
- [55] Chan, Z. L., Qin, G. Z., Xu, X. B., Li, B. Q. et al., Proteome approach to characterize proteins induced by antagonist yeast

- and salicylic acid in peach fruits. *J. Proteome Res.* 2007, *6*, 1677–1688.
- [56] Sghaier-Hammami, B., Saidi, M. N., Castillejo, M. A., Jorriño, J. V. et al., Proteomics analysis of date palm leaves affected at three characteristic stages of brittle leaf disease. *Planta* 2012, *236*, 1599–1613.
- [57] Bonghi, C. L., Manganaris, G. A., in: Benkeblia, N. (Ed.), *OMICS Technologies: Tools for Food Science*, CRC Press 2012, pp. 201–226.
- [58] Lee, J. M., Joung, J.-G., McQuinn, R., Chung, M.-Y. et al., Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor SIERF6 plays an important role in ripening and carotenoid accumulation. *Plant J.* 2011, *70*, 191–204.
- [59] Giovannoni, J. J., Molecular biology of fruit maturation and ripening. *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 2001, *52*, 725–749.
- [60] Qin, G., Wang, Y., Cao, B., Wang, W., Tian, S., Unraveling the regulatory network of the MADS box transcription factor RIN in fruit ripening. *Plant J.* 2012, *70*, 243–255.
- [61] Zhang, L., Jiang, L., Shi, Y., Luo, H. et al., Post-harvest 1-methylcyclopropene and ethephon treatments differently modify protein profiles of peach fruit during ripening. *Food Res. Int.* 2012, *48*, 609–619.
- [62] Prinsi, B., Negri, A. S., Fedeli, C., Morgutti, S. et al., Peach fruit ripening: a proteomic comparative analysis of the mesocarp of two cultivars with different flesh firmness at two ripening stages. *Phytochemistry* 2011, *72*, 1251–1262.
- [63] Nilo, R. P., Campos-Vargas, R., Orellana, A., Assessment of *Prunus persica* fruit softening using a proteomics approach. *J. Proteomics* 2012, *75*, 1618–1638.
- [64] Hu, H., Liu, Y., Shi, G.-L., Liu, Y.-P. et al., Proteomic analysis of peach endocarp and mesocarp during early fruit development. *Physiol. Plantarum* 2011, *142*, 390–406.
- [65] Lounifi, I., Arc, E., Molassiotis, A., Job, D. et al., Interplay between protein carbonylation and nitrosylation in plants. *Proteomics* 2013, *13*, 568–578.
- [66] Qin, G., Meng, X., Wang, Q., Tian, S., Oxidative damage of mitochondrial proteins contributes to fruit senescence: a redox proteomics analysis. *J. Proteome Res.* 2009, *8*, 2449–2462.
- [67] Guarino, C., Arena, S., De Simone, L., D'Ambrosio, C. et al., Proteomic analysis of the major soluble components in Annurca apple flesh. *Mol. Nutr. Food Res.* 2007, *51*, 255–262.
- [68] Marondedze, C., Thomas, L. A., Apple hypanthium firmness: new insights from comparative proteomics. *Appl. Biochem. Biotechnol.* 2012, *168*, 306–326.
- [69] Nogueira, S. B., Labate, C. A., Gozzo, F. C., Pilau, E. J. et al., Proteomic analysis of papaya fruit ripening using 2DE-DIGE. *J. Proteomics* 2012, *75*, 1428–1439.
- [70] Huerta-Ocampo, J. Á., Osuna-Castro, J. A., Lino-López, G. J., Barrera-Pacheco, A. et al., Proteomic analysis of differentially accumulated proteins during ripening and in response to 1-MCP in papaya fruit. *J. Proteomics* 2012, *75*, 2160–2169.
- [71] Toledo, T. T., Nogueira, S. B., Cordenunsi, B. R., Gozzo, F. C. et al., Proteomic analysis of banana fruit reveals proteins that are differentially accumulated during ripening. *Postharvest Biol. Tec.* 2012, *70*, 51–58.
- [72] Andrade, J. de M., Toledo, T. T., Nogueira, S. B., Cordenunsi, B. R. et al., 2D-DIGE analysis of mango (*Mangifera indica* L.) fruit reveals major proteomic changes associated with ripening. *J. Proteomics* 2012, *75*, 3331–3341.
- [73] Minas, I. S., Tanou, G., Belghazi, M., Job, D. et al., Physiological and proteomic approaches to address the active role of ozone in kiwifruit post-harvest ripening. *J. Exp. Bot.* 2012, *63*, 2449–2464.
- [74] Katz, E., Fon, M., Lee, Y., Phinney, B. et al., The citrus fruit proteome: insights into citrus fruit metabolism. *Planta* 2007, *226*, 989–1005.
- [75] Katz, E., Fon, M., Eigenheer, R. A., Phinney, B. S. et al., A label-free differential quantitative mass spectrometry method for the characterization and identification of protein changes during citrus fruit development. *Proteome Sci.* 2010, *8*, 68.
- [76] Song, J., Sun, R., Li, D., Tan, F. et al., An improvement of shotgun proteomics analysis by adding next-generation sequencing transcriptome data in orange. *PLoS ONE* 2012, *7*, e39494.
- [77] Katz, E., Boo, K.-H., Kim, H. Y., Eigenheer, R. A. et al., Label-free shotgun proteomics and metabolite analysis reveal a significant metabolic shift during citrus fruit development. *J. Exp. Bot.* 2011, *62*, 5367–5384.
- [78] Muccilli, V., Licciardello, C., Fontanini, D., Russo, M. P. et al., Proteome analysis of *Citrus sinensis* L. (Osbeck) flesh at ripening time. *J. Proteomics* 2009, *73*, 134–152.
- [79] Pan, Z., Liu, Q., Yun, Z., Guan, R. et al., Comparative proteomics of a lycopene-accumulating mutant reveals the important role of oxidative stress on carotenogenesis in sweet orange (*Citrus sinensis* [L.] osbeck). *Proteomics* 2009, *24*, 5455–5470.
- [80] Pan, Z., Zeng, Y., An, J., Ye, J. et al., An integrative analysis of transcriptome and proteome provides new insights into carotenoid biosynthesis and regulation in sweet orange fruits. *J. Proteomics* 2012, *75*, 2670–2684.
- [81] Zeng, Y., Pan, Z., Ding, Y., Zhu, A. et al., A proteomic analysis of the chromoplasts isolated from sweet orange fruits [*Citrus sinensis* (L.) Osbeck]. *J. Exp. Bot.* 2011, *62*, 5297–5309.
- [82] Esteve, C., Del Rio, C., Marina, M. L., Garcia, M. C., Development of an ultra-high performance liquid chromatography analytical methodology for the profiling of olive (*Olea europaea* L.) pulp proteins. *Anal. Chim. Acta* 2011, *690*, 129–134.
- [83] Esteve, C., Cañas, B., Moreno-Gordaliza, E., Del Rio, C. et al., Identification of olive (*Olea europaea*) pulp proteins by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and nano-liquid chromatography tandem mass spectrometry. *J. Agric. Food Chem.* 2011, *59*, 12093–12101.

- [84] Esteve, C., D'Amato, A., Marina, M. L., García, M. C. et al., Identification of olive (*Olea europaea*) seed and pulp proteins by nLC-MS/MS via combinatorial peptide ligand libraries. *J. Proteomics* 2012, 75, 2396–2403.
- [85] Bevan, M., Bancroft, I., Bent, E., Love, K. et al., Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thaliana*. *Nature* 1998, 39, 1485–1488.
- [86] Fay, L. B., Kussmann, M., Mass spectrometry in nutrition research. *RSC Food Analysis Monographs*, RSC Publishing, Norwich, UK 2010.
- [87] Marzban, G., Herndl, A., Maghuly, F., Katinger, H. et al., Mapping of fruit allergens by 2D electrophoresis and immunodetection. *Expert Rev. Proteomics* 2008, 5, 61–75.
- [88] Larocca, M., Rossano, R., Santamaria, M., Riccio, P., Analysis of pineapple [*Ananas comosus* (L.) Merr.] fruit proteinases by 2-D zymography and direct identification of the major zymographic spots by mass spectrometry. *Food Chem.* 2010, 123, 1334–1342.
- [89] Salekdeh, G. H., Komatsu, S., Crop proteomics: aim at sustainable agriculture of tomorrow. *Proteomics* 2007, 7, 2976–2996.
- [90] D'Ambrosio, C., Arena, S., Rocco, M., Verrillo, F. et al., Proteomic analysis of apricot fruit during ripening. *J. Proteomics* 2013, 78, 39–57.
- [91] Vanholme, R., Storme, V., Vanholme, B., Sundin, L. et al., A systems biology view of responses to lignin biosynthesis perturbations in *Arabidopsis*. *Plant Cell* 2012, 24, 3506–3529.
- [92] van de Poel, B., Bulens, I., Markoula, A., Hertog, M. L. A. T. M. et al., Targeted systems biology profiling of tomato fruit reveals coordination of the Yang cycle and a distinct regulation of ethylene biosynthesis during post-climacteric ripening. *Plant Physiol.* 2012, 160, 1498–151.
- [93] Yu, Z., Jin, S., Ding, Y., Wang, Z. et al., Comparative transcriptomics and proteomics analysis of citrus fruit, to improve understanding of the effect of low temperature on maintaining fruit quality during lengthy post-harvest storage. *J. Exp. Bot.* 2012, 63, 2873–2893.

Supplementary Table I (Molassiotis et al.)

Proteins differentially accumulated in climacteric and non-climacteric fruit of fruit tree species during various ripening conditions.

List of the proteins identified in Climacteric fruits

Legend:

Protein name, identified peptide names based on the corresponding reference cited and also on database search;

Functional category, proteins ontologically classified into functional categories proposed by of Bevan et al.;

Species, Fruit species used for protein extraction according to the corresponding reference cited;

Tissue/organelle, Localization was assigned based on the reference cited;

Reference,

Protein name	Functional category	Species	Reference
Climacteric Fruits			
(R)-mandelonitrile lyase	02.16-Energy/Fermentation	<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
1,4-alpha-glucan-protein synthase	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
14-3-3 family protein	10.04-Signal transduction/Mediators	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
20S Proteasome α subunit	06.13-Protein destination and storage/Proteolysis	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
20S Proteasome β subunit	06.13-Protein destination and storage/Proteolysis	<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149

		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
26S proteasome subunit	06.13-Protein destination and storage/Proteolysis	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
2-cys Peroxiredoxin	11.06-Disease/Defence/Detoxification	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
40S ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
60S ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
6-phosphogluconate dehydrogenase	02.07-Energy/Pentose phosphate	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Absciscic stress ripening protein	11.05-Disease/Defense/Stress responses	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
ACC oxidase	01.01-Metabolism/Amino acid	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116

		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Acidic chitinase	11.02-Disease/defense/Defense-related	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
Aconitase	02.10-Energy/TCA pathway	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
Actin	09.04-Cell structure/Cytoskeleton	<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Giraldo et al., Journal of Proteomics 75 (2012) 5774-5782
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149

		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Actin-depolymerizing factor	09.04-Cell structure/Cytoskeleton	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Actinidin	06.13-Protein destination and storage/Proteolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Acyl-[acyl-carrier-protein] desaturase	01.06-Metabolism/Lipid and sterol	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Acyl-CoA oxidase	01.06-Metabolism/Lipid and sterol	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Adenine nucleotide alpha hydrolases-like protein (F26k24.22 protein)	11.05-Disease/Defense/Stress responses	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Adenine phosphorybosyl transferase	01.03-Metabolism/Nucleotides	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Adenosine kinase	01.03-Metabolism/Nucleotides	<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
ADP-glucose pyrophosphorylase small subunit	01.05-Metabolism/Sugars and polysaccharides	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
ADP-ribosylation factor	10.04-Signal transduction/Mediators	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
ADP-ribosyltransferase	03.16-Cell growth/division/DNA synth/replication	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326

Agglutinin	03.26-Cell growth/division/Growth regulators	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Alanine aminotransferase	01.01-Metabolism/Amino acid	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Alcohol acyl transferase	01.06-Metabolism/Lipid and sterol	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Alcohol dehydrogenase	02.16-Energy/Fermentation	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Aldo/keto reductase	11.06-Disease/Defence/Detoxification	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
Aldolase	02.01-Energy/Glycolysis	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Alpha-1,4 glucan phosphorylase	01.05-Metabolism/Sugars and polysaccharides	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
Alpha-1,4-glucan-protein synthase	09.01-Cell structure/Cell wall	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Alpha-soluble NSF attachment protein	08.07-Intracellular traffic/Vesicular	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Aminobutyrate transaminase gamma	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
Amylase alpha	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194

		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Annexin	11.05-Disease/Defense/Stress responses	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Anthocyanidin reductase	20.99-Secondary metabolism/Other	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Anthocyanidin synthase	20.99-Secondary metabolism/Other	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Arg10	12-Unclear classification	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Ascorbate peroxidase	11.06-Disease/Defence/Detoxification	<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Aspartate aminotransferase	01.01-Metabolism/Amino acid	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Aspartate transaminase	01.01-Metabolism/Amino acid	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326

ATP synthase subunit α	07.22-Transporters/Transport ATPases	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
ATP synthase subunit β	07.22-Transporters/Transport ATPases	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406

ATP synthase subunit δ	07.22-Transporters/Transport ATPases	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
ATP synthase subunit E	07.22-Transporters/Transport ATPases	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
ATPase	07.22-Transporters/Transport ATPases	<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
AVBC007680 clone	12-Unclear classification	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Bet v 1 allergen protein	11.02-Disease/defense/Defense-related	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Beta-1,3-glucanase	01.05-Metabolism/Sugars and polysaccharides	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Beta-cyanoalanine synthase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Caffeoyl-CoA-O-methyltransferase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Calcineurin like protein	11.05-Disease/Defense/Stress responses	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Calmodulin	10.99-Signal Transduction/Others	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169

		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200
Catalase	11.06-Disease/Defence/Detoxification	<i>Prunus persica</i>	Giraldo et al., Journal of Proteomics 75 (2012) 5774-5782
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Cell division cycle protein 48	03.22-Cell growth/division/Cell cycle	<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Cell division inhibitor	03.22-Cell growth/division/Cell cycle	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Cell wall invertase	09.01-Cell structure/Cell wall	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
Chalcone isomerase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Chalcone synthase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Chaperonin 21	06.01-Protein destination and storage/Folding and stability	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Chaperonin 60	06.01-Protein destination and storage/Folding and stability	<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Chitinase	11.02-Disease/defense/Defense-related	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341

		<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Prunus persica</i>	Giraldo et al., Journal of Proteomics 75 (2012) 5774-5782
Chymopapain	06.13-Protein destination and storage/Proteolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Cinnamyl-alcohol dehydrogenase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Cobalamine-independent methionine synthase	02.10-Energy/TCA pathway	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Coproporphyrinogen oxidase	20.99-Secondary metabolism/Other	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Cpn10	06.01-Protein destination and storage/Folding and stability	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Cyanoalanine beta synthase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Cysteine protease	06.13-Protein destination and storage/Proteolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
Cysteine proteinase inhibitor	06.13-Protein destination and storage/Proteolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
Cysteine synthase	01.01-Metabolism/Amino acid	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
Cytochrome b	02.20-Energy/Electron-transport	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
Cytochrome c oxidase	02.20-Energy/Electron-transport	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262

Cytochrome c peroxidase	02.20-Energy/Electron-transport	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Dehydrin	11.05-Disease/Defense/Stress responses	<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
Dehydroascorbate reductase	11.06-Disease/Defence/Detoxification	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
Dienelactone hydrolase	20.99-Secondary metabolism/Other	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex	02.10-Energy/TCA pathway	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
Disulfide isomerase	06.01-Protein destination and storage/Folding and stability	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
DNA-damage-repair/toleration protein	03.19-Cell growth/division/Recombination/repair	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Dynein heavy chain isoform	09.04-Cell structure/Cytoskeleton	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326

Electron transfer flavoprotein-ubiquinone oxidoreductase	07.99-Transporters/Others	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Embryogenic potential marker	03.19-Cell growth/division/Recombination/repair	<i>Malus domestica</i>	Maronedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Endo-beta-1,4-glucanase	09.01-Cell structure/Cell wall	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Endochitinase	11.02-Disease/defense/Defense-related	<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
Endopolygalacturonase	09.01-Cell structure/Cell wall	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Endoxylanase	01.05-Metabolism/Sugars and polysaccharides	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
Enolase	02.01-Energy/Glycolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Enoyl-ACP reductase	01.06-Metabolism/Lipid and sterol	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Prunus persica</i>	Giraldo et al., Journal of Proteomics 75 (2012) 5774-5782
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262

Ethylene response sensor protein	10.99-Signal Transduction/Others	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Expansin	09.01-Cell structure/Cell wall	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
F13M22.16 Protein	12-Unclear classification	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
F3H7.1 protein	11.02-Disease/defense/Defense-related	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Ferredoxin-dependent glutamate synthase	01.01-Metabolism/Amino acid	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Ferredoxin-NADP (H) oxidoreductase	02.30-Energy/Photosynthesis	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Ferritin	06.20-Protein destination and storage/Storage proteins	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Fibrillin	11.05-Disease/Defense/Stress responses	<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
Flavanone 3-hydroxylase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Formate dehydrogenase	11.06-Disease/Defence/Detoxification	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Fructose-bisphosphate aldolase	02.01-Energy/Glycolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200

Fruit protein oxidoreductase NAD-binding	02.20-Energy/Electron-transport	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Galactose mutarotase	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Galactosidase alpha	01.05-Metabolism/Sugars and polysaccharides	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
Galactosidase beta	01.05-Metabolism/Sugars and polysaccharides	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
GcpE	20.2-Secondary metabolism/Terpenoids	<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
Glucanase putative	11.05-Disease/Defense/Stress responses	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Glucose-6-phosphate 1-dehydrogenase	02.07-Energy/Pentose phosphate	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Glutamate dehydrogenase	01.01-Metabolism/Amino acid	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Glutamine synthetase	01.01-Metabolism/Amino acid	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194

		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Glutathione reductase	11.06-Disease/Defence/Detoxification	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Glutathione S-transferase	11.06-Disease/Defence/Detoxification	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Glutathione-disulfide reductase	11.06-Disease/Defence/Detoxification	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Glyceraldehyde-3-phosphate dehydrogenase	02.01-Energy/Glycolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462

		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Glycine-rich RNA-binding protein	11.05-Disease/Defense/Stress responses	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
GTP-binding protein	08.07-Intracellular traffic/Vesicular	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Guanosine nucleotide diphosphate dissociation inhibitor	01.03-Metabolism/Nucleotides	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Histidine-containing phosphotransfer	11.05-Disease/Defense/Stress responses	<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Homocysteine S-methyltransferase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
HSP 70	06.01-Protein destination and storage/Folding and stability	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326

		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
HSP 90	06.01-Protein destination and storage/Folding and stability	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
HSP small	06.01-Protein destination and storage/Folding and stability	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200

		<i>Prunus persica</i>	Giraldo et al., Journal of Proteomics 75 (2012) 5774-5782
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Hydroperoxide Lyase	01.06-Metabolism/Lipid and sterol	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Hypersensitive induced reaction protein	11.02-Disease/defense/Defense-related	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
Invertase inhibitor	09.01-Cell structure/Cell wall	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Iron-binding protein	12-Unclear classification	<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Isocitrate dehydrogenase	02.10-Energy/TCA pathway	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194

Isoflavone reductase	20.99-Secondary metabolism/Other	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Ketol-acid reductoisomerase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Kiwellin	11.02-Disease/defense/Defense-related	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Lactoylglutathione lyase	20.99-Secondary metabolism/Other	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Leucine aminopeptidase	06.13-Protein destination and storage/Proteolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Leucoanthocyanidin dioxygenase	20.99-Secondary metabolism/Other	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Lipoxygenase	01.06-Metabolism/Lipid and sterol	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326

		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Lissencephaly type-1-like homology motif	09.04-Cell structure/Cytoskeleton	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Magnesium-chelatase subunit ch II	20.99-Secondary metabolism/Other	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Major allergen protein	11.02-Disease/defense/Defense-related	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Giraldo et al., Journal of Proteomics 75 (2012) 5774-5782
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Malate dehydrogenase	02.10-Energy/TCA pathway	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341

		<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
Maturase	04.22-Transcription/mRNA processing	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Methionine synthase	01.01-Metabolism/Amino acid	<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
Methylcrotonoyl-CoA carboxylase	01.01-Metabolism/Amino acid	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464

MLA7	11.06-Disease/Defence/Detoxification	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Monodehydroascorbate reductase	11.06-Disease/Defence/Detoxification	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
MyosinI heavy chain	09.04-Cell structure/Cytoskeleton	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
NAD(P)-binding Rossmann-fold superfamily protein	12-Unclear classification	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
NADH-ubiquinone dehydrogenase	02.20-Energy/Electron-transport	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
NADP-dependent isocitrate dehydrogenase	02.10-Energy/TCA pathway	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
NADP-dependent sorbitol-6-phosphate dehydrogenase	01.05-Metabolism/Sugars and polysaccharides	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
NADP-Malate dehydrogenase	02.01-Energy/Glycolysis	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462

		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
N-terminal nucleophile aminohydrolase	06.13-Protein destination and storage/Proteolysis	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Nucleoside disphosphate kinase	01.03-Metabolism/Nucleotides	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
Nudix hydrolase	12-Unclear classification	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Osmotin	11.05-Disease/Defense/Stress responses	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
Oxygen-evolving enhancer protein	02.30-Energy/Photosynthesis	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Pectate lyase	09.01-Cell structure/Cell wall	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
Pectinesterase	09.01-Cell structure/Cell wall	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
Pectinmethylesterase inhibitor	09.01-Cell structure/Cell wall	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464

Peptide methionine sulfoxide reductase	11.05-Disease/Defense/Stress responses	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
Peptidyl-prolyl cis-trans isomerase	06.01-Protein destination and storage/Folding and stability	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Peroxidase	11.06-Disease/Defence/Detoxification	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Peroxiredoxin	11.05-Disease/Defense/Stress responses	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Phosphatidylinositide phosphatase	12-Unclear classification	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Phosphoenolpyruvate carboxykinase	02.01-Energy/Glycolysis	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Phosphoglucomutase	02.01-Energy/Glycolysis	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Phosphoglycerate dehydrogenase	01.01-Metabolism/Amino acid	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Phosphoglycerate kinase	02.01-Energy/Glycolysis	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326

		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Phospholipase	01.06-Metabolism/Lipid and sterol	<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Phosphoribulokinase	02.30-Energy/Photosynthesis	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Phosphoserine aminotransferase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Photosystem II stability/assembly factor	02.30-Energy/Photosynthesis	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
Phytochrome kinase substrate	10.04-Signal Transduction/Mediators	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Plasma membrane intrinsic polypeptide	12-Unclear classification	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Plastid-lipid-associated protein	12-Unclear classification	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
P-loop containing nucleoside triphosphate hydrolase	01.03-Metabolism/Nucleotides	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Polygalacturonase inhibitor	11.02-Disease/defense/Defense-related	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Polyphenol oxidase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406

		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Porin	07.99-Transporters/Others	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Porphyromonas-type peptidyl-arginine deiminase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Processing peptidase	06.13-Protein destination and storage/Proteolysis	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
Profilin	09.04-Cell structure/Cytoskeleton	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
Pyruvate decarboxylase	02.01-Energy/Glycolysis	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Quinone oxidoreductase	02.20-Energy/Electron-transport	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464

		<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Malus domestica</i>	Qin et al., Proteomics 9 (2009) 4241-4253
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
RAD23 PROTEIN	03.19-Cell growth/division/Recombination/repair	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Ras-related protein	10.0410-Signal transduction/G proteins	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Reversibly glycosylated polypeptide	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Ribonuclease-like PR-10b	11.02-Disease/defense/Defense-related	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
Ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
Ripening-associated protein	11.05-Disease/Defense/Stress responses	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
RuBisCO large subunit	02.30-Energy/Photosynthesis	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200

		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
		<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
RuBisCO subunit-binding protein	06.01-Protein destination and storage/Folding and stability	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
S-Adenosyl-l-homocysteine hydrolase	01.01-Metabolism/Amino acid	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
S-adenosyl-L-methionine synthetase	01.01-Metabolism/Amino acid	<i>Musa acuminata (banana)</i>	Toledo et al., Postharvest Biology and Technology 70 (2012) 51–58
		<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Feng et al., Protein Journal 30 (2011) 194-200
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638

		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Serine hydroxymethyl transferase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Serine-rich protein	20.99-Secondary metabolism/Other	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Soluble inorganic pyrophosphatase	11.02-Disease/defense/Defense-related	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
Succinyl CoA ligase	02.10-Energy/TCA pathway	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Sucrose synthase	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Cu/Zn-Superoxide dismutase	11.06-Disease/Defence/Detoxification	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Mn-Superoxide dismutase	11.06-Disease/Defence/Detoxification	<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262

		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Synptobrevin-related protein	03.22-Cell growth/division/Cell cycle	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
T-complex protein	06.01-Protein destination and storage/Folding and stability	<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Temperature-induced lipocalin	07.99-Transporters/Others	<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
Thaumatococin	11.02-Disease/defense/Defense-related	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Prunus persica</i>	Zhang et al., Amino Acids 39 (2010) 181-194
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
Thioredoxin	11.05-Disease/Defense/Stress responses	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Transaldolase	02.07-Energy/Pentose phosphate	<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464

Translation initiation factor	05.04-Protein synthesis/Translation factors	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Lara et al., Journal of Experimental Botany 60 (2009) 4315–4333
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Translational elongation factor	05.04-Protein synthesis/Translation factors	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
Translationally controlled tumor protein	11.02-Disease/defense/Defense-related	<i>Carica papaya</i>	Huerta-Ocampo et al., Journal of Proteomics 75 (2012) 2160-2169
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262

		<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
Transposase	03.22-Cell growth/division/Cell cycle	<i>Malus domestica</i>	Marondedze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
Triosephosphate isomerase	02.01-Energy/Glycolysis	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Carica papaya</i>	Nogueira et al., Journal of Proteomics 75 (2012) 1428-1439
		<i>Malus domestica</i>	Guarino et al., Molecular Nutrition & Food Research 51 (2007) 255-262
		<i>Mangifera indica</i>	Andrade et al., Journal of Proteomics 75 (2012) 3331-3341
		<i>Pyrus communis</i>	Pedreschi et al., Postharvest Biology and Technology 50 (2008) 110–116
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Prunus persica</i>	Prinsi et al., Phytochemistry 72 (2011) 1251-1262
Tubulin alpha chain	09.04-Cell structure/Cytoskeleton	<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
		<i>Pyrus communis</i>	Pedreschi et al., Proteomics 7 (2007) 2083–2099
		<i>Pyrus communis</i>	Pedreschi et al., Journal of Agriculture and Food Chemistry 57 (2009) 6997-7004
		<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406

Ubiquitin-conjugating enzyme	06.13-Protein destination and storage/Proteolysis	<i>Prunus persica</i>	Zhang et al., Journal of Proteomics 74 (2011) 1135-1149
UDP-glucosyl transferase	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
UDP-glucuronate decarboxylase	01.05-Metabolism/Sugars and polysaccharides	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
UTP-glucose-1-phosphate uridylyltransferase	01.05-Metabolism/Sugars and polysaccharides	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
		<i>Malus domestica</i>	Maroneddze and Thomas, Applied Biochemistry and Biotechnology 168 (2012) 306-326
		<i>Prunus persica</i>	Nilo et al., BMC Genomics (2010) 11 art. no. 43
		<i>Prunus persica</i>	Nilo et al., Journal of Proteomics 75 (2012) 1618-1638
Voltage-dependent anion-selective channel	07.99-Transporters/Others	<i>Prunus persica</i>	Qin et al., Journal of Proteome Research 8 (2009) 2449–2462
Xyloglucan endotransglycosylase	09.01-Cell structure/Cell wall	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Xylose isomerase	01.05-Metabolism/Sugars and polysaccharides	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
Zinc metalloprotease	06.13-Protein destination and storage/Proteolysis	<i>Prunus persica</i>	Zhang et al., Food Research International 48 (2012) 609-619
β-cyanoalanine synthase	01.01-Metabolism/Amino acid	<i>Prunus persica</i>	Hu et al., Physiologia Plantarum 142 (2011) 390-406
Zinc finger protein	04.05.01.04-Transcription/transcriptional control	<i>Actinidia deliciosa</i>	Minas et al., Journal of Experimental Botany 63 (2012) 2449-2464
Non-Climacteric Fruits			
(S)-2-hydroxy-acid oxidase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
[acyl-carrier-protein] S-malonyltransferase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

1,4-alpha-glucan branching enzyme	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
1,4-benzoquinone reductase	04.32-Transcription/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
10-hydroxygeraniol oxidoreductase	20.2-Secondary metabolism/Terpenoids	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
14-3-3 family protein	10.04-Signal transduction/Mediators	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
1-deoxy-D-xylulose-5-phosphate reductoisomerase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
1-phosphatidylinositol phosphodiesterase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
2,3-biphosphoglycerate-independent phosphoglycerate mutase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
20 kDa chaperonin	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
20S Proteasome subunit	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
20S proteasome β subunit	06.13-Protein destination and storage/Proteolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
26S proteasome AAA-ATPase subunit	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
26S proteasome non-ATPase regulatory subunit	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

26S proteasome subunit	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
2-cys Peroxiredoxin	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
2-isopropylmalate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Dihydrolipoyllysine residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
30S ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
3-beta hydroxysteroid dehydrogenase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
3-dehydroquinate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
3-isopropylmalate dehydratase large subunit	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
3-isopropylmalate dehydratase small subunit	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
3-isopropylmalate dehydrogenase large subunit	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
3-keto-acyl-ACP dehydratase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
3-ketoacyl-CoA thiolase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

3-phosphoshikimate 1-carboxyvinyltransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
40S ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
4-coumarate-CoA ligase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
4-hydroxy-3-methylbut-2-en-1-yl diphosphate	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
4-Hydroxyphenyl pyruvate dioxygenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
5,10-methylenetetrahydrofolate dehydrogenase	01.01-Metabolism/Amino Acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
5-methylthioribose kinase	01.01-Metabolism/Amino Acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
6,7-dimethyl-8-ribityllumazine synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
60S acidic ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
60S ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
6-phosphofructokinase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

6-phosphogluconate dehydrogenase	02.07-Energy/Pentose phosphate	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
6-phosphogluconolactonase	02.07-Energy/Pentose phosphate	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
9-cis-epoxycarotenoid 4 dioxygenase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Apetala/ethylene responsive factor	03.99-Cell growth/division/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
ABA-responsive protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ABC transporter	07.25-Transporters/ABC-type	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Abnormal inflorescence meristem 1 / fatty acid multifunctional protein	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Absciscic stress ripening protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Acetohydroxy acid isomeroeductase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Acetolactate synthase small subunit	01.01-Metabolism/Amino Acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Acetyl co-enzyme A carboxylase biotin carboxylase subunit	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Acetyl-CoA C-acyltransferase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Acetyl-CoA carboxylase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

Acetylglutamate kinase	01.01-Metabolism/Amino Acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Acetylornithine aminotransferase	01.01-Metabolism/Amino Acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Acetyltranferase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Acidic ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aconitase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Actin	09.04-Cell structure/Cytoskeleton	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Actin-depolymerizing factor	09.04-Cell structure/Cytoskeleton	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Acyl carrier protein	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
		<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Acyl-[acyl-carrier-protein] desaturase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Acyl-CoA oxidase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Acyl-CoA synthetase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Acyl-CoA thioesterase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Acyl-CoA:1-acylglycerol-3-phosphate acyltransferase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Acyl-CoA-binding protein	07.13-Transporters/Lipids	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Adenine phosphory transferase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Adenosine kinase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Adenosylhomocysteinase	01.01-Metabolism/Amino acid	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Adenylosuccinate synthetase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
ADP/ATP carrier protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
ADP-ribosylation factor	10.04-Signal transduction/Mediators	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Alanine aminotransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Alcohol dehydrogenase	02.16-Energy/Fermentation	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Aldehyde dehydrogenase	02.16-Energy/Fermentation	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aldo/keto reductase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Aldolase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aldose 1-epimerase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Allantoate Amidohydrolase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Allene oxide cyclase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Allyl alcohol dehydrogenase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Alpha-1,4 glucan phosphorylase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Alpha-galactosidase	09.01-Cell structure/Cell wall	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Alpha-soluble NSF attachment protein	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Alternative oxidase	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Aluminium-induced protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Amidophosphoribosyltransferase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Amine oxidase-related	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Aminoacylase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aminobutyrate transaminase gamma	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aminotransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Amylase alpha	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Ankyrin-repeat protein	10.04-Signal transduction/Mediators	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Annexin	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Antiporter/ drug transporter	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Antiporter/ glucose-6-phosphate transporter	07.07-Transporters/Sugars	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Antiviral protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Apyrase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aquaporin	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
ARD-like protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Arginine decarboxylase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Argininosuccinate lyase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Argininosuccinate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Ascorbate peroxidase	11.06-Disease/Defence/Detoxification	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Aspartate aminotransferase	01.01-Metabolism/Amino acid	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Aspartate semialdehyde dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Aspartate transaminase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Aspartate-tRNA ligase	05.10-Protein synthesis/tRNA synthases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Aspartic proteinase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Aspartokinase-homoserine dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Aspartyl aminopeptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP synthase subunit G	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP synthase subunit α	07.22-Transporters/Transport ATPases	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP synthase subunit β	07.22-Transporters/Transport ATPases	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
ATP synthase subunit γ	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP synthase subunit δ	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP synthase subunit E	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP synthase subunit H	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP/ADP translocator	07.99-Transporters/Others	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
ATPase	07.22-Transporters/Transport ATPases	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
ATPase inhibitor	10.04-Signal transduction/Mediators	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP-dependent Clp protease	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
ATP-dependent protease subunit	06.13-Protein destination and storage/Proteolysis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Succinate dehydrogenase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Auxin polar transport, establishment and/or maintenance of transmembrane electrochemical gradient	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Auxin/aluminum-responsive protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Auxin-induced protein	10.99-Signal transduction/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
AX110P-like protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Band 7 protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Basic chitinase	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Benzodiazepine receptor	10.01-Signal Transduction/Receptors	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Bet v 1 allergen protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Beta transducin-like protein	04.01-Transcription/rRNA synthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Beta-1,3-galactosyltransferase	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Beta-1,3-glucanase	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684

Beta-hydroxyacyl-ACP dehydratase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Bifunctional aspartokinase/homoserine dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Bifunctional purine biosynthesis protein	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Biotin carboxylase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
bis(5'-adenosyl)-triphosphatase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
b-keto acyl reductase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Branched-chain aminotransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Brassinosteroid insensitive1-associated receptor kinase	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
BSD domain-containing protein	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
C2 domain-containing protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
CAAX protease	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ca ²⁺ /Na ⁺ exchanger	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Calcineurin like protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Calcium ion binding protein	10.99-Signal Transduction/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Calcium-activated potassium channel	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

Calcium-transporting ATPase	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Calcium-dependent lipid binding protein	10.99-Signal Transduction/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Calcium-dependent protein kinase	10.99-Signal Transduction/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Calmodulin	10.99-Signal Transduction/Others	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Calnexin	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Calreticulin	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Carbonic anhydrase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Carboxylesterase	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Carboxymethylenebutenolidase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Carnitine/acylcarnitine translocase	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Carrier protein	07.99-Transporters/Others	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Casein kinase alpha chain	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Caspase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Catalase	11.06-Disease/Defence/Detoxification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

CBS domain-containing protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cell division cycle protein 48	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cell division protein ftsH	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Cell elongation protein diminutio	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chalcone isomerase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Chalcone synthase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chaperone	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Chaperone DnaJ	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chaperone protein DnaK	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Chaperonin 21	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chaperonin 60	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chitinase	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chlorophyll A/B binding protein	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

		<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Chloroplast outer envelope protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chorismate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
CHP-rich zinc finger protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Chromatin remodeling complex subunit	03.22-Cell growth/division/Cell cycle	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Cinnamate 4-hydroxylase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Citrate lyase α-subunit	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Citrate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Citrin	07.99-Transporters/Others	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Clathrin heavy chain	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Clathrin light chain	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Clp protease	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Coatomer subunit alpha	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Cobalamine-independent methionine synthase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Complex 1 family protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Component of the TOM complex	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Copalyl diphosphate	20.2-Secondary metabolism/Terpenoids	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Copper chaperone	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Coproporphyrinogen oxidase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cpn10	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Cryptochrome	10.99-Signal transduction/Others	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Cyclase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cystathionine beta lyase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Cystathionine gamma synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Cysteine protease	06.13-Protein destination and storage/Proteolysis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Cysteine proteinase inhibitor	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cysteine synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470

Cytidylyltransferase family	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cytochrome b	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cytochrome b6	02.20-Energy/Electron-transport	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Cytochrome b-f	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Cytochrome c	02.20-Energy/Electron-transport	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cytochrome c oxidase	02.20-Energy/Electron-transport	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Cytochrome P450	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Defensin	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Dehydrin	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Dehydroascorbate reductase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

Dehydroquinase dehydratase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Delta 1-pyrroline-5-carboxylate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Diacylglycerol kinase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Diaminopimelate decarboxylase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Dicarboxylate/tricarboxylate carrier	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Dihydrodipicolinate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Dihydrolipoamide dehydrogenase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Dihydroxy-acid dehydratase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Dimethylmenaquinone methyltransferase	02.07-Energy/Pentose phosphate	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Disease resistance protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Disulfide isomerase	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
D-limonene synthase	20.2-Secondary metabolism/Terpenoids	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
DNA repair ATPase-related	03.19-Cell growth/division/Recombination/repair	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
DNA-binding family protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
DNA-damage-repair/toleration protein	03.19-Cell growth/division/Recombination/repair	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Dolichyl-di-phosphooligosaccharide protein	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Drought-induced protein SDi-6-like	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Dynamin	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Early nodulin	09.01-Cell structure/Cell wall	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Early-responsive to dehydration stress protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Elicitor-inducible protein	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
embryo-specific protein-related	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Emp24	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Endo-1,3;1,4-beta-D-glucanase	09.01-Cell structure/Cell wall	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Endoplasmic reticulum membrane fusion protein	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Endoplasmic reticulum oxidoreductin	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Endoplasmin homolog	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Enod93 protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Enolase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Enoyl-ACP reductase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Esterase/lipase/thioesterase family protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ethanolamine-phosphate cytidyltransferase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ethylene response sensor protein	10.99-Signal Transduction/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Exo-beta-glucanase	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Expansin	09.01-Cell structure/Cell wall	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

Expressed protein-Unknown	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
FAD-dependent glycerol-3-phosphate dehydrogenase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Fasciclin-like arabinogalactan protein	08.99-Intracellular traffic/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Fatty acid hydroperoxide lyase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
F-box family protein	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Fiber annexin	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Fiber protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Fibrillin	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Flavanone 3-hydroxylase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
Flavonoid 3'-monooxygenase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Formaldehyde dehydrogenase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Formate dehydrogenase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Fra e 12.01 allergen	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Fructokinase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152

		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Fructose-bisphosphate aldolase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Fruit protein	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Fumarase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Galacturonate binding	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Gamma-aminobutyrate transaminase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
GcpE	20.2-Secondary metabolism/Terpenoids	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
GDP dissociation inhibitor	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
GDP-Mannose-3', 5' -Epimerase	20.1-Secondary metabolism/Phenylpropanoids/Phenolics	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470

Geranyl geranyl pyrophosphate synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Geranylgeranyl reductase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Germin	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
GF14 protein	10.04-Signal transduction/Mediators	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Globulin	06.20-Protein destination and storage/Storage proteins	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
GluB-5 long variant	12-Unclear classification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Glucan phosphorylase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Glucan water dikinase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Glucanase-b-1,4	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Glucose-6-phosphate isomerase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glucose-6-phosphate/phosphate translocator	07.07-Transporters/Sugars	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Glucose-repressible alcohol dehydrogenase transcriptional effector	04.99-Transcription/Others	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Glucosyltransferase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutamate decarboxylase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutamate dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutamate-1-semialdehyde 2,1-aminomutase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Glutamate-cysteine ligase	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Glutamine synthetase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutamyl-tRNA(Gln) amidotransferase	05.99-Protein Synthesis/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutaredoxin	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutathione peroxidase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutathione reductase	11.06-Disease/Defence/Detoxification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutathione S-transferase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glutathione-dependent formaldehyde dehydrogenase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glyceraldehyde-3-phosphate dehydrogenase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycerol-3-phosphate dehydrogenase-FAD dependent	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycerophosphoryl diester phosphodiesterase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycine hydroxymethyltransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycine-rich RNA binding protein	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycolate oxidase/ oxidoreductase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycosyltransferase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Glycyl-tRNA synthetase	05.10-Protein Synthesis/tRNA synthases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
GPI-anchored protein	07.13-Transporters/Lipids	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68

GTP-binding nuclear protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
GTP-binding protein	08.07-Intracellular traffic/Vesicular	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Guanine nucleotide regulatory protein	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Heme oxygenase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Hexokinase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
Hexose transporter	07.07-Transporters/Sugars	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Histone	03.22-Cell growth/division/Cell cycle	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Histone deacetylase	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Homeobox-leucine zipper protein	04.99-Transcription/Others	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Homocysteine S-methyltransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
HSP 101	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
HSP 60	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
HSP 70	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
HSP 80	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
HSP 90	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
HSP associated protein	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
HSP small	06.01-Protein destination and storage/Folding and stability	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684

Hydrolase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Hydrolase, alpha/beta fold family protein	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Hydroxymethylbutenyl 4-diphosphate synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Hydroxyproline-rich glycoprotein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Hypersensitive induced reaction protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Hypoxia-responsive family protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Imidazole glycerol phosphate synthase subunit hisf	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Import inner membrane translocase	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Importin subunit alpha	07.99-Transporters/Others	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Indole-3-acetic acid-amido synthetase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Indole-3-glycerol phosphate synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Inner envelope protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Inorganic pyrophosphatase	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Inosine monophosphate dehydrogenase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Integral membrane protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Iron-binding protein	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

Iron-deficiency-responsive protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Isocitrate dehydrogenase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Isoflavone reductase	20.99-Secondary metabolism/Other	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Isopentenyl pyrophosphate:dimethylallylpyrophosphate isomerase	20.99-Secondary metabolism/Other	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Isopentenyl-diphosphate delta-isomerase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
K(+) efflux antiporter	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
kelch repeat containing protein	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ketoacyl-thiolase beta	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ketol-acid reductoisomerase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
KH, type 1	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Kinase/ ribokinase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Kinesin light chain	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

Kunitz-type proteinase inhibitor	06.13-Protein destination and storage/Proteolysis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Lactoylglutathione lyase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Late embryogenesis abundant protein	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Leucine aminopeptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Leucine-rich repeat protein	12-Unclear classification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
leucine-rich repeat transmembrane protein kinase	12-Unclear classification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
L-galactose-1-phosphate phosphatase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Light-harvesting chlorophyll a/b-binding protein	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Light-induced protein	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Limonoid UDP-glucosyltransferase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Lipid associated protein	07.13-Transporters/Lipids	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Lipid transfer protein	07.13-Transporters/Lipids	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Lipocalin	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Lipoxygenase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
LL-diaminopimelate aminotransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Long-chain-fatty-acid CoA ligase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Lycopene beta cyclase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Lycopene epsilon cyclase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Magnesium transporter CorA	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Major intrinsic protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Malate dehydrogenase	02.10-Energy/TCA pathway	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Mangrin	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Mannose 6-phosphate reductase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Maturase	04.22-Transcription/mRNA processing	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Mce-related family protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Metalloendopeptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Methionine synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Microsomal signal peptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Microtubule associated protein	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Miraculin	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Mitochondrial import receptor subunit	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Mitochondrial phosphate translocator	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Mitogen-activated protein kinase kinase kinase	10.04.04-Signal transduction/Kinases	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Mo25 family protein	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Monodehydroascorbate reductase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Monooxygenase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Myo inositol monophosphatase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Myo-inositol 1-phosphate synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
MyosinI heavy chain	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
N-acetyl-gamma-glutamyl-phosphate reductase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
N-acetylglutamate kinase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

N-acylethanolamine amidohydrolase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NAD(P)-linked oxidoreductase domain-containing protein	12-Unclear classification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
NAD-dependent epimerase/dehydratase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NADH-cytochrome b5 reductase	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NADH-ubiquinone oxidoreductase	02.20-Energy/Electron-transport	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NADP-dependent isocitrate dehydrogenase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NADP-malate dehydrogenase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Nascent polypeptide associated complex alpha chain	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NB-ARC domain containing protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
NBS-containing resistance-like protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Neoxanthin cleavage enzyme	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Nine-cis-epoxycarotenoid dioxygenase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Nitrate transporter	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NLI interacting factor	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Non-green plastid inner envelope membrane protein	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Non-symbiotic hemoglobin	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

NTGB2	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
NtSar1 protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Nuclear RNA-binding protein	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Nucleoside disphosphate kinase	01.03-Metabolism/Nucleotides	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Nucleoside-diphosphate-sugar dehydratase	01.03-Metabolism/Nucleotides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Oleosin	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Oligomycin sensitivity conferring protein	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Oligopeptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Oligosaccharyl transferase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ornithine carbamoyltransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Outer membrane lipoprotein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Outer membrane OMP85 family protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Oxidoreductase, zinc-binding dehydrogenase	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Oxoglutarate dehydrogenase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Ozone-responsive stress-related protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
P450 monooxygenase	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Patellin	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
PDR-like ABC transporter	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Pectin methylesterase inhibitor	09.01-Cell structure/Cell wall	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Pectinesterase	09.01-Cell structure/Cell wall	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Peptidyl-prolyl cis-trans isomerase	06.01-Protein destination and storage/Folding and stability	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Perakine reductase	20.99-Secondary metabolism/Other	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Perchloric acid soluble translation inhibitor	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Peroxidase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Peroxidase anionic	11.06-Disease/Defence/Detoxification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

Peroxin	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Peroxiredoxin	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
peroxisomal biogenesis factor	09.19-Cell Structure/Perioxosome	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phenylcoumaran benzylic ether reductase	20.99-Secondary metabolism/Other	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphatase	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphate transporter	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphate-induced protein	03.99-Cell growth/division/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphoenolpyruvate carboxykinase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphoenolpyruvate carboxylase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphoethanolamine cytidyltransferase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphoglycerate mutase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Phosphoglycerate dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Phosphoglycerate kinase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Phosphoinositide-specific phospholipase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phospholipase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phospholipid hydroperoxide glutathione peroxidase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Phosphoribosylaminoimidazolecarboxamide formyltransferase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

Phosphoribulokinase	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Phosphoserine aminotransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Photosystem I precursor	02.30-Energy/Photosynthesis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Photosystem II precursor	02.30-Energy/Photosynthesis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Phox (PX) domain-containing-like protein	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
PII protein	02.30-Energy/Photosynthesis	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Plant uncoupling mitochondrial protein	08.04-Intracellular traffic/Mitochondria	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Plasma membrane H ⁺ ATPase	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Plasma membrane protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Plastid division protein FtsZ	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Plastidic 6-phosphogluconate dehydrogenase	02.07-Energy/Pentose phosphate	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Plastidic ATP/ADP transporter	07.99-Transporters/Others	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Plastid-lipid-associated protein	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Plastocyanin-like domain-containing protein	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Pleiotropic drug resistance like protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Poly(A)-binding protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Polyol transporter	07.07-Transporters/Sugars	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Polygalacturonase inhibitor	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Polyubiquitin	03.19-Cell growth/division/Recombination/repair	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Porin	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Presequence protease	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Prli-interacting factor	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Processing peptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Profilin	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Progesterone 5-beta-reductase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Prohibitin	03.16-Cell growth/division/DNA synth/replication	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Proline iminopeptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Prolyl 4-hydroxylase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Protease inhibitor/seed storage/lipid transfer protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Proteasome subunit α	06.13-Protein destination and storage/Proteolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Proteasome subunit β	06.13-Protein destination and storage/Proteolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Protein kinase	10.04.04-Signal transduction/Kinases	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Protein phosphatase	10.04.07-Signal transduction/Phosphatases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Protein TIC	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Protein TOC75	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Protein transport protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Proton pump interactor	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

PS1 reaction center subunit III	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Pseudouridine synthase	05.10-Protein Synthesis/tRNA synthases	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Pyrophosphate-energized vacuolar membrane proton pump	07.22-Transporters/Transport ATPases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
Pyruvate decarboxylase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Pyruvate dehydrogenase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Pyruvate dehydrogenase kinase	02.01-Energy/Glycolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Pyruvate kinase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Quinone oxidoreductase	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ran-binding protein	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Ras-related protein	10.0410-Signal transduction/G proteins	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Receptor-protein kinase	10.04.04-Signal transduction/Kinases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Regulator of ribonuclease-like protein	04.22-Transcription/mRNA processing	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Remorin	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Reticulon	08.99-Intracellular traffic/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Reversibly glycosylated polypeptide	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ribonuclease	04.22-Transcription/mRNA processing	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Ribonucleoprotein	04.01-Transcription/rRNA synthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Ribose-5-phosphate isomerase	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
Ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ribosome recycling factor	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
RNA binding protein	04.22-Transcription/mRNA processing	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
RNA recognition motif	04.22-Transcription/mRNA processing	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
RNA-binding region RNP-1 (RNA recognition motif)	04.22-Transcription/mRNA processing	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Rotamase	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Rubber elongation factor	05.99-Protein Synthesis/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
RuBisCO activase	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
RubisCo large subunit	02.30-Energy/Photosynthesis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
RubisCo small subunit	02.30-Energy/Photosynthesis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
RuBisCO subunit-binding protein	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309

S-Adenosyl-l-homocysteine hydrolase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
S-adenosyl-L-methionine synthetase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Salt tolerance protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Sec14p-like lipid-binding domain	07.13-Transporters/Lipids	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Secretory carrier membrane protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Selenium-binding protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Senescence-associated protein	11.05-Disease/Defense/Stress responses	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Serine acetyltransferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Serine hydroxymethyl transferase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Serine proteinase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Serine/threonine phosphatase	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Serine/threonine protein kinase	10.04.04-Signal transduction/Kinases	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Seryl-tRNA synthetase	05.10-Protein Synthesis/tRNA synthases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
S-formylglutathione hydrolase	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
SGT1	04.32-Transcription/Other	<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Signal peptidase subunit family protein	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Sodium/calcium exchanger family protein	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
SOUL heme-binding family protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
St12p	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
STARCH EXCESS 1	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Stearoyl-ACP desaturase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Steroid membrane binding protein	03.26-Cell growth/division/Growth regulators	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Stress related protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Strictosidine synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Structural constituent of ribosome	05.01-Protein synthesis/Ribosomal proteins	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Substrate carrier family protein	08.04-Intracellular traffic/Mitochondria	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Subunit of the TOM complex	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Succinate dehydrogenase flavoprotein	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Succinate-semialdehyde dehydrogenase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Succinyl CoA ligase	02.10-Energy/TCA pathway	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Sucrose synthase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Sucrose-phosphatase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Sugar transporter	07.07-Transporters/Sugars	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Superoxide dismutase Cu/Zn	11.06-Disease/Defence/Detoxification	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Superoxide dismutase Fe	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Superoxide dismutase Mn	11.06-Disease/Defence/Detoxification	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
SWIB complex BAF60b domain-containing protein	04.32-Transcription/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Synaptotagmin	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Synptobrevin-related protein	03.22-Cell growth/division/Cell cycle	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Syntaxin	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
T-complex protein	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Tetrahydrofolate dehydrogenase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Tetra-ubiquitin	03.19-Cell growth/division/Recombination/repair	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
TGB12K interacting protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Thaumatococin	11.02-Disease/defense/Defense-related	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
		<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Thiamin biosynthetic enzyme	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470

		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Thimet oligopeptidase	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Thioredoxin	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Thioredoxin peroxidase	11.06-Disease/Defence/Detoxification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Threonine synthase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Thylakoid lumenal 29.8 kDa protein	02.30-Energy/Photosynthesis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Tocopherol cyclase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
TPR domain containing protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Trans-2-enoyl-CoA reductase	01.06-Metabolism/Lipid and sterol	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Transaldolase	02.07-Energy/Pentose phosphate	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Transaminase	01.01-Metabolism/Amino acid	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Transcription coactivator DNA binding	04.05.01.04-Transcription/transcriptional control	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Transcription factor	04.1904-Transcription/Specific TFs	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Transferase family protein	12-Unclear classification	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005

Transketolase	02.07-Energy/Pentose phosphate	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Translation initiation factor	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Translational elongation factor	05.04-Protein synthesis/Translation factors	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Translational inhibitor protein	05.99-Protein Synthesis/Others	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Translationally controlled tumor protein	11.02-Disease/defense/Defense-related	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
Translocon inner membrane	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Translocon outer membrane complex	06.04-Protein destination and storage/Targeting	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Transmembrane protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Transposon protein	03.22-Cell growth/division/Cell cycle	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Triosephosphate isomerase	02.01-Energy/Glycolysis	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Tripeptidyl peptidase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Triticin	12-Unclear classification	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

tRNA/rRNA methyltransferase family protein	04.32-Transcription/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Trypsin and protease inhibitor family protein	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Tubulin alpha chain	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Tubulin beta chain	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Tubulin FtsZ	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Ubiquinol-cytochrome-c reductase	02.20-Energy/Electron-transport	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ubiquitin	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ubiquitin fusion-degradation protein	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ubiquitin-40S ribosomal protein	05.01-Protein synthesis/Ribosomal proteins	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ubiquitin-conjugating enzyme	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Ubiquitin-protein ligase	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
UDP-D-apiose/UDP-D-xylose synthase	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
UDP-D-glucose/UDP-D-galactose 4-epimerase	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403

UDP-glucoronosyl/UDP-glucosyl transferase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
UDP-glucose dehydrogenase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
UDP-glucose pyrophosphorylase	02.07-Energy/Pentose phosphate	<i>Citrus sinensis</i>	Katz et al., Journal of Experimental Botany 62 (2011) 5367–5384
		<i>Citrus sinensis</i>	Pan et al., Journal of Proteomics 75 (2012) 2670-2684
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
UDP-glucose:protein transglucosylase	09.01-Cell structure/Cell wall	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
UDP-glucuronate 5-epimerase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
UDP-glucuronate decarboxylase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Uncoupling protein	07.99-Transporters/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Universal stress protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Uricase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Uridine 5'-monophosphate synthase	01.03-Metabolism/Nucleotides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
UTP-glucose-1-phosphate uridylyltransferase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
UV-B and ozone similarly regulated protein	11.05-Disease/Defense/Stress responses	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Vacuolar ATP sythase	07.22-Transporters/Transport ATPases	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Vacuolar protein sorting-associated protein	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68

Valencene synthase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Muccilli et al., J. Proteomics 73 (2009) 134-152
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Vesicle transport protein	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Vesicle transport v-SNARE	08.07-Intracellular traffic/Vesicular	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Villin	09.04-Cell structure/Cytoskeleton	<i>Citrus sinensis</i>	Katz et al., Proteome Science 8 (2010) 68
Voltage-dependent anion-selective channel	07.01-Transporters/Ions	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Wall-associated kinase	10.04.04-Signal transduction/Kinases	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
WD-40 repeat family protein / auxin-dependent protein	04.32-Transcription/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Wrp15	07.99-Transporters/Others	<i>Olea europaea</i>	Esteve et al., Journal of Proteomics 75 (2012) 2396-2403
Xanthine/uracil permease protein	08.99-Intracellular traffic/Others	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
		<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
YGGT family protein	12-Unclear classification	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Zinc dependent protease	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Zinc metalloprotease	06.13-Protein destination and storage/Proteolysis	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
β-fructofuranosidase	01.05-Metabolism/Sugars and polysaccharides	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101

β-hydroxyacyl-ACP dehydratase	01.06-Metabolism/Lipid and sterol	<i>Olea europaea</i>	Esteve et al., Journal of Agriculture and Food Chemistry 59 (2011) 12093-12101
β-OHase 1	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Brassinosteroid biosynthetic protein	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Zeta carotene desaturase	20.99-Secondary metabolism/Other	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
Zinc finger protein	04.05.01.04-Transcription/transcriptional control	<i>Citrus sinensis</i>	Zeng et al., Journal of Experimental Botany 62 (2011) 5297-5309
		<i>Citrus sinensis</i>	Pan et al., Proteomics 9 (2009) 5455–5470
Multispanning membrane protein	06.01-Protein destination and storage/Folding and stability	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005
Xylose isomerase	01.05-Metabolism/Sugars and polysaccharides	<i>Citrus sinensis</i>	Katz et al., Planta 226 (2007) 989-1005