Analysis of Isolated Barley Tissues using Proteomic Approaches

Dissertation

zur Erlangung des akademisches Grades
Doctor rerum naturalium (Dr. rer. nat.)

vorgelegt der

Naturwissenschaftlichen Fakultät I
Biowissenschaften

der Martin-Luther-Universität Halle-Wittenberg

von

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Geboren am 08.03.1983 in Lutherstadt Wittenberg

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Halle (Saale), 08.03.2011

1. Abstract

Barley (*Hordeum vulgare* L.) is an important cereal crop and therefore high interest in the determination of factors influencing grain quality and stress tolerance exists. The elucidation of protein networks affecting grain developmental processes and protective functions of the leaf epidermis were in focus of the presented study.

Comprehensive methods elucidating factors influencing the complex biochemical processes in plants are available and mainly focussed on transcript profiling approaches for the tissues investigated in the presented work. But as transcript levels not always correlate to the proteome level, protein analyses are necessary to gain detailed information about the actual state of a tissue, organ, or cell. Proteomics is a valuable tool to determine biochemical aspects of plant tissue specificity, growth and adaption to biotic and abiotic stresses on protein level. 2-dimensional gel electrophoresis (2-DE) is still the standard method to perform protein profiling approaches, but gel-free methods mainly based on liquid-chromatography (LC) separation coupled to mass spectrometry (MS) detection are on their way to be used routinely. In the present study the applicability of nanoLC-based separation coupled to label-free MS detection with regard to the quantification efficiency and the usage in micro-proteomics approaches could be shown.

Molecular functions of barley leaf epidermis tissue from 5 day old seedlings were successfully unveiled by the combination of gel-based (2-DE) and gel-free (nanoLC-MS) proteome profiling approaches. A high number of proteins related to disease and defence processes were detected, e.g. reactive oxygen species-scavenging enzymes, and secondary metabolite synthesis, and point towards a protective function of barley leaf epidermis tissue on proteome level. Differences between mesophyll and epidermis tissue according to the metabolite distribution were analysed using gas chromatography-based separation coupled to MS detection as well as LC-based separation coupled to fluorescence detection and indicate an accumulation of glucose and fructose in the epidermis tissue.

Proteome analyses were additionally applied to gain insights into biochemical processes during different grain developmental phases (pre-storage until storage phase). The analysis of 5 different time points (ranging from 3 to 16 days after flowering) using label-free LC-MS revealed complex data sets. Multivariate statistics was applied for the determination of developmental patterns. Results showed developmental-dependent expression of proteins, at which ROS-scavenging enzymes, proteins related to protein synthesis, histones, and photosynthesis-related proteins were higher expressed in the middle phase of development, displaying high metabolic activities. Proteins higher expressed within the storage phase are important for storage protein accumulation, grain texture, and the protection of starch reserves against pathogens. Thus, different biochemical processes occurring during barley grain development were detected and were correlated to the developmental stages. Nevertheless, analyses of whole grains may mask tissue- or organ-specific changes in protein expression profiles. Till now tissue-specific protein analyses of barley grains were mainly focussed on manually dissected material. As the nucellar projection (NP) and endosperm transfer cells (ETC), both important for the nutrient transfer from maternal to filial tissue, are not accessible by manual dissection, laser-micro-dissection was applied for sampling. Protein extracts were analysed by the label-free LC-MS approach in a qualitative and quantitative manner. The majority of the ~160 identified proteins were involved in translation, protein synthesis or protein destination. The NP proteome was enriched for stress defence molecules. Proteins related to the assimilate transport and the mobilization of nutrients were common to both tissues. The combined qualitative and quantitative data set enabled the identification of several proteins showing tissue specificity in their expression.

2. Introduction

2.1. Barley as a major crop and model plant

Barley (*Hordeum vulgare* L.) is a monocotyledonous plant and belongs to the grass family (*Gramineae*). Grains of this important cereal crop are used for human and animal nutrition, and in the brewing industry due to their high contents of sugars, starch, storage proteins and fatty acids. Barley is a highly adapted cereal, able to grow at extreme climates, e.g. Himalayan regions, Ethiopia, and Morocco. It is one of the most genetically diverse cereals giving the opportunity to identify and breed varieties for specific uses, such as the application as a “chemical biofactory” over-producing pharmaceuticals or nutriceuticals (Baik and Ullrich 2008). Besides its worth as one of the major world crops, barley serves as an important model plant species for studies in malting and brewing industry, plant breeding methodology, genetics, biotechnology, etc. (Nilan and Ullrich 1993). As researchers have put their efforts into several sequencing projects, 415,381 expressed sequence tags (EST) are currently already available for barley (http://www.ncbi.nlm.nih.gov). Thus, nowadays barley can be used to a great extent as model plant. Important objectives of barley research projects, especially for plant breeders, are the processing and nutritional characteristics of grains, adaption to local environments, resistance to diseases and tolerance to abiotic stresses such as drought, heat, cold, and atmospheric pollutants (Mannonen *et al.* 1994).

2.1.1. Barley leaf epidermis

The barley leaf is composed of different tissue types. The cuticle, which is the outermost part of a leaf, is impermeable for gases. Photosynthesis is mainly accomplished in the chloroplast-rich mesophyll tissue. The epidermis is a surface cell layer in plants and makes up 27% of the total leaf volume (Winter *et al.* 1993). Several cell types are present within the leaf epidermal cell layer, namely pavement and basal cells, trichomes and stomata with pavement cells occurring most frequently (Esau 1977). Due to its location at the leaf surface, the epidermis has several functions in the protection and separation of underlying tissues from the environment and plays an important role for the perception of environmental signals (Dietz *et al.* 1994). This includes the control of the stomatal and nonstomatal water loss, cuticle synthesis and the compartmentation of ions, assimilates and compounds of secondary metabolism, including flavonoids, terpenes, and alkaloids (Hollenbach *et al.* 1997).

The underlying mechanisms of these highly complex physiological functions are far away from being completely understood, but some main biochemical characteristics are known (Murata *et al.* 2008). One of the aspects studied in more detail in epidermis tissue is the vacuolar solute composition. As different tissues are specialized for different functions, the solute compositions and concentrations also differ between those tissues (Fricke 2004). This aspect was analysed in leaf epidermis tissue compared to mesophyll and showed that they differ in their vacuolar calcium, phosphor, and organic solutes concentrations (Fricke *et al.* 1996). Additionally, the function of leaf epidermis as intermediary storage compartment has been widely discussed in barley. Dietz *et al.* (1994) postulated intermediate epidermal storage of glucose and fructose as their levels increased concomitant to levels in the mesophyll. However, single cell analyses of barley leaf epidermis and mesophyll showed that epidermal cells contained negligible concentrations of sugars and no accumulation of such could be detected (Koroleva *et al.* 1998). Therefore, the epidermis was supposed not to take part in carbohydrate storage, as it was also described by others (Fricke *et al.* 1994, Koroleva *et al.* 1997). This obvious contradiction concerning the accumulation of glucose and fructose has not yet been addressed in literature but may originate from the usage of different growing conditions (soil culture/harvest primary leaf of 10 day old seedlings *vs.* hydroponic culture/harvest third leaf of 19 to 24 day old seedlings). Besides, all studies are in agreement, that leaf epidermis tissue does not contain sucrose at detectable concentrations and therefore does not act as buffer for leaf sucrose accumulation.

Several factors pointing towards a possible protective function of leaf epidermis tissue are described. It was shown that flavonoids known to be efficient protectors against UV-B radiation are mainly localized in the epidermis and, upon UV-B stress treatment, accumulated in the epidermis and only to a minor extent in the mesophyll tissue (Kaspar *et al.* 2010, Schmitz-Hoerner and Weissenbock 2003). Further investigations showed that barley leaf epidermis tissue is involved in defence mechanisms against pathogens (Fujita *et al.* 2004). Barley plants have developed two different responses towards pathogen attacks in epidermis tissue, namely, the formation of papillae at sites of attempted penetration and hypersensitive cell death (Panstruga and Schulze-Lefert 2002).

Even though several studies dealt with diverse aspects of leaf epidermis tissue in terms of its function, global investigations with regard to gene, protein, and metabolite expression patterns are still missing for barley. Using the *Arabidopsis thaliana* (L.) Heynh. (*A. thaliana)* model system to investigate cell type-specific gene and protein expression profiles, transcript and proteome analyses of epidermal tissue were performed out of single cells (Brandt *et al.* 2002, Lieckfeldt *et al.* 2008). A high expression of transcripts related to sulphur metabolism and detoxification was found, whereas only few transcripts related to photosynthesis were detected. Wienkoop and colleagues (2004) performed the detection of proteins present in single epidermal cells extracted from *A. thaliana* leaves by nanoLC-MS. In total 26 proteins were detected in epidermis tissue, whereas none of them could be found in the trichomes, which were also analysed as parts of the leaf epidermis surface. Additionally, the number of proteins found in the single cell extracts was to low to perform intensive studies on defining possible molecular functions of this tissue type.

The work presented here aimed at the disclosure of possible molecular functions of barley leaf epidermis on proteome level by the detection of all proteins visualisable using 2-D gel electrophoresis (2-DE) as well as liquid chromatography (LC)-based separation and on metabolite level using gas chromatography (GC)- as well as LC-based separation.

2.1.2. Barley grain development

The barley caryopsis is a single-seeded fruit that is composed of several organ and tissue types, like the embryo and the carbohydrate-rich endosperm (Figure 1).

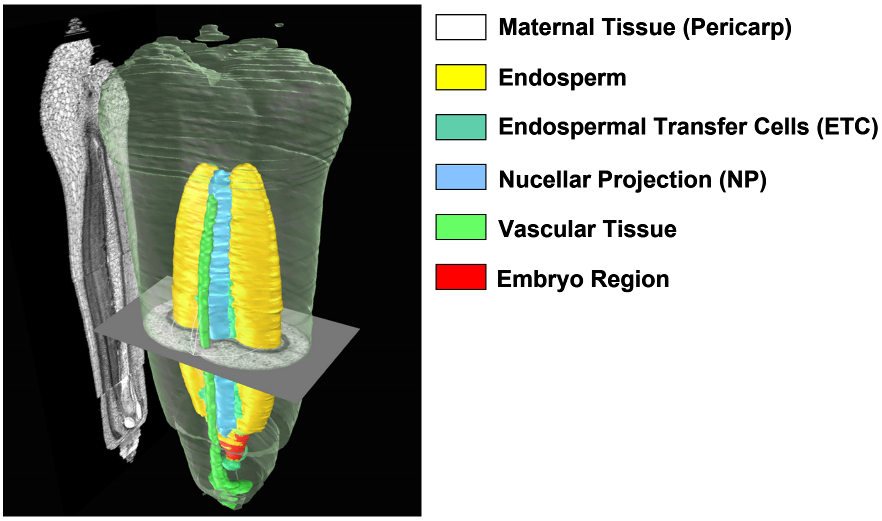


Figure 1: Histological 3-dimensional model of a developing barley grain at 8 days after flowering (DAF) displaying the location of the different organs. The picture is courtesy of Felix Bollenbeck (IFF Magdeburg) and Winfriede Weschke (IPK Gatersleben).

A detailed histological study of barley caryopsis development revealed at least 18 different tissues (Gubatz *et al.* 2007) displaying the high complexity. Detailed understanding of physiological, metabolic, and biochemical aspects of the development of cereal caryopses is of high interest, because of its importance for final grain weight and quality, at which the composition of the grain is a prime focus due to its nutritional importance.

A number of factors influence the developmental processes and the accumulation of storage products in barley grains (Barnabas *et al.* 2008). These processes are genetically programmed and occur successively starting with the maternal organs and followed by the filial organs, which then differentiate into highly specialized storage organs (Borisjuk *et al.* 2004). The barley grain development can be divided into distinct phases, ranging from the pre-storage and intermediate phase to the storage phase (maturation) followed by the desiccation phase (Figure 2).

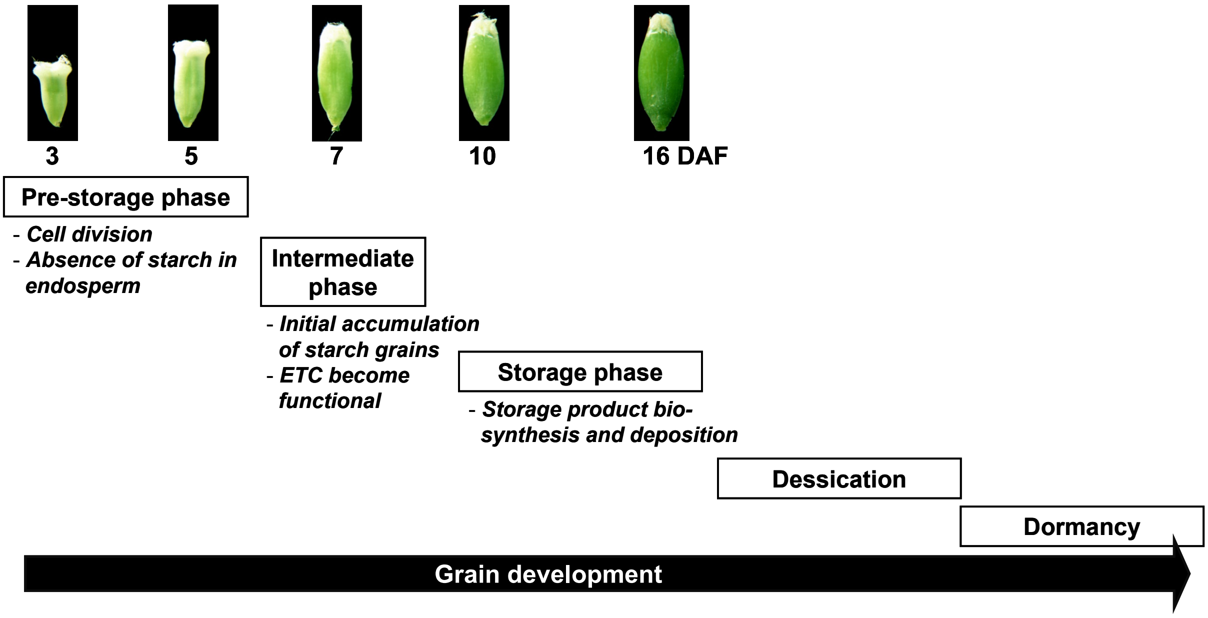


Figure 2: Schematic overview of the grain development processes, which can be divided into distinct phases (pre-storage phase, intermediate phase, storage phase, desiccation and dormancy).

These sequential developmental phases are dominated by different biological processes (Weschke *et al.* 2003). Early grain development (pre-storage phase) is characterized by the growth of the pericarp and cellularisation processes occurring in the endosperm. During the intermediate phase (also called transition phase) endosperm transfer cells (ETC) become functional. The intermediate phase represents the transition from cell division/elongation towards storage product accumulation in the endosperm. The following storage phase is determined by storage product biosynthesis and deposition in the endosperm in conjunction with an increase in the caryopsis volume. Water loss characterizes the desiccation phase. The embryo and aleurone hold desiccation tolerance and dormancy to assure a continuation of life cycle during germination. Dormancy can be considered as a block to the completion of germination of an intact viable seed under favourable conditions and thus controls germination timing (Finch-Savage and Leubner-Metzger 2006). During germination, starch and storage proteins, which were deposited in the endosperm during storage phase, are degraded by hydrolases to supply the growing embryo with assimilates.

The different developmental phases are characterized by different metabolite levels. For example, levels of sucrose, which is imported into the filial storage organs without prior cleavage, peak in the transition phase. The overall starch content on the other hand increases steadily throughout the development and highest levels can be detected in the maturation phase. Transcript profiling has already been successfully applied to examine the complex biological processes during grain development (Sreenivasulu *et al.* 2004). It could be shown that the intermediate phase is characterized by massive transcriptional reprogramming processes and a transient burst of gene expression related to photosynthesis and energy production.

Even though proteins more likely reflect the actual state of the organism as they are the final gene products, analyses of grain development on proteome level are still rare and mainly focus on mature or germinating seeds. Among these studies spatio-temporal profiling approaches of proteins in barley grains have been performed and included a comparison of different tissue types (embryo, endosperm, and aleurone layer) in mature seeds (Finnie and Svensson 2003) and at different developmental stages during germination and radicle elongation (Bonsager *et al.* 2007). Dramatic changes upon imbibition of the quiescent seed were detected on proteome level. Many of the proteins showing changes in expression patterns could be related to the desiccation state, like the loss of desiccation-related LEA (late embryogenesis abundant) proteins from the embryo and aleurone layer. Observed changes on proteome level were detected during early germination and supported the concept of programming of the germination process already during maturation. This means that components important for subsequent processes are already present in the dry mature seed prior to germination. The overlap of the proteomic data gained in these studies to the previously recorded transcriptome data (Potokina *et al.* 2002, Watson and Henry 2005) was limited highlighting the value of proteomics as complementary approach. Additionally, proteome profiling has already been applied to screen barley cultivars for differences in the seed protein profiles (Finnie *et al.* 2009). Results showed that some spot variations were caused by amino acid differences encoded by single nucleotide polymorphisms (SNPs) and thus a possible link between cultivar traits, the proteome and the genome was found.

Studies dealing with proteome analyses of barley grain development mainly focussed on later developmental stages (e.g. maturation and germination). However, early developmental processes are important for final grain yield and quality as they for example determine storage product synthesis. Only limited information about these early processes exist on proteome level, and thus the presented study aimed at temporal protein profiling of barley grain development from 3 to 16 days after flowering (DAF).

The nutrient transfer during grain development from the maternal tissue to the filial endosperm is mediated via the nucellar projection (NP)/ ETC complex (Thiel *et al.* 2009, Figure 3). The NP is a rather heterogeneous tissue as it consists of mitotically active, differentiating/elongating, as well as disintegrating cells. It differentiates from the nucellus tissue. The release of nutrients from the nucellus and the NP is partially associated with programmed cell death (PCD). Transcript analyses revealed a high activity of genes involved in amino acid catabolism and ammonia re-fixation, suggesting a possible role of the NP in protein degradation and remobilization of nitrogen (Thiel *et al.* 2008). Additionally, a possible function of NP as metabolic interface to precondition amino acid supply has been concluded (Thiel *et al.* 2009).

Figure 3: Cross section of a barley caryopsis at 8 DAF (A) and magnification of the maternal-filial boundary (B) consisting of the nucellar projection (surrounded by green lines) as well as the endosperm transfer cells (surrounded by yellow lines). Picture taken from Thiel *et al.* (2008).

Transfer cells in general are plant cells with secondary ingrowths specialized for solute transport and enhance plasma membrane transport activity (Offler *et al.* 2003). Transfer cells have been observed in all plant classes, fungi, and red algae holding different functions in higher plants, like solute uptake by leaf minor veins, distribution of xylem and phloem sap in stem nodes, and for phloem and xylem uploading in flowers and fruits (Thompson *et al.* 2001). The transfer cells located in the grain endosperm are called ETC and differentiate from the first epidermal cell row. ETC in barley grains become functional for sucrose uptake at around 6 DAF. It is a persisting tissue developing cell wall ingrowths to increase transport-active surfaces (Thiel *et al.* 2008). In contrast to NP, ETC do not accumulate starch during storage events that take place in the caryopsis. Besides its function in the efficient transfer of sugars and amino acids, ETC also act as a barrier against pathogens (Li *et al.* 2008). The differentiation and development of both tissues, ETC and NP, needs to be coordinated with the changing sink strength of the developing endosperm.

The functions of the different tissue types present in barley grains are likely to be reflected by the presence or absence of proteins. However, analyses carried out on whole grains are likely to mask unique localized responses (Balestrini and Bonfante 2008). Thus, the analysis of spatial distribution patterns of proteins using laser-micro-dissected material would reveal valuable information about the complex course of events ongoing during grain development. Until now, the analyses of specific cell types involved in developmental processes are still scarce. The appliance of laser-micro-dissection (LMD) as sampling strategy greatly improves the profiling of proteins present in a distinct tissue as it allows dissecting tissues not accessible by manual dissection. This technique has already been used for the analyses of gene expression profiles in plants, e.g. in maize epidermis, vascular tissues, shoot apical meristem, and roots (Nakazono *et al.* 2003, Ohtsu *et al.* 2007, Woll *et al.* 2005). On the proteome level only proof-of-principle studies have been performed for the analyses of laser-micro-dissected plant material (Hennig 2007). As both, the NP and the ETC, are important for nutrient transfer from maternal to filial tissue, it was aimed to perform proteome analyses of those tissues in the presented work to gain further insights into their molecular functions.

2.2. Proteomics for qualitative and quantitative profiling of tissues and developmental processes

Several genomes have already been sequenced nowadays and include a few plant species (*A. thaliana*, *Oryza sativa* L. and *Populus* L.). As the correlation between the levels of mRNA and proteins is limited (Anderson and Seilhamer 1997, Futcher *et al.* 1999), it is ineluctable to analyse the end product of the genome in order to elucidate functional properties. Proteomics in general describes the entire profile of all proteins expressed from an organism, organ, tissue or a cell under well defined conditions and at a given time. Even though the genome is constant, the proteome varies in correlation to the developmental stage, changes in the environment, and further influences, like biotic and abiotic stresses. Additionally, splicing and post-translational modifications can lead to further variation between the gene and its product giving the potential for more than one gene product. As proteomic approaches cannot benefit from amplification protocols, generally far fewer proteins than transcripts can be detected (Hennig 2007). Nevertheless, post-translational modifications, which are relevant for the biological function of a protein, cannot be detected using transcript profiling approaches. The first proteomic technique enabling the separation of protein mixtures was 2-DE introduced by O'Farrell (1975). Only with the development of mass spectrometry (MS) methods in the 1990s, like matrix-assisted laser desorption/ionisation (MALDI, Karas and Hillenkamp 1988) and electrospray ionisation (ESI, Fenn *et al.* 1989) allowing the ionization of large biomolecules, it was possible to use the potential of this method as the subsequent identification of separated proteins became feasible. Nowadays, 2-DE is still the standard method (Gevaert *et al.* 2007), but gel-free proteomics approaches have been developed to overcome some of the limitations posed by 2-DE, e.g. the separation of very basic proteins and integral membrane proteins. The standard workflows of both methods are shown in Figure 4.

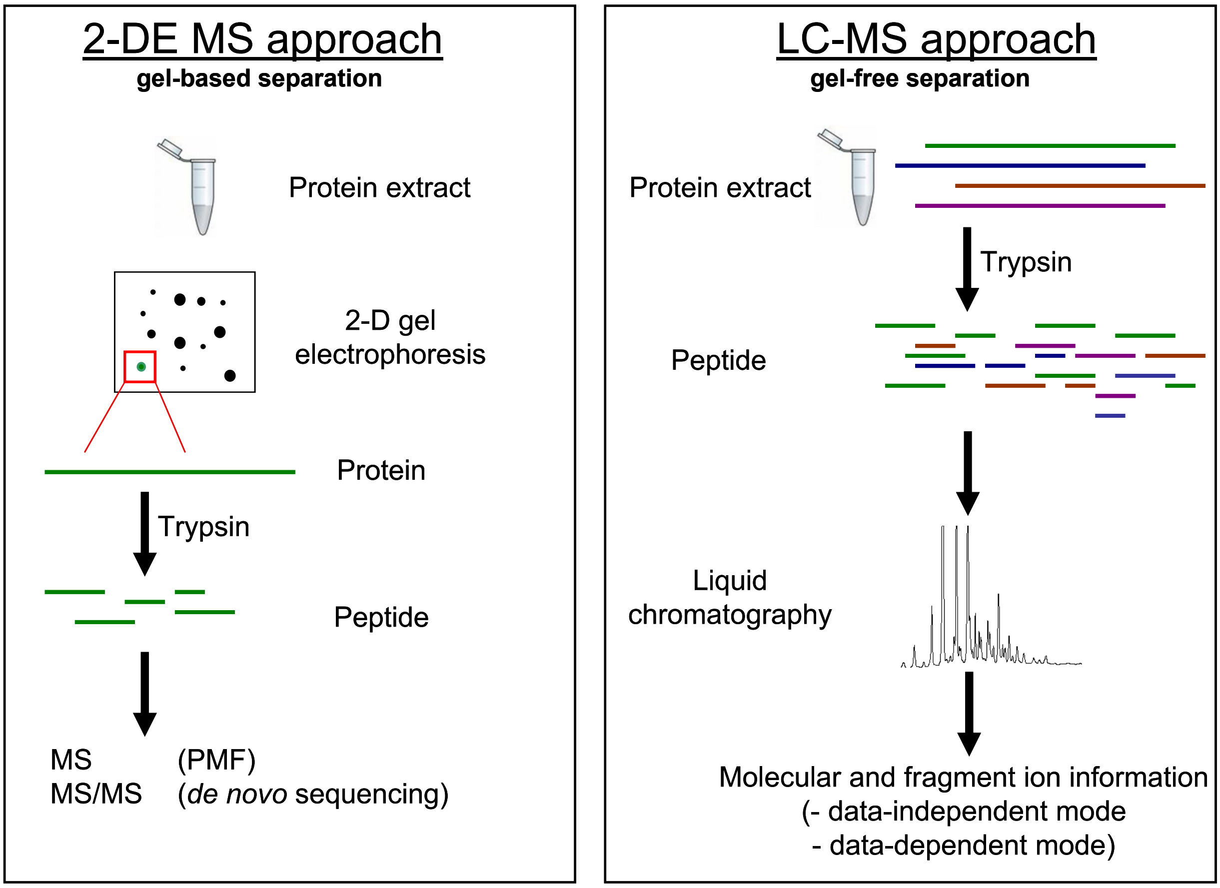


Figure 4: Schematic workflows for the analysis of proteins using 2-D gel electrophoresis (2-DE), and liquid chromatography (LC)-MS. Within the 2-DE approach proteins are separated in a 2-dimensional manner (based on their isoelectric point and molecular weight), stained and quantified based on pixel intensities. Subsequently, spots of interest are cut out of the gel and the proteins are digested. Identification is done on the basis of tryptic peptides using mass spectrometry methods (peptide mass fingerprinting (PMF), *de novo* sequencing). Separation and quantification within the LC-based approach is done on peptide level. Complete protein extract is digested, generated peptides are separated using liquid chromatography (in either one or two dimensions) and analysed using mass spectrometric detection. Quantification is based on the gained mass signals.

The main difference between the techniques is the level of quantification. Whereas the abundance of proteins is quantified based on pixel intensities of the stained gel spots during 2-DE, quantification using the LC-MS approach is performed on peptide level on the basis of mass spectra data. Methods for measurements of protein abundances in gel-free approaches can either include the incorporation of stable isotope labels or tags into proteins or peptides (Roe and Griffin 2006). Subsequent quantification is done on the basis of these introduced molecules. On the other hand label-free approaches can be applied. The methods either include quantification on the basis of measured peptide signal intensities, which are compared among the samples and replicates to determine fold changes in protein abundance or on the number of MS/MS spectra matched to a protein within an experiment, called spectral counting (Matros *et al.* submitted, Neilson *et al.* 2010).

As the protein identification heavily relies on the availability of complete genome sequence information, the appliance of proteomics on plant material is still challenging due to incomplete databases (Matros *et al.* 2010). Nevertheless, a large number of protein profiling approaches of different plant species, tissue types and also organelles have already been performed, whereas most of them have used 2-DE. Proteome analyses can be divided into mapping approaches aiming at the identification of all detectable proteins, and into approaches aiming at the identification of proteins showing changes in their expression pattern in connection to various biotic and abiotic stresses as well as developmental changes, tissue types or organelles. Plant proteomic approaches have been mainly used for analyses of *A. thaliana* and *O. sativa*, because they have completely sequenced genomes. Even though protein identification is more difficult, when only incomplete genome information exist, several proteomic approaches focussed on traditional monocot crop species such as wheat and maize, and on trees, fruit crops, and legumes (Rampitsch and Srinivasan 2006). The proteome profiling approaches performed on different plant species not only included the analyses of different genotypes, mutants, and transgenics, but also of different organs, tissues, and cells, like seeds, roots, stems, and leaves (Jorrin *et al.* 2007). As the thousands of gene products in plants are targeted to specific locations, subcellular proteomics is one of the growing areas in researchers' interest and has been applied for *A. thaliana* plastids, mitochondria, nuclei, and peroxisomes (Haynes and Roberts 2007). Comparative proteome profiling aiming at the detection of differently expressed proteins has been applied to analyse the responses of maize leaf tissue upon UV-stress (Casati *et al.* 2005), of *A. thaliana* rosette leaves upon cold stress (Amme *et al.* 2006), and of barley root tissue upon salt stress (Witzel *et al.* 2009).

First analyses applying gel-based separation combined with gel-free methods have been successfully adopted for the investigation of proteins within *A. thaliana* leaf peroxisomes (Reumann *et al.* 2007) and showed a complementary character of both methods. Additionally, several studies employing gel-free LC-based methods solely have been performed. The application of LC-based separation coupled to MS detection led to the successful identification of around 6,000 proteins from *Populus* xylem tissue (Kalluri *et al.* 2009). Especially the analyses of small protein amounts out of laser-micro-dissected material can benefit from gel-free techniques, mainly when nanoLC-based separation is applied, as it allows the identification of a substantial number of biologically diverse proteins from limited protein quantities. The analyses of ~3,000 LMD-derived tumour cells from breast carcinoma tissue for example led to the identification of around 1,000 proteins using nanoLC-based separation coupled to FT-ICR analyses (Umar *et al.* 2007). Nevertheless, analyses of laser-micro-dissected material out of plant tissues are rare at the moment. One of the aims of this work is to resolve spatial protein profiling patterns using LMD-derived material. Thus the development and verification of a nanoLC-based separation method allowing the detection and quantitative protein analyses of small protein amounts was aimed.

2.3. Scientific aims of the work

The work described here is focused on the proteome profiling of different isolated barley tissues. The quality and yield of barley, being a major crop plant, is partly determined by the composition of proteins during grain development, but also by the potential of the growing plant to cope with different exogenic stress factors. Proteomics is a valuable tool to understand biochemical aspects of plant developmental processes and tissue specific functions. Most of the analyses performed until now were done using 2-DE. Nevertheless, gel-free approaches are originating, which circumvent several limitations of gel-based methods. One aim of this thesis was to develop and verify a gel-free LC-based separation method coupled to MS detection applicable for the analyses of different tissue types and especially for the profiling of laser-micro-dissected material.

The barley leaf epidermis is known to be an effective protector against various stresses. Only few in-depth analyses of this tissue exist, especially on proteome level. Possible biochemical functions of the epidermis tissue should be disclosed in this thesis by application of proteomic tools. Thus the creation of a reference map, containing all proteins detectable using 2-DE as well as LC-based separation of barley leaf epidermis, was aimed. Epidermis tissue separated manually from mesophyll of growing seedlings of the cultivar Barke was analysed. The study also aimed at the functional classification of detected proteins. Additionally, analyses of metabolites found within the epidermis was performed as the combination of protein and metabolite data reveals a more entire data set to unveil detailed understanding of barley leaf epidermis tissue.

Several studies of barley grain development based on metabolite and gene expression profiles have already been performed. Nevertheless, analyses of the early grain developmental phases on proteome level are still rare and therefore it was another aspect of the thesis to monitor protein expression changes during barley grain development using a label-free LC-based approach coupled to MS detection. Besides temporal distribution patterns of proteins also the spatial arrangement within the barley grain should be determined, as it gives first insights into the allocation of functions within the caryopses. A special focus was laid on the analyses of the NP as well as ETC as they are important for the nutrient transfer from maternal to filial tissues, endosperm/embryo nutrition, and grain development. Thus, the detailed understanding of the functions of these tissues can yield additional information important for example for optimizing grain yield. LMD should be applied for the purchase of NP and ETC sample material and gained results of both tissues should be compared qualitatively and quantitatively.

3. Materials and Methods

3.1. Plant Material

3.1.1. Barley leaf tissues

Barley (*Hordeum vulgare* L., cv. 'Barke') seedlings were grown under green house conditions at a day/night rhythm of 14/10 h and 20/18 °C. Leaf mesophyll and lower epidermis were separated using scalpel and forceps. Leaves were first slightly scratched for the detachment of mesophyll and epidermis. Afterwards the mesophyll was removed using a forceps as shown in Figure 5 and then both tissue types were separately snap frozen under liquid nitrogen.

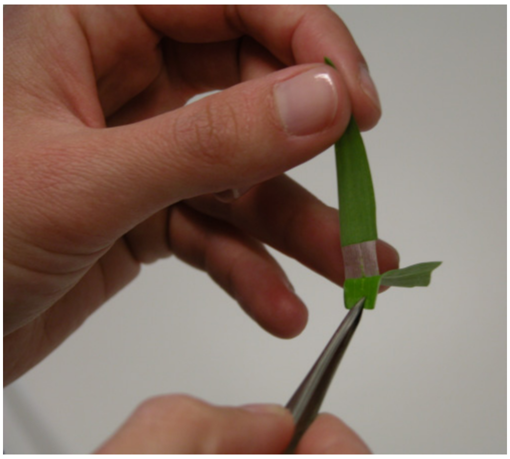


Figure 5: Separation of epidermis and mesophyll in barley leaf tissue.

After separation tissues were ground using mortar and pistil and stored at -80 °C until sample preparation for the respective analyses.

3.1.2. Barley caryopsis

Barley (*Hordeum vulgare* L., cv. 'Barke') plants were grown under controlled conditions in growth chambers as described by Weschke *et al.* (2000). In short, during generative phase plants were grown at a day/night rhythm of 16/8 h and 18/10 °C. Caryopses were harvested at 3, 5, 7, 8, 10, and 16 DAF and directly frozen in liquid nitrogen. Samples were stored until sample preparation at -80 °C.

3.1.3. Dissected material of barley caryopsis

Dissection of distinct tissues of the barley grain was performed using laser capture micro-dissection combined with pressure catapulting (LMPC) according to Thiel *et al.* 2008. Frozen caryopses at the developmental stage 8 DAF were transferred to a cryostat and fixed at one end of the caryopsis onto the sample plate using Tissue-Tek O.C.T compound (Sakura Finetek Europe B.V., Zoeterwoude, Netherlands). The middle part of the caryopses was cut out using a razor blade and thin sections of 20 µm were either placed into a tube for analyses of complete sections or glued onto the sample plate (PEN membrane slides, PALM, Bernried, Germany) using thaw mounting for further processing of samples by LMD. Slides were stored for five to seven days in the cryostat at -20 °C until complete dryness. Prior to micro-dissection, dry cryosections were adapted to room temperature. PEN slides with dehumidified sections were placed into a PALM Laser Microbeam instrument (Carl Zeiss MicroImaging GmbH, Jena, Germany) and the ETC and the NP were dissected. Using the “CloseCut & AutoLPC” function of the PALM RoboSoftware, the region of NP and ETC was first separated from the surrounding tissue with the aid of a cutting line and then carried away by a number of laser shots and catapulted into the lid of a 0.5 ml PALM Adhesive Cap. The power of the laser beam was adjusted to 45 to 60 mW for cutting procedure and to 70 to 90 mW for laser pressure catapulting.

Typically, between 70 and 75 sections were processed per experiment for dissection of ETC referring to about 4,500,000 µm^2 of section area. For dissection of NP, about 40 sections were processed per experiment, which refers to about 2,500,000 µm^2 section area. For each cell type three individual preparations were performed.

3.2. Analyses of protein expression profiles

3.2.1. Protein extraction

Extraction of proteins from barley leaf tissue

Proteins were extracted from frozen ground leaf tissue following the Schlesier and Mock (2006) TCA/Acetone method. One part of frozen material was mixed with ten parts of extraction buffer (10% trichloroacetic acid (TCA), 0.07% (w/v) 2-mercaptoethanol in acetone). The incubation for 45 min at -20 °C was followed by a centrifugation step to precipitate the pellet (Mikro 22R, Hettich, Tuttlingen, Germany; 15 min, 4 °C, 36,000*g*) and a washing step using 2-mercaptoethanol in acetone (0.07% w/v). The pellet was dried in a vacuum centrifuge (Concentrator 5301, Eppendorf, Hamburg, Germany). In dependency on the applied method for protein separation and detection, the resulting pellet was further processed. For 2-DE the pellet was dissolved for 1 h at 37 °C under shaking conditions in rehydration buffer (8 M urea, 2% (w/v) 3-[(3-cholamidopropyl) dimethylammonio]-1-propanesulfonate (CHAPS), 0.005% (v/v) 3,3',5,5'-tetrabromphenolsulfonphthalein, 0.5% immobilized pH-gradient (IPG)-buffer, 20 mM dithiothreitol (DTT)). The resulting solution was purified through an Ultrafree MC Amicon filter (Durapor PVDF 0.45 µm, Millipore, Schwalbach, Germany) to remove solid residues. Contaminating salts and metabolites were removed by dialysis against 40 times rehydration buffer using the Quant Dialysis Kit (GE Healthcare, München, Germany). When label-free LC-MS was chosen for the analysis, the TCA/acetone pellet was dissolved in 0.1% RapiGest^{TM} SF (Waters, Eschborn, Germany) in 50 mM ammonium bicarbonate. Contaminating low molecular weight substances were removed through an iterative filtration step with a cut-off filter (10 kDa, Vivaspin, Vivascience AG, Hannover, Germany).

Extraction of proteins from barley caryopses

Water-soluble proteins from barley caryopses were extracted following the protocol according to Schlesier and Mock (2006) with minor modifications. Grinding and protein extraction were performed using FastPrep FP120/BIO 101 machine (ThermoSavant, Waltham, MA, USA). Three to five frozen caryopses were added to a chilled tube containing 100 mg of zirconium beads. Ten parts of extraction buffer (10% TCA, 0.07% (w/v) 2-mercaptoethanol in acetone) were added and tubes were shook three times for 5 s using the FastPrep machine. Subsequent extraction steps were performed as described above (section 3.2.1., Extraction of water-soluble proteins from barley leaf tissue). Three mg of the protein pellet was dissolved in 100 µl 0.1% RapiGest^{TM} SF (Waters) in 50 mM ammonium bicarbonate. Insoluble material was removed by centrifugation through an Ultrafree MC Amicon filter (Durapor PVDF 0.45 µm, Millipore). Contaminating low molecular weight substances were removed as described above.

Extraction of proteins from dissected tissue

For protein isolation out of laser-micro-dissected material, the dissected cells were directly dissolved in 30 µl (ETC) or 20 µl (NP) RapiGest^{TM} SF buffer (0.1% RapiGest^{TM} SF in 50mM ammonium bicarbonate) according to Mustafa *et al.* 2007. Ten sonicaton steps a 5 s were applied for cell disruption and protein extraction. Between each sonication step samples were cooled down on ice to minimize protein degradation processes. Proteins were solubilised by shaking for 1 h at 37 °C.

3.2.2. Determination of protein concentration

2-D Quant Kit

The concentration of proteins dissolved in buffers containing CHAPS or DTT were determined with the 2-D Quant-Kit (GE Healthcare) according to the manufacturer's instructions. Bovine serum albumin (BSA) was used a reference.

Bradford assay

The concentration of proteins resolved in RapiGest^{TM} SF was determined by the method according to Bradford (1976) using BSA as a reference.

3.2.3. Protein profiling using 2-D gel electrophoresis

2-D gel electrophoresis

2-DE was performed as described in Schlesier and Mock (2006). Briefly, 400 µg protein extract was loaded onto a 24 cm IPG-strip (GE Healthcare, pH 3-11, nonlinear) by rehydration for 12 hours using an IPGphor II unit (GE Healthcare) for the separation in the first electrophoretic dimension. Proteins were focussed with following parameters: 2 h gradient to 150 V, 2 h gradient to 300 V, 2 h gradient to 1000 V, 3 h gradient to 3000 V, 3 h gradient to 6000 V and 10 h 6000 V. After isoelectric focussing (IEF) IPG-strips were equilibrated for 15 min in buffer 1 (50 mM Tris-HCl pH 8.8, 6 M urea, 30% v/v glycerine, 2% w/v sodium dodecyl sulfate (SDS), 20 mM DTT, 0.01% 3,3',5,5'-tetrabromphenolsulfonphthalein), followed by an incubation for 15 min in buffer 2 (50 mM Tris-HCl pH 8.8, 6 M urea, 30% v/v glycerine, 2% w/v SDS, 135 mM iodoacetamide, 0.01% 3,3',5,5'-tetrabromphenolsulfonphthalein). Equilibrated IPG-strips were placed on top of an 11.25% SDS polyacrylamide gel for the second electrophoretic dimension and separation was performed using an Ettan DALTsix Electrophoresis unit (GE Healthcare) at following conditions: 0.5 h at 30 V and 14 h at 80 V.

Protein staining and image acquisition

Proteins were visualized with colloidal Coomassie Blue (GelCodeBlue Stain Reagent, Pierce Chemical Company, Rockford, USA) following the manufacturer’s instructions. Image acquisition was done using a UMAX Power Look III scanner (UMAX Systems GmbH, Willich, Germany) with the MagicScan software (v.4.5, UMAX).

Image analyses and data processing for relative quantification of protein patterns

Image analysis of 2-D gel patterns was performed using TT900 S2S software (Nonlinear Dynamics, Newcastle upon Tyne, United Kingdom) for image alignment and Progenesis PG220v2006 software (Nonlinear Dynamics) for comparative image analysis. The following default parameters were applied: ‘mode of non-spot’ with margin 45 as background subtraction method, spot matching with vector box size 12 and search box size 64, volumes were normalized by multiplying the total spot volume by 100, and spot detection with an area > 300 and a volume > 1500.

Protein identification using mass spectrometry

Peptide mass fingerprint using MALDI-TOF MS

Protein spots selected for protein identification were excised from the gel using an automatic spot picker (Proteineer sp, Bruker Daltonics Bremen, Germany). Gel pieces were directly placed into a 96 well plate and washed in 200 µl 10 mM ammonium bicarbonate (in 50% acetonitrile) for 30 min at room temperature under shaking conditions. The supernatant was removed and the gel pieces were allowed to dry overnight at room temperature. Proteins in the washed and dried gel pieces were digested with 10 µl trypsin solution (Sequencing Grade Modified Trypsin V511, Promega; 10 ng/µl in 5 mM ammonium bicarbonate/5% acetonitrile) for 5 h at 37 °C. The digestion was stopped by the addition of 1 µl 1% trifluoroacetic acid (TFA). Digests were cleaned and concentrated using ZipTip C18 columns (Millipore) as described in the manufacturer's procedures.

The acquisition of Peptide Mass Fingerprints (PMF) was performed with a REFLEX III MALDI-Time of Flight (TOF) mass spectrometer (Bruker Daltonics) as described in Brumbarova *et al.* 2008. External calibration and subsequent internal mass correction of spectra were performed with the Flex Analysis software (Bruker Daltonics). Biotools 3.0 software (Bruker Daltonics) with the implemented MASCOT search engine (Matrix Science, London, United Kingdom) was utilized for database search in the HarvEST Hv database. The search parameters were: 100–200 ppm tolerance for mass accuracy, one missed cleavage site, oxidation (Met), propionamide (Cys) and carbamidomethyl (Cys) as allowed variable modifications.

MS/MS for de novo sequencing

When identification using MALDI-TOF MS failed, samples were additionally analysed using liquid chromatography (LC)–based separation coupled to mass spectrometric detection (MS) and *de novo* sequencing according to Witzel *et al.* (2007). An aliquot of 2 µl protein digest was separated on a NanoAcquity system (Waters) equipped with a 20 mm x 180 µm Symmetry (5 µm) pre-column coupled to a 100 mm x 100 µm BEH (1.7 µm) C18 column with a gradient of 3–40% acetonitrile over 30 min at a constant flow rate of 600 nl/min. Solvent A consisted of water with 0.1% formic acid and solvent B of acetonitrile with 0.1% formic acid. The lockmass, [Glu1]-Fibrinopeptide B human (Sigma-Aldrich, Selze, Germany) at a concentration of 1 pmol/µl, was delivered at a constant flow rate of 600 nl/min through the auxiliary pump of the NanoAcquity pump to the reference sprayer of the NanoLockSpray source.

Mass spectrometric detection was done on a Q-TOF Premier mass spectrometer (Waters) in a data-dependent analysis (DDA) mode using following conditions: MS was operating in v-mode and positive nanoelectrospray ion mode. The applied source temperature was 80 °C and cone gas flow 50 l/h. Mass spectra for the calibrant were acquired in continuous fragmentation mode at a collision energy of 22 eV. MS data were acquired in the m/z range of 400–1600 with a survey scan time of 0.95 s and an interscan time of 0.05 s. MS/MS was performed in the m/z range of 50–1600 when total ion chromatogram (TIC) intensity was above a threshold of 2000.

Protein Lynx Global Server (PLGS) 2.3 software (Waters) was used for processing and identification of obtained spectra. Resulting sequences were entered as search strings in the HarvEST Hv database, with search parameters: 10 ppm mass tolerance, 0.1 Da fragment mass tolerance, one missed cleavage site, oxidation (Met), propionamide (Cys), and carbamidomethyl (Cys) as variable modifications. BLAST homology based and similarity searches were performed with same database.

3.2.4. Protein expression analysis using label-free LC-MS

Separation and detection of complex peptide mixtures

Digestion of proteins was performed prior to the analyses. Protein extracts dissolved in 0.1% RapiGest^{TM} buffer (in 50 mM ammonium bicarbonate) were held at 80 °C for 10 min before incubation at 60 °C for 10 min in the presence of 2.5 mM DTT in water. Free cysteines were alkylated in the presence of 7.5 mM iodoacetamide in water at room temperature for 30 min in the dark. Proteins were digested by adding 0.2 µg Sequencing Grade Modified Trypsin V511 (Promega) and incubating overnight at 37 °C. RapiGest^{TM} SF was hydrolyzed after protein digestion by adjusting the pH to ~2 with 1N HCl and the resulting pellet was removed by centrifugation (20 min, 18000*g*, 4 °C),

Separation and mass spectrometric analysis of complex tryptic digests was performed on a nanoLC-ESI-Q-TOF MS/MS instrument (Waters) as described previously (Kaspar *et al.* 2010). Separation of peptides was performed as described in section 3.2.3 (*MS/MS for de novo sequencing*) using modified conditions. Tryptic peptides were separated on a 20 mm x 180 µm Symmetry (5 µm) C18 pre-column coupled either to a 150 mm x 75 µm BEH (1.7 µm) C18 column or a 100 mm x 100 µm BEH (1.7 µm) C18 column. The flow rate for the gradient (3-33% acetonitrile) was set to 600 nl/min and the gradient length varied according to the complexity of the measured sample (70, 80, and 110 min). Solvent A consisted of water with 0.1% formic acid and solvent B was acetonitrile with 0.1% formic acid. Detailed information about the parameters used for the experiments are given in Table 1.

MS detection of eluting peptides was done by a data-independent MS mode and the conditions included a source temperature of 80 °C and a cone gas flow of 50 L/h. A voltage of 2.8 kV was applied to the nano flow probe tip. The instrument was calibrated with 1 pmol/µl [Glu1]-Fibrinopeptide B delivered through the reference sprayer of the NanoLockSpray source at a flow rate of 600 nl/min. Mass spectra for the calibrant were acquired in continuous fragmentation mode at a collision energy of 22 eV. LC-MS data were collected in an alternating high and low energy acquisition mode (multiplexed LC-MS mode) using MassLynx 4.1 software (Waters) with a spectra acquisition time of 1 s with a 0.02 s interscan delay. During each 1 s data collection cycle constant collision energy of 4 eV was applied for the low energy mode and a collision energy gradient from 10 to 28 eV was used for high energy mode.

For the analyses of protein expression changes during barley grain development the applied conditions for the two conducted experiments differed slightly according to the LC-based separation (Table 1). These changes affected the protein amount used for injection, column and gradient length, in which modifications of the last two parameters are closely linked to each other as the column length has a strong influence on the gradient length. Detection parameters were kept unaltered besides an adaption of data acquisition time according to the gradient length.

Table 1: Overview about the parameters applied for the performed experiments to analyse proteome profiles using LC-MS approach. Given are the amount used for injection, the column parameters and gradient information. The pre-column used for the experiments was a 20 mm x 180 µm Symmetry (5 µm) C18 column.

	Amount	Column	Gradient
Barley grain development			
Experiment 1	0.15 µg protein + 75 fmol enolase	150 mm x 75 µm BEH (1.7 µm, C18 column) with pre-column	3-33% acetonitrile (+0.1% formic acid) 110 min
Experiment 2	0.5 µg protein + 75 fmol enolase	100 mm x 100 µm BEH (1.7 µm, C18 column) with pre-column	3-33% acetonitrile (+0.1% formic acid) 80 min
Epidermis mapping	0.5 µg protein + 100 fmol enolase	150 mm x 75 µm BEH (1.7 µm, C18 column) without pre-column	3-33% acetonitrile (+0.1% formic acid) 110 min
Laser-micro-dissected material	200,000 µm^2 + 100 fmol enolase	100 mm x 100 µm BEH (1.7 µm, C18 column) with pre-column	3-33% acetonitrile (+0.1% formic acid) 70 min

Processing of data obtained from LC-based separation experiments

Multiplexed LC-MS data processing using PLGS software

The multiplexed LC-MS data were processed as described by Silva *et al.* (2006) using the PLGS 2.3. software. Molecular ion information from the low energy MS trace and fragment ion data from the high energy MS trace were subjected to the protein identification process using the Identity Algorithm implemented in the PLGS software. Database searches were conducted against a UniProt reference database, consisting of manually assembled entries of *Oryza sativa* and *Hordeum vulgare* with 90% homology and the *H. vulgare* index of the HarvEST database, both of them complemented with sequences for human keratin, porcine trypsin and yeast enolase. Search parameters were: automatic peptide fragment tolerance, 3 minimum fragment ion matches per peptide and 7 minimum fragment ion matches per protein, one minimum peptide match per protein, carbamidomethyl (Cys) as fixed modification, variable oxidation (Met) and propionamide (Cys) modification and a false positive rate of 4%. The intensities of mass signal were used for quantification, which was either performed on protein or peptide level as described in Kaspar *et al.* (2010). Briefly, quantification on protein level included mapping of each peptide to its related protein. The pooled peptides from one protein were then used to calculate an overall change value, which is affected by the probability score of each individual peptide. For peptide level quantification each detected component was matched by its exact mass and retention time (EMRT) signature. The peptides were clustered across the LC runs and between samples, and subsequently the intensities of the peptide signals (deisotoped and charge state-reduced) were used for quantification. Absolute quantities were calculated out of the average intensities of the top three intense peptides per protein in each injection with a response factor calculated from the average intensity of the three most intense peptides matched to the applied amount of enolase internal standard (Cheng *et al.* 2009). Results from replicates were evaluated using replicate filters (at least two out of three LC runs and detected in each of the conducted experiments) and calculated quantities were combined to generate a mean value. Comparative profiling was either performed on the basis of the absolute protein quantities or relative signal intensities of single EMRTs.

Multiplexed LC-MS data processing using clustering algorithms

Additional data processing was applied for the elucidation of statistically significant and objective kinetic patterns within the barley grain development. Prior to this, data pre-processing was performed. Missing values occurring in the data set were eliminated by setting a mean value of existing values, when only a single data point was missing. In case more time data points of one sample were missing, these values were set to “eps”, which is the smallest machine readable number. The computational intelligence-based clustering algorithm Neural Gas was applied for the clustering task. This algorithm is a specialized artificial neural network and was initially suggested by Martinetz & Schulten (1991). Neural Gas belongs to the class of unsupervised trained neural networks. The algorithm receives a set of feature vectors as input data. During an iterative training process, an a-priori defined and randomly initialized number of prototype vectors is adapted to optimally represent the properties of the given data set according to a specified similarity metric. Multivariate data processing was done in corporation with Prof. Dr. Udo Seiffert (IFF Magdeburg).

3.3. Validation of protein patterns

3.3.1. Western blot analyses

Immunoblotting analysis was performed as described in Amme *et al.* (2005). Five µg (for alcoholdehydrogenase (ADH), ascorbate peroxidase (APX), superoxide dismutase (SOD), chitinase (PR-Q), stress-inducible protein in *Nicotiana tabacum* L. (STINT)) or 10 µg (for phenylalanine ammonia-lyase (PAL)) of protein were separated on a 1-D SDS-Page. Proteins were blotted onto a polyvinylidene fluoride (PVDF) membrane (Immobilon-P, pore size 0.45 µm, Millipore, Eschborn, Germany) using a semidry apparatus (Schütt, Göttingen, Germany). Antibodies for immunodetection were either obtained from Agrisera (polyclonal SOD antibody from spinach) and Lifespan Biosciences (polyclonal ADH antibody from yeast), or kindly provided by B. Fitig (Université Louis Pasteur, Straßbourg/France, monoclonal PR-Q antibody from tobacco), T. Saji (National Institute for Environmental Studies, Tsububa/Jana, monoclonal APX antibody from spinach), and M. Okazaki (Shinshu University, Ueda/Japan, PAL antibody from tobacco). The STINT antibody was raised against the tobacco homologue of the stress-inducible protein AT1G62740 (Hedtmann and Mock, unbublished results). Signal visualization was achieved by the addition of anti-rabbit IgG coupled with alkaline phosphatase (Boehringer, Mannheim, Germany), in the presence of 5-bromo-4-chloro-3-indolyl (BCIP), and nitroblue tetrazolium chloride (NBT).

3.3.2. Enzymatic measurements

Enzyme assay measurements were performed for fructose-bisphosphate aldolase (FBP aldolase) and alanine aminotransferase (ALA AT) as described in Gibon *et al.* (2004). A combination of stopped and cycling assays was used for detection leading to an increase in the detected metabolites (Gibon *et al.* 2002). Proteins were extracted out of 20 mg grounded barley grain material by intense shaking with 500 µl buffer (2 mM leupeptin, 500 mM DTT, 100 mM phenylmethylsulfonyl fluoride) and a small amount (tip of a spatula) of polyvinylpyrrolidone. The samples were kept cold during a short shaking step and the following centrifugation procedure (10 min, 13000 rpm, 4 °C). The supernatant containing extracted enzymes was then diluted to generate appropriate activities for the corresponding enzyme assay using extraction buffer (ALA AT 1:40,000, FBP aldolase 1:2,000) to ensure that measurements are performed at optimal concentrations. These optimal dilutions were determined in pilot studies by Kathleen Merx (Applied Biochemistry Group, IPK Gatersleben). The assay mixes were freshly prepared and differed for the enzymes. Exact composition is described in Table 2.

Table 2: Composition of the assay mixes used for the determination of enzymatic activity of alanine aminotransferase (A) and fructose-bisphosphate aldolase (B) in developing barley grains. The compositions for blank measurement as well as for the determination of maximum activity are displayed.

A

Alanine aminotransferase

Compound	Blank	Maximum activity
H_2O	1495 µL	1495 µL
Extraction buffer (5x)	520 µl	520 µl
LDH (60 u/ml)	52 µl	52 µl
NADH (5 mM)	13 µl	13 µl
H_2O	260 µl	0 µl
2-oxoglutarate (25 mM)	0 µl	260 µl

B

Fructose-bisphosphate aldolase

Compound	Blank	Maximum activity
H_2O	552.5 µL	552.5 µL
Extraction buffer (5x)	260 µl	260 µl
GDH (200 u/ml)	13 µl	13 µl
TPI (100 u/ml)	13 µl	13 µl
NADH (60 mM)	6.5 µl	6.5 µl
H_2O	325 µl	0 µl
F1,6BP (20 mM)	0 µl	325 µl

Enzymatic reaction was started by the addition of 2 µl of the diluted extract to 18 µl of the respective assay mix. Samples were held at room temperature for 25 min and the reaction was stopped by adding 20 µl HCl (0.5 M in 100 mM Tricine/KOH pH 9). Subsequent to an incubation step for 5 min at 95 °C (ALA AT) or for 10 min at room temperature (FBP aldolase), 20 µl NaOH (0.5 M) were added for both enzyme assays to adjust the pH to 9.0. Activity measurements were performed by addition of 50 µl of the corresponding determination mix (Table 3). Products were monitored at an absorbance wavelength of 570 nm (ALA AT) or 340 nm (FBP aldolase) using a microplate spectrophotometer (SpectraMax Plus, Molecular Devices).

Table 3: Composition of determination mixes used for the analysis of enzymatic activity of alanine aminotransferase (A) and fructose-bisphosphate aldolase (B) in developing barley grains.

A

Alanine aminotransferase

Compound	Amount
H_2O	3.96 ml
Extraction buffer (5x)	2.2 ml
MTT	2.2 ml
EDTA (200 mM)	0.88 ml
ADH	0.22 ml
Ethanol (50%)	0.44 ml
PES	1.1 ml

B

Fructose-bisphosphate aldolase

Compound	Amount
H_2O	4.476 ml
Extraction buffer (5x)	1.2 ml
$MgCl_2$	0.024 ml
GDH (200 u/ml)	0.060 ml
GPOx (500 u/ml)	0.060 ml
TPI (100 u/ml)	0.060 ml
NADH (60 mM)	0.120 ml

3.4. Analyses of metabolites

3.4.1. Chlorophyll extraction and determination

Chlorophyll was extracted from barley leaf tissue according to Lichtenthaler *et al.* (1987). Equal amounts of fresh weight (15 mg) were used for mesophyll and epidermis tissue. Frozen material was dissolved in 1.5 ml acetone and centrifuged for 5 min at 36,000*g*. The supernatant was transferred into a quartz cuvette and absorption was measured immediately at defined wavelengths for chlorophyll a (645 nm) and chlorophyll b (662 nm). Chlorophyll a (Chl_a), b (Chl_b), and the total content (Chl_total) were calculated out of the recorded absorption units (A) using following formulas:

$$Chl\_a = 11{,}27A_{662} - 2{,}04A_{645}$$
$$Chl\_b = 20{,}13A_{662} - 4{,}19A_{645}$$
$$Chl\_total = 7{,}05A_{662} + 18{,}09A_{645}$$

Total amount of chlorophyll within the epidermis tissue was correlated to the amounts detected in mesophyll tissue (set to 100%).

3.4.2. Amino acid analyses using LC-based separation

Fifty mg of frozen and ground epidermis and leaf material was extracted using 800 µl 80% ethanol followed by an incubation step for 60 min at 80 °C. The extract was allowed to cool down and centrifuged for 15 min (36,000*g*, 4 °C). The supernatant was transferred into a new reaction tube and dried in vacuum for at least 2 h at 50 °C. The dried residue was dissolved in 200 µl water. Amino acids were derivatized in 10 µl of ACQ reagent (Waters) and 80 µl of borate buffer (pH 8.8) added to 10 µl sample volume and incubated for 10 min at 55 °C to allow fluorescence detection. Ten µl of the extract were used for separation of amino acids using a High Performance Liquid Chromatography (HPLC, Alliance 2690, Waters, Eschborn, Germany) system. Gradient for separation ran from 100% A (140 mM sodium acetate, pH 5.8, 7 mM thriethanolamine) to 18% acetonitrile within 47.5 min. The temperature for the column (AccQ.Tag, 3.6 mm x 150 mm, Waters) was kept at 37 °C and for the auto sampler at 10 °C. Detection was performed using a fluorescence detector (Waters 474 Scanning Fluorescence Detector) at an excitation wavelength of 300 nm and an emission wavelength of 400 nm.

3.4.3. Metabolite analyses using GC-MS

Metabolite extraction and analyses followed the protocol previously described by Lippmann *et al.* (2009). Briefly, 50 mg sample of frozen and ground epidermis and leaf material was extracted with 700 µl methanol for 10 min at 70 °C. Three hundred-fifty µl chloroform and 700 µl water were added to the extract and cell debris was removed by a centrifugation step (15 min, 10,000*g*). The sample was transferred into a fresh reaction tube and dried in vacuum. The derivatization of metabolites included two steps: first 80 µl methoxyaminohydrochloride (20 mg/ml in pyrridine), which contained alkanes (C7-C30, Sigma-Aldrich, Munich, Germany) at a concentration of 10 µg/µl used as retention time standards, was added and samples were incubated for 2 h at 37 °C. During the second step 80 µl N-Methyl-N-(trimethylsily)-trifluoroacetamide was added and samples were incubated for 30 min at 37 °C. One µl of each sample was injected at a temperature of 240 °C using splitless mode into the GC-MS system consisting of a gas chromatograph A7890 (Agilent, Böblingen Germany) coupled to a TOF mass spectrometer GCT Premier (Waters). Separation, performed on a 30 m DB5ms column (Phenomenex, Aschaffenburg, Germany) with 0.25 mm inner diameter and 0.25 µm film thickness including a 5 m guard column, followed a temperature regime: 3 min at 80 °C, followed by a gradient of 5 °C/min to 310 °C for 50 min. MassLynx 4.1 software (Waters) was used for data acquisition at following parameters: 10 spectra/s in a range of 50-650 m/z centroid mode using the dynamic enhancement modus (DRE). Metabolite identification was performed automatically with the internal software ChromaLynx using NIST 05 library and interesting components were validated manually by comparison with reference spectra and with retention time of individual standards. Retention time indices (RI), calculated in correlation to retention time of added alkanes, were used to verify the identified metabolites, when corresponding values were available in the database. For principle component analysis (PCA) MarkerLynx (Waters) was utilized with following settings: 20 masses per retention time were isolated at a threshold at 5% of base peak intensity. The retention time window was set between 6.5 and 37 min, and mass window between 100 and 850 with a mass tolerance at 0.05 Da. Pareto algorithm was used for visualization of loading and score plot.

4. Results

The work presented here aims at the protein analysis of different tissue types to unveil the molecular functions of barley leaf epidermis tissue (chapter 4.2), and to analyse spatial and temporal protein expression patterns in developing barley grains (chapter 4.3). A main focus is to determine protein profiles of tissues important for nutrient transfer processes in the barley grain. Therefore the development and establishment of a gel-free LC-based method coupled to MS detection was required, enabling the analysis of small protein amounts as well as confident protein identification and quantification processes (chapter 4.1).

4.1. Development of a gel-free LC-MS method for protein profiling

4.1.1. Optimization of the sample preparation procedure

Sample preparation is a critical issue, when applying LC-MS for protein profiling approaches, as substances interfering with a reproducible LC separation and MS detection need to be removed. Especially when using nano-scale columns, samples have to be particle-free for unhindered analyses. At the same time additional purification steps can lead to significant sample losses, and thus need to be chosen with great care. Optimization of the sample preparation procedure was done using epidermis tissue, as pilot experiments showed that this tissue type contains high amounts of flavonoids, mainly saponarin, which can still be detected after protein extraction (Figure A 1 in the appendix). These substances interfere with the MS detection due to ion suppression effects influencing peptide signals. Thus, their amount needs to be reduced and/or heavily diluted within the protein extract. Two different methods, namely the treatment of solubilised proteins using a) In-Solution digestion, and b) On-Filter digestion were compared.

a) In-Solution digestion

Protein extract out of barley epidermis tissue was loaded onto a 10 kDa cut-off filter and an equal volume of solubilisation buffer (0.1% RapiGest^{TM} SF in 50 mM ammonium bicarbonate) was added. The sample was washed twice by centrifugation and filtration to remove disturbing substances smaller than 10 kDa. In the case of epidermis tissue the level of saponarin and further flavonoids should be reduced by passing the 10 kDa filter, whereas the proteins stay in the retentate. A schematic overview of the workflow for the In-Solution digestion is shown in Figure 6.

After removal of interfering substances, proteins were reduced with DTT, alkylated with iodoacetamide, and digested using trypsin directly in the purified solution as described in Material and Methods (section 3.2.4). The resulting peptide mixture was used for LC-MS analysis. Three injections were performed and the peptides eluting from the nanoLC system were detected by an ESI-Q-TOF MS. The corresponding chromatograms of samples treated with In-Solution digestion were complex and reproducible. However, a complete depletion of saponarin could not be achieved as the corresponding signal was still abundant (Figure 8) and represented the dominant mass detected.

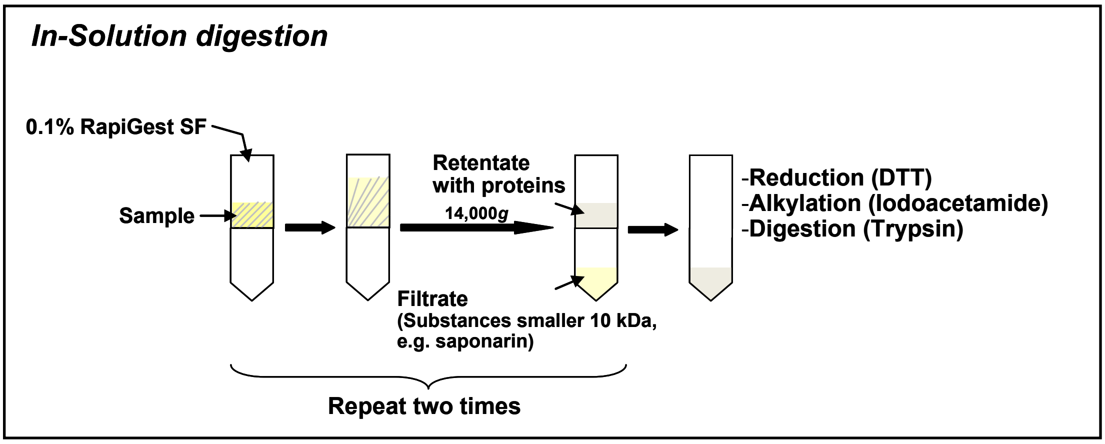


Figure 6: Workflow for In-Solution digestion of complex protein extracts. The protein extract is placed on a filter (cut-off 10 kDa) together with the same volume of solubilisation buffer (0.1% RapiGest™ SF in 50 mM ammonium bicarbonate). Afterwards all compounds smaller than 10 kDa, e.g. saponarin in the case of epidermis tissue, are removed by a filtration step, whereas proteins cannot pass the filter and stay in the retentate. The volume is reduced to the starting sample volume. Steps are repeated twice and retentate is used afterwards for reduction, alkylation and digestion of the proteins.

b) On-Filter digestion

Solubilised proteins were placed on a filter with a cut-off of 10 kDa. Remaining liquid residues were removed by filtration leaving the corresponding proteins on the filter. Proteins were directly digested on the filter and tryptic peptides were eluted by filtration. The application of this method should lead to a reduction of disturbing substances smaller than 10 kDa, like saponarin in the case of epidermis tissue, as they will pass the filter during the filtration step. A schematic overview of the On-Filter digestion workflow is shown in Figure 7.

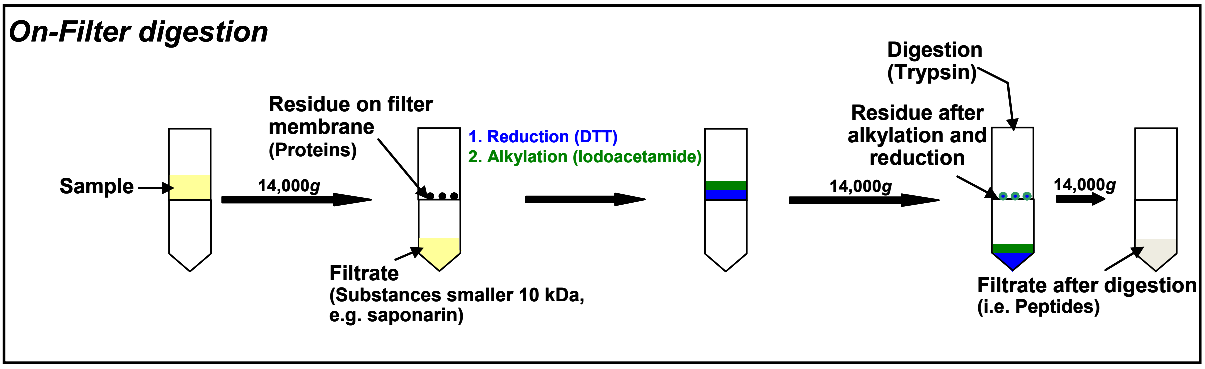


Figure 7: Description next page

Figure 7: Workflow for On-Filter digestion of complex protein extracts. The protein extract is placed on a filter and substances smaller than 10 kDa are removed by filtration. Afterwards DTT, iodoacetamide and trypsin are added consecutively for reduction, alkylation and digestion of the proteins directly on the filter. Remaining solutions are removed by filtration. Obtained peptides are eluted from the filter by centrifugation and washed with 0.2 M ammonium bicarbonate solution.

Analyses of the obtained tryptic peptides have been performed for barley leaf epidermis tissue as described for In-Solution digestion. An estimated total protein amount of 0.5 µg was injected for both experiments. The sample was measured in triplicate runs. Visual inspection of corresponding chromatograms showed less complexity for the On-Filter digestion method compared to the In-Solution digestion procedure, and individual signal intensities were higher for the latter method. The saponarin peak was still detectable for both methods reflecting the fact, that saponarin could not be removed completely (Figure 8). Nevertheless, its amount could be reduced compared to previous experiments, where proteins out of epidermis tissue were digested directly without additional sample preparation steps (corresponding chromatogram is shown Figure A 1 in the appendix). Thus, even though a complete reduction of saponarin could not be achieved, its amount was decreased by the aid of additional cleaning steps using filter devices.

The signal intensities throughout the complete spectrum based on the base peak intensity (BPI) chromatograms were higher for the In-Solution digestion (BPI signal = $3.21e^3$) compared to the On-Filter digestion (BPI signal = $1.13e^3$), which on the one hand can be correlated to a higher abundance of proteins but also of saponarin. The retention time shift of around 3 min for saponarin observed for the two different sample preparation methods can be explained by the usage of two different column batches (pre-column and analytical column).

Subsequent protein identification was performed by searching against a manually assembled UniProt reference database. The In-Solution digestion of epidermis-specific proteins led to an identification of around 500 proteins per run, of which 470 were found to be reproducible in two out of three runs and 240 proteins were detected in all three LC runs. All detected proteins were equally distributed over all three runs (see Figure A 2 a in the appendix). A lower number of proteins could be identified in each single run for the On-Filter digestion method compared to the In-Solution digestion approach, leading to 107 proteins showing an overlap for two out of three runs and 57 proteins found in all three runs (Figure 9). Whereas nearly the same number of proteins could be detected in second and third run, a higher number was detected in the first run. Thus, only small number of these proteins contributed to the complete data set (Figure A 2 b in the appendix), whereas the rest of them were removed as they were detected just once.

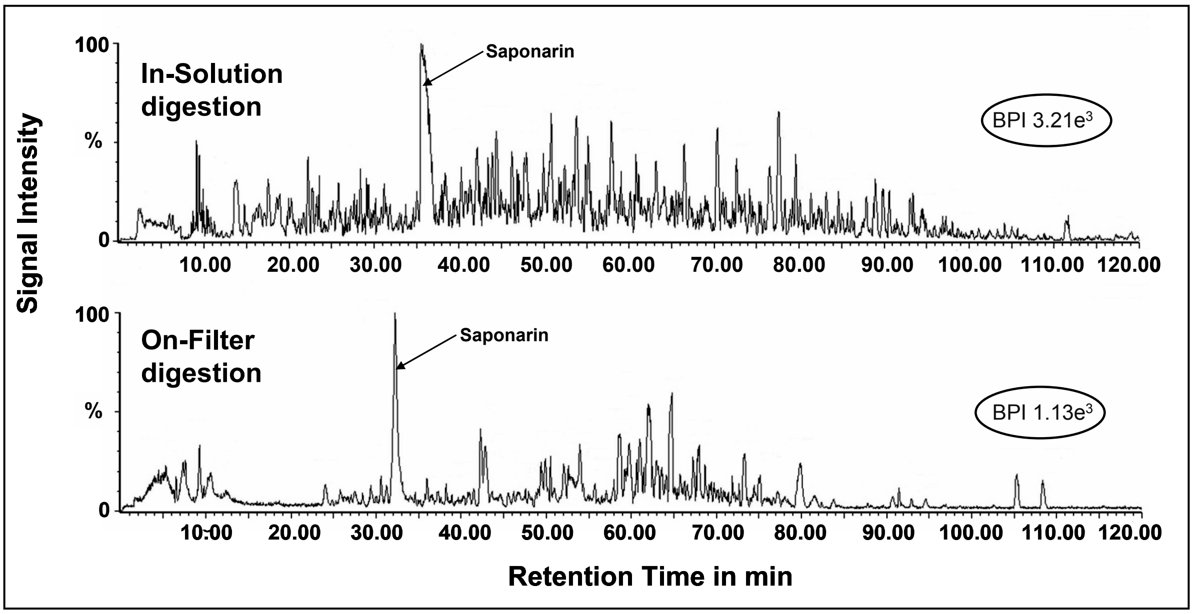


Figure 8: Comparison of sample preparation using In-Solution (upper panel) and On-Filter digestion (lower panel). Corresponding base peak intensity (BPI) chromatograms of the low energy trace from the peptide mixture of barley leaf epidermis tissue are shown. Separation was done on a nanoLC-column (C18, 15 cm) using a gradient ranging from 0-33% acetonitrile within 110 min. Subsequent detection of eluting peptides was performed using an ESI-Q-TOF mass spectrometer. An estimated total protein amount of 0.5 µg on column was injected for both experiments. The arrows mark the saponarin peak.

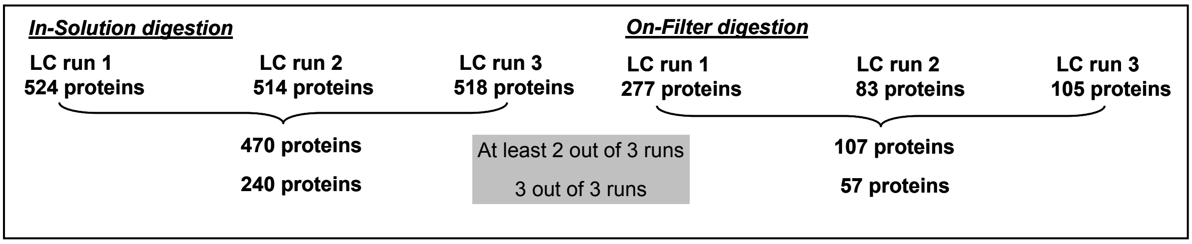


Figure 9: Comparison of the number of identified proteins for the In-Solution digestion and the On-Filter digestion procedure for the analyses of barley leaf epidermis tissue. The numbers for each of the three executed LC runs as well as the overlap of proteins found in at least two out of three runs and the number of proteins found in all three runs are given.

The results revealed that with the aid of In-Solution digestion the content of saponarin could be reduced. Even though the reduction was less than with the On-Filter digestion (denoted by the intensities of BPI signals), In-Solution digestion led to the identification of a significant higher number of proteins, and thus was applied for all samples analysed using gel-free LC-based separation.

4.1.2. Verification of LC-based separation coupled to label-free MS detection

Separation and subsequent quantification of peptide mixtures from complex protein extracts using LC-MS heavily relies on different parameters. The determination of:

- retention time stability,
- stability of mass to charge (m/z) values,

- properness of quantification based on signal intensities;

based on standard peptides was inevitable to verify the applicability of nanoLC-based separation coupled to label-free MS detection using an ESI-Q-TOF MS system prior to the analysis of biological samples.

Within the approach proteins were detected in a data-independent mode in a low and a high energy trace. Thus, peptides eluting from the nanoLC-column are constantly fragmented without precursor ion selection, leading to a continuum multiplexed LC-MS data set. Intact molecular ions obtained out of the low energy trace and associated produced fragment ions obtained out of the high energy trace have the same chromatographic profile and were therefore merged according to their retention time and m/z values to so-called EMRT clusters. A schematic diagram of the workflow is illustrated in Figure 10.

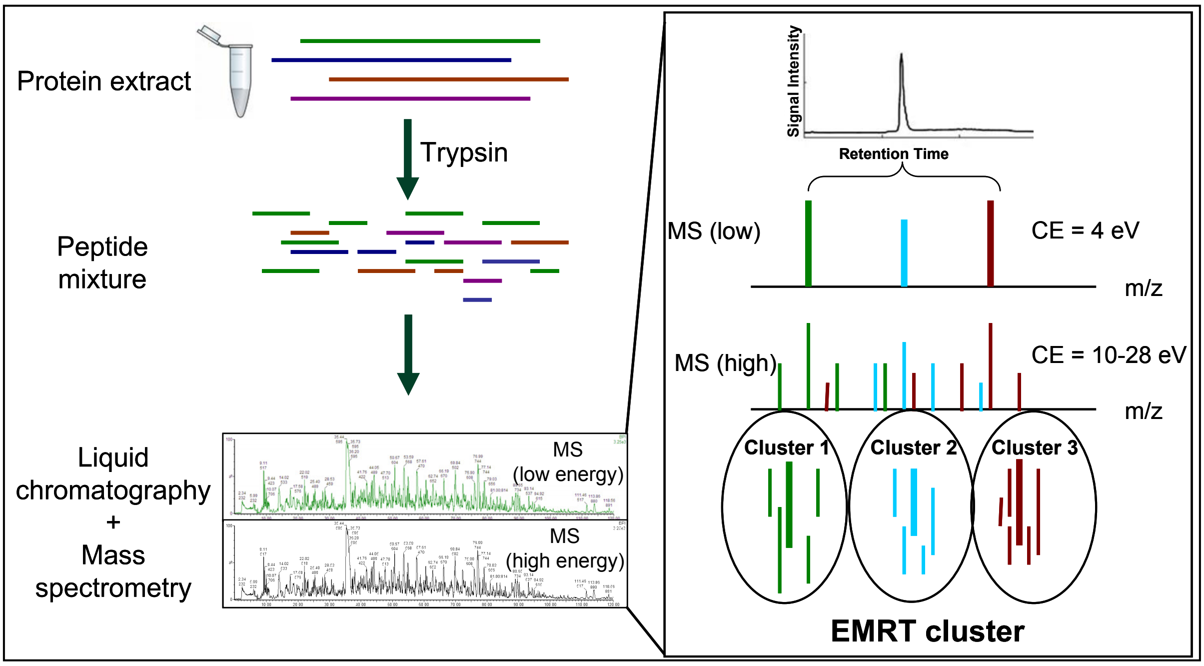


Figure 10: Schematic diagram displaying the principles of the label-free LC-MS method for quantification and identification of proteins using a multiplexed approach. A complete protein extract is digested, e.g. with porcine trypsin, and the resulting peptide mixture is subsequently separated using liquid chromatography in a reversed phase manner. Detection is performed in a data-independent mode, collecting ions in alternating low and high energy data acquisition trace. Low energy MS mode (collision energy (CE) = 4 eV) provides molecular ion and quantification information, whereas high energy MS mode (CE ranging from 10-28 eV) contains fragment ion information. Produced fragment ions and intact molecular ions have the same chromatographic profile and can therefore be grouped to exact mass retention time (EMRT) clusters.

Verification of the nanoLC-ESI-Q-TOF MS system regarding retention time and m/z stability has been carried out using standard tryptic peptides of the protein enolase derived from yeast. Retention times were determined out of BPI chromatograms and accurate m/z values out of the corresponding mass spectra. In total 5 peaks differing in their retention times and m/z values were selected for system verification and thus were monitored over 5 different injections. Corresponding data evaluation showed a high stability over the 5 LC runs for the two determined parameters (Figure 11). The average mass deviation for the monitored range was 34 ppm (5 mDa) and the average retention time deviation was 1000 ppm (6 s) at typical peak widths of 40 s at 10% basis of the bottom.

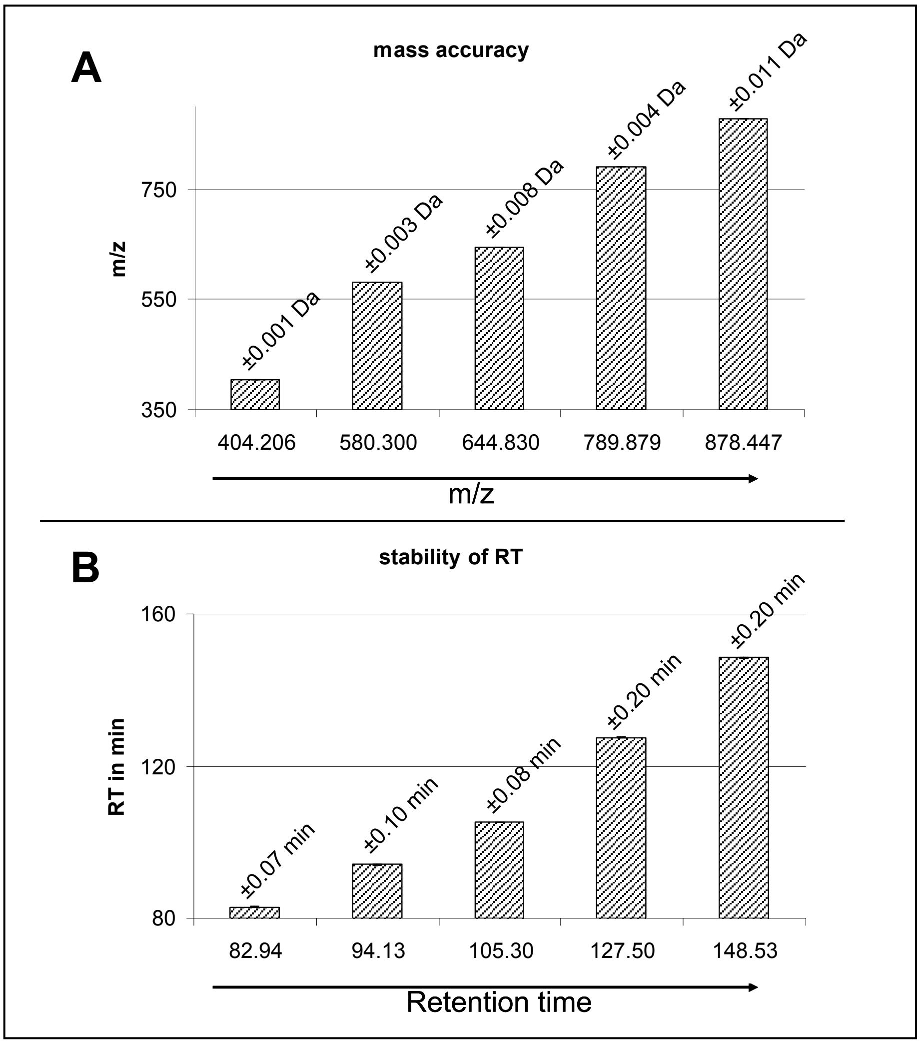


Figure 11: Verification of nanoLC-ESI-Q-TOF MS/MS system using a reference substance (100 fmol enolase (yeast)). Mass accuracy was determined for five defined m/z values (404.2; 580.3; 644.9; 789.9; 878.5) over five LC runs and showed an average deviation of 34 ppm/5 mDa (A). Retention time (RT) stability was determined for five different values distributed over the gradient (82.9; 94.1; 105.3; 127.5; 148.5 min) for five runs and showed an average deviation of 6s (1000 ppm, B).

Besides its accuracy according to retention time and m/z values, also properness of the LC-MS system for the quantification process, which is dependent on the stability of mass signal intensities, was determined. Therefore, peptides of 4 different standard proteins (yeast alcohol dehydrogenase, rabbit glycogen phosphorylase b, bovine serum albumin, yeast enolase I) were spiked in defined ratios into a complex background consisting of a protein extract of barley leaf epidermis material. Samples were injected three times and quantification efficiency was determined after data processing and database search as mean values of the three replicates. Theoretical ratios were compared with experimentally gained results (Table 4).

Table 4: Verification of the quantification efficiency of LC-based separation coupled to label-free MS detection for protein profiling. Peptides of 4 standard proteins were spiked into a complex protein background (consisting of barley leaf epidermis tissue) in defined ratios (theoretical ratio). Data processing and calculation of experimental ratios was performed subsequent to the measurements. Corresponding values together with their standard deviation are given. Peptides of yeast alcohol dehydrogenase were used for data normalization.

Protein	Amount 1	Amount 2	Ratio (theoretical)	Ratio (experimental)
Yeast alcohol dehydrogenase	50 pmol	50 pmol	1:1	-
Rabbit glycogen phosphorylase	50 pmol	25 pmol	1:0.5	1:0.5 [±0.02]
Bovine serum albumin	50 pmol	400 pmol	1:8	1:7.2 [±0.03]
Yeast enolase I	50 pmol	100 pmol	1:2	1:1.9 [±0.03]

The verification of the quantification efficiency clearly showed a high correlation between theoretical values of spiked proteins and experimentally gained results in a complex biological background.

In summary, high stability of retention times and m/z values as well as the high quantification efficiency demonstrated the feasibility of LC-based separation coupled to label-free MS detection for protein profiling approaches. Therefore, the verified method was applied for the analyses of barley leaf epidermis tissue and grain material.

4.1.3. Determination of the applicability of gel-free LC-based separation for small sample amounts

Besides the verification of the LC-MS system according to stability and quantification efficiency, the capability to analyse small sample amounts had to be determined. Therefore, different quantities of thin cryosections (5, 10, 15, and 20 cuttings) prepared from developing barley grains (8 DAF) were used for sample preparation. Bradford assay of protein extracts was performed to determine the protein concentrations and showed a coherent increase of the protein amount with the number of sections used (Table 5). Equal protein amounts (0.5 µg) of each sample were loaded onto a nanoLC-system and detection was done as described in Material and Methods section 3.2.4. Visual inspection revealed comparable BPI chromatograms of the different samples and no obvious differences in dependency on the number of cuttings used for protein extraction could be found (Figure 12).

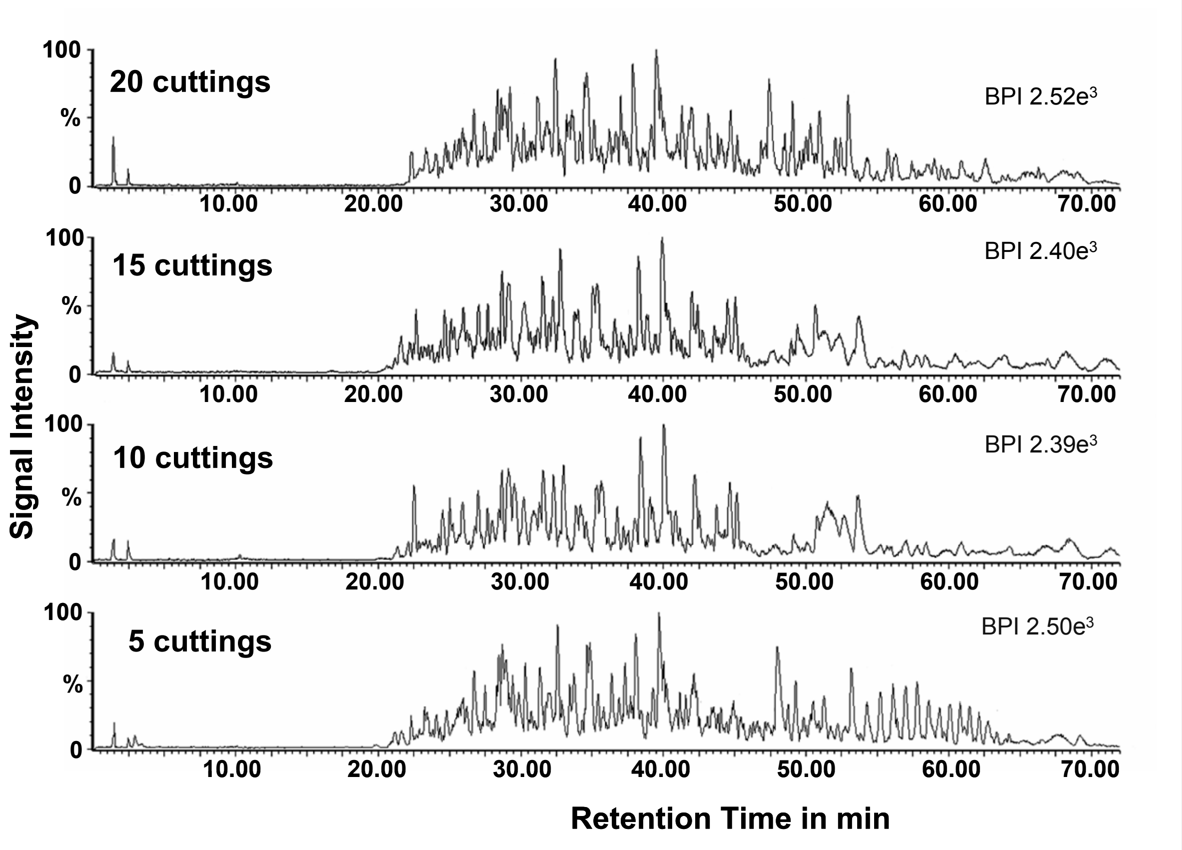


Figure 12: Base peak intensity (BPI) chromatograms of the low energy trace from LC-based separation of peptides from cryodissected cuttings gained out of barley grain material (8 DAF). Different quantities of cuttings (5, 10, 15, and 20) were used for protein extraction. Tryptic peptides (0.5 µg total amount) were separated on a nanoLC-column with a gradient from 0-33% acetonitrile and detected using an ESI-Q-TOF MS system.

Protein identification was performed against a manually assembled UniProt reference database and only proteins were taken into account for data interpretation appearing in at least two out of three technical replicates per sample. Comparable numbers of proteins were identified for the different extracts (Table 5). Results revealed applicability of the described method down to the analyses of 5 cuttings referring to 15,000,000 µm^2 of cells (417,000 µm^2 per injection) and therefore confirmed its utility for small sample amounts. Nevertheless, the experiments using different amounts of cuttings were used as pilot studies to test the properness of protein extraction and subsequent separation method. Further sophistication of the applied methods has been performed on biological relevant laser-microdissected material and included the analysis of biological replicates.

Table 5: Results of the analyses of cryodissected cuttings out of barley grains (8 DAF). Shown are the number of cuttings used for protein extraction and corresponding protein amounts. Third column displays the number of identified proteins, when protein extracts were analysed using a nanoLC-ESI-Q-TOF MS system. Protein identification was done by searching against a manually assembled UniProt reference database.

Number of cuttings	Protein amount in µg	Number of identified proteins out of 0.5 µg
5	18	261
10	22	185
15	27	213
20	45	320

In summary, the determination of optimal methods for sample preparation, protein separation, quantitative detection, and needed sample amount led to the following parameters, which were used for the analyses barley grain and leaf epidermis material presented in this work:

- In-Solution digestion has been proven to be more suitable for protein extraction compared to On-Filter digestion.
- The applicability of gel-free LC-based separation coupled to label-free MS-detection could be shown according to retention time stability and mass accuracy as well as according to the reliability of the quantification.
- Five cuttings, referring to 417,000 µm^2 sample area, were adequate for the proteome analyses of cryodissected material using nanoLC-based separation.

4.2. Protein and metabolite profiling of barley epidermis tissue

Several stress factors can dramatically effect plant growth and crop yield. It is known that the epidermis of leaves acts as an effective protector against different stresses. Nevertheless, only marginal knowledge about the proteome and metabolite profile of epidermal tissue exists. The work presented here is related to the detailed analyses of the leaf epidermis tissue of barley plants (cv. Barke) using protein and metabolite profiling techniques to gain a closer insight into its possible biological functions. Five day old seedlings, which were grown under green house conditions, were used for the analyses. Proteins and metabolites were extracted out of manually separated mesophyll and epidermis tissue.

4.2.1. Determination of chlorophyll content in barley leaf epidermis tissue

Sample preparation of epidermis is a critical issue and profiling results are reliant on the quality of separated tissue. Visual inspection of the epidermis separated from the remaining leaf did not show contamination with mesophyll. Additionally, chlorophyll content was determined in comparison to mesophyll tissue to reassure the purity of the samples. Extraction of chlorophyll was performed for all three harvests in three replicates per harvest (Material and Methods section 3.4.1). Results revealed chlorophyll amounts below 10% for all three harvests in epidermis tissue compared to mesophyll (set to 100%), displaying a good separation of epidermis tissue from the mesophyll (Table 6).

Table 6: Determination of chlorophyll content in barley leaf epidermis tissue compared to mesophyll. Chlorophyll was extracted and measured as described in Material and Methods section 3.4.1. Three technical replicates per harvest were performed and values for epidermis were calculated in correlation to the chlorophyll content in mesophyll (set to 100%). Average values (in %) together with their standard deviation are given.

Harvest	Chlorophyll content in % (± standard deviation)
1	9.3 (0.8)
2	6.6 (0.8)
3	6.0 (0.1)

4.2.2. Mapping the proteome of barley leaf epidermis tissue

Epidermis protein profiling using 2-D gel electrophoresis

With the aim to obtain more insights into the molecular functions of barley leaf epidermis tissue, a protein reference map using 2-DE was established. The application of 2-DE for the analysis of barley leaf epidermis tissue was feasible as sufficient sample material could be prepared. Protein extraction using TCA/Acetone method, separation by 2-DE and visualisation using colloidal Coomassie Brilliant Blue was performed as described in Materials and Methods section 3.2.3. The technical reproducibility of protein separation was ensured by setting up three 2-D gels per sample. Spots were detected using image analysis software. Proteins found in three independent harvests in at least two technical replicates per harvest were included in the reference map. Three-hundred and seventy-four proteins fitted these criteria and were collected from 2-D gels using an automated spot picker. A representative 2-DE image is shown in Figure 13. All spots included in the reference map are marked in Figure A 3 and corresponding spot list is provided in Table A 1.

Protein identification was performed as described in Materials and Methods section 3.2.3 on the basis of peptide mass fingerprint data (MALDI-TOF MS) and/or *de novo* sequencing data (nanoLC-ESI-Q-TOF MS). Following the described procedures, protein identification was successful for 318 spots by searching against the barley EST database HarvEST using Biotools 3.0 (Bruker Daltonics) with the implemented MASCOT search engine (Matrix Science) for peptide mass fingerprint data and PLGS 2.3. software (Waters) for *de novo* sequencing. About 75% of the protein spots could be identified using peptide mass fingerprinting and additional 8% were identified by *de novo* sequencing of tryptic peptides.

Spot 544, identified using MALDI-TOF MS as succinyl-CoA ligase alpha 2 subunit with a sequence coverage of 28%, is shown as an example in Figure 14A. Spot 667 could be successfully identified as glyceraldehyde 3 phosphate dehydrogenase using LC-ESI-Q-TOF MS with a sequence coverage of 10% (Figure 14B).

In total, 387 proteins could be detected within the 318 excised protein spots. The higher number of identified proteins compared to the number of detected spots was caused by multiple protein identifications in single spots. Among the identified proteins, 168 were found to be unique. Proteins with multiple observations revealed similar molecular weight but differed in the isoelectric point (spot number 204, 206, 207; Figure 13 B, identified as vacuolar ATP synthase) and vice versa (spot number 913, 924, 932; Figure 13 C, identified as RNA binding protein). Changes in the isoelectric point or the molecular weight can be caused by post-translational modifications, and/or are due to isoforms or degradation processes. A more detailed consideration of this aspect can be found in the discussion (chapter 4.2.2). The most abundant protein appeared in six different spots (spot number 421, 423, 429, 431, 432, 445; Figure 13 D), and was identified as S-adenosylmethionine synthetase. The complete list of identified proteins is provided in the appendix, Table A 1.

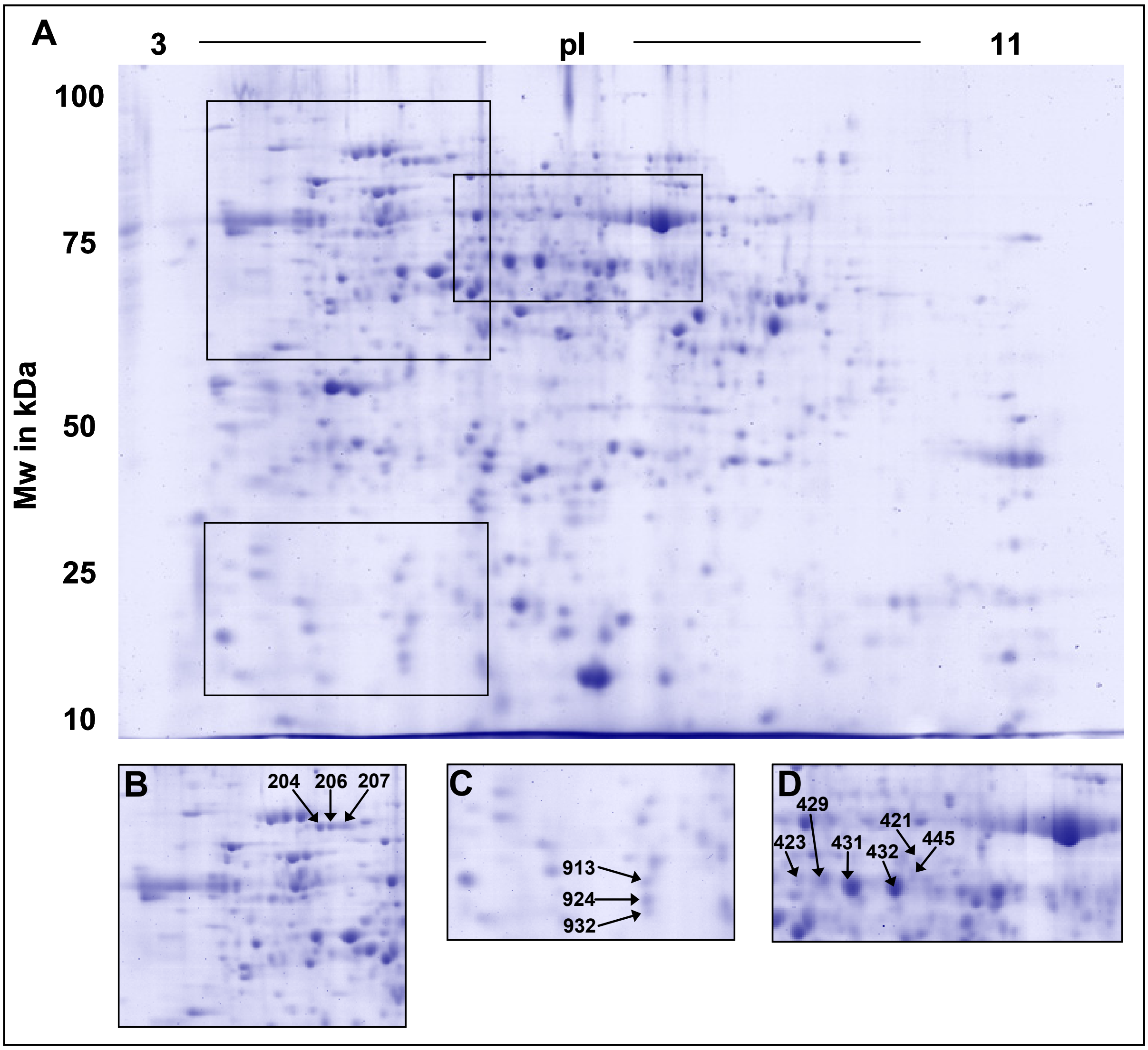


Figure 13: (A) Representative 2-DE image for the mapping of barley leaf epidermis proteins. Polypeptides were extracted using TCA/Acetone method, separated by 2-DE (first dimension: non-linear pH gradient from 3-11; second dimension: 11.25% SDS-Page) and stained using colloidal Coomassie Brilliant Blue (cCBB). (B, C, D) Enlarged regions of the gel. A reference map displaying the spots and their corresponding spot number is provided in Figure A 3.

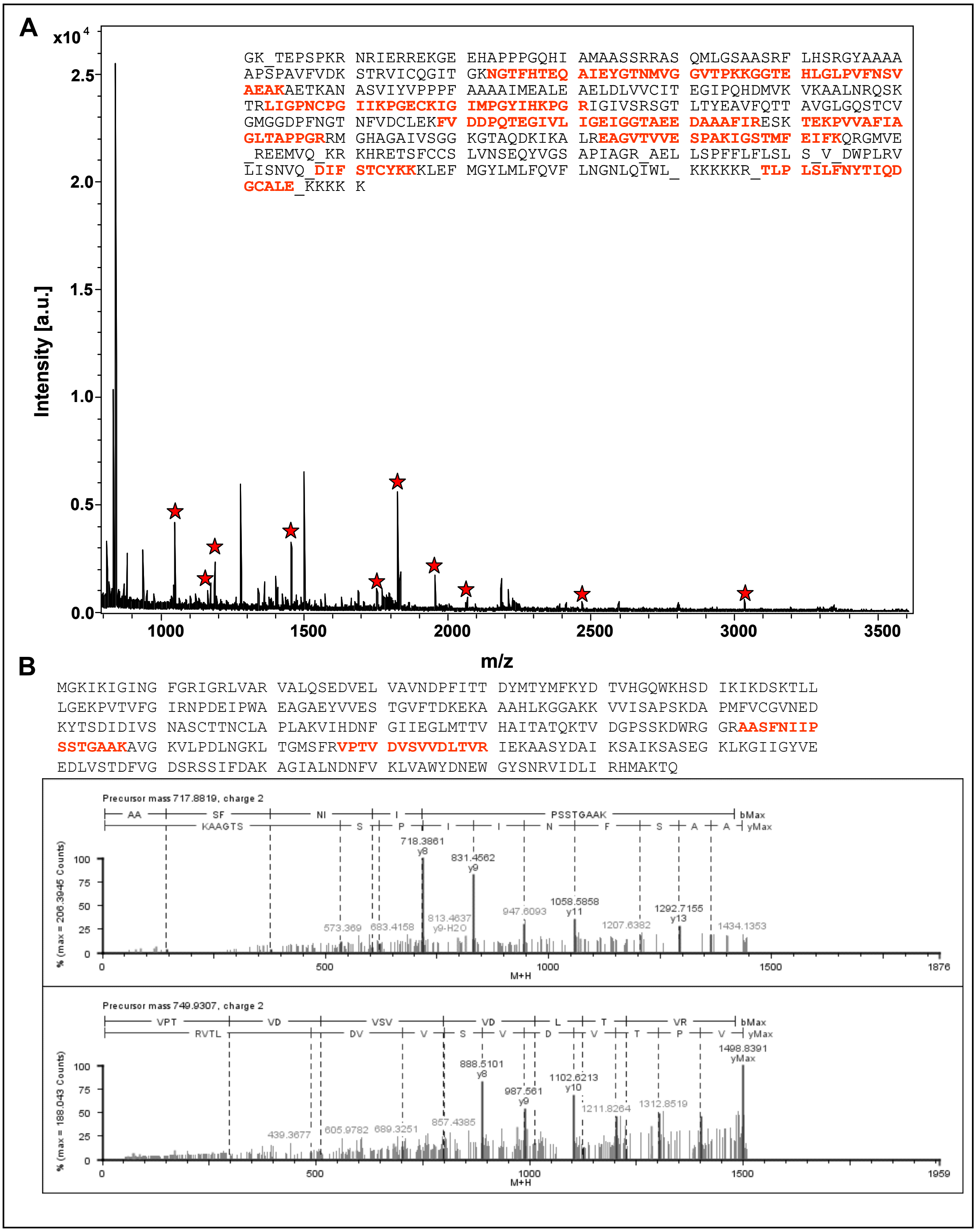


Figure 14: (A) Identification of spot 544 as succinyl-CoA ligase alpha 2 subunit using MALDI-TOF MS is shown. The amino acid sequence (black), the peptides detected (red) and the corresponding mass spectrum are shown. Masses that were used for the identification were marked with a red star. A sequence coverage of 28% was obtained. (B) Identification of spot 667 as glyceraldehyde-3-phosphate dehydrogenase using LC-ESI-Q-TOF MS with a sequence coverage of 10%. Shown above are the amino acid sequence (black) and the detected peptides (red). The fragment spectra of the peptides with m/z 717.88 [M+H$^+$] (sequence: AASFNIIPSSTGAAK, upper panel) and m/z 749.93 [M+H$^+$] (sequence: VPTVDVSVVDLTVR, lower panel) are displayed.

Epidermis protein profiling using gel-free LC-MS approach

It has already been described that gel-based and gel-free separation methods lead to complementary data sets and thus the additional appliance of nanoLC-MS analysis should increase the number of identified proteins in barley leaf epidermis tissue.

Protein extracts processed using In-Solution digestion (as described in Results section 4.1.1.) were separated and analysed by nanoLC-MS approach in three injections per sample for three independent harvests. BPI chromatograms of the triplicate runs for the first experiment are shown in Figure 15.

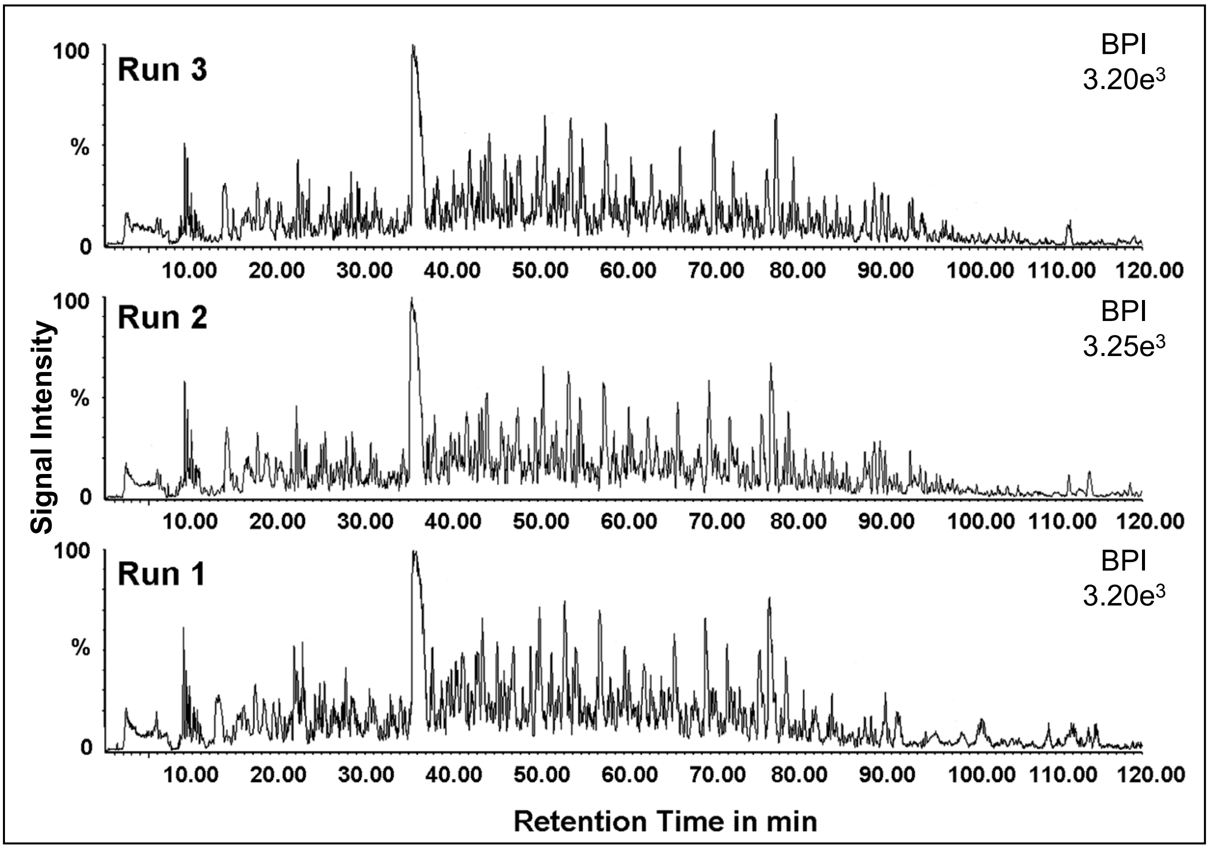


Figure 15: Base peak intensity (BPI) chromatograms of the low energy trace from LC-based separation of peptide mixture of barley leaf epidermis tissue. Tryptic peptides were obtained using In-Solution digestion. Separation was done on a nanoLC-column (C18, 15 cm) using a gradient ranging from 0-33% acetonitrile within 110 min. Subsequent detection of eluting peptides was performed using an ESI-Q-TOF MS in a multiplexed mode. Triplicate runs of one sample are displayed and show the high degree of similarity for retention time (x-axis) as well as signal intensity (y-axis) across the injections.

Protein identification was done subsequent to data processing by searching against the HarvEST database. Proteins had to be identified with at least two different peptides in one LC run. In total 230 proteins were found in all three harvests in at least two technical replicates per harvest. Seventy-five proteins were found to overlap with 2-DE approach. The complete protein list is shown in the appendix (Table A 2).

Functional classification of identified proteins in barley epidermis tissue

Using 2-DE as well as LC-MS approach 542 proteins (2-DE: 387 proteins, LC-MS: 230 proteins, 75 proteins detected in both approaches) were identified. Among those proteins, 321 unique features occurred. The complete list of identified proteins is provided in Table A 1 for the 2-DE approach and Table A 2 for the LC-based separation. The detected proteins were grouped due to their functional distribution according to an established scheme described for plants (Bevan *et al.* 1998). The assignment of proteins into their function is shown in Figure 16 for the proteins found exclusively either in the 2-DE or the LC-MS approach, and for the proteins found in both approaches (LC-MS + 2-DE).

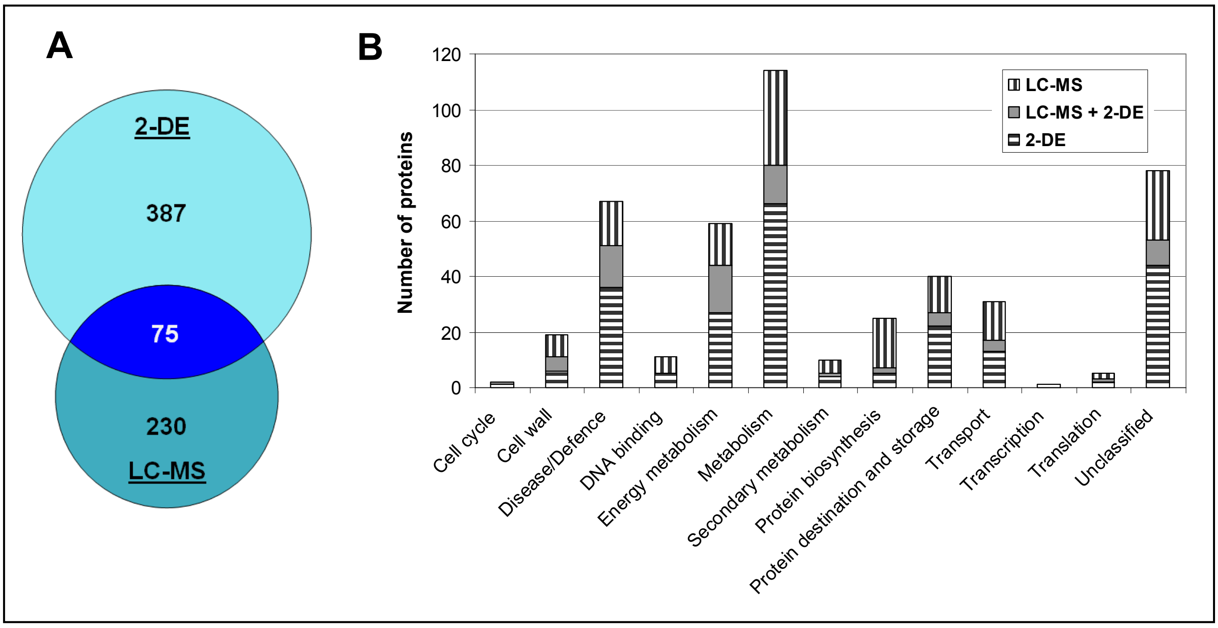


Figure 16: Results of the protein profiling of barley leaf epidermis tissue using 2-DE and gel-free LC-MS analysis. (A) Number of identified proteins in the 2-DE and the LC-MS approach are given, together with the number of overlapping proteins. (B) Assignment of proteins identified within the profiling of barley leaf epidermis tissue according to their functional classification. Total number of proteins gained out of 2-DE and LC-MS, and in both approaches (LC-MS + 2-DE), is shown. Classification was done according to a previous described assignment scheme (Bevan *et al.* 1998).

The functional grouping patterns looked similar for both methods, even though the overlap of identified proteins was only around 35% (75 proteins). Most proteins of the combined data set were allocated towards general metabolism (114 proteins), whereas the second largest group encoded for proteins with no classification as yet (80 proteins). The proteins of the third major group are involved in disease and defence processes (67 proteins). Only few proteins were found that are involved in transcription, translation, and cell cycle processes. In the group of secondary metabolite-related proteins, key enzymes required for the synthesis of flavonoids could be detected (phenylalanine ammonia-lyase, chalcone synthase, chalcone isomerase, chalcone-flavone isomerase).

In general, the resolved proteome of barley epidermis tissue revealed a proportion of proteins related to primary metabolism and energy metabolism. Nevertheless, disease and defence-related proteins were higher in frequency than energy metabolism-related proteins. Out of the disease and defence-related proteins, a high number of detoxification-related proteins, like peroxidase, ascorbate peroxidase, glutathione peroxidase, dehydroascorbate peroxidase, and superoxide dismutase Cu/Zn 2, were detected. Additionally, a putative stress-induced protein and a stress-related like protein interactor were detected in multiple spots in the 2-DE approach.

Proteins detected exclusively by 2-DE or by LC-MS were broadly distributed in their molecular function and with regard to their biochemical aspects. Method specific differences in the separation range occurred and thus were responsible for the detection of some of the proteins in only one of the approaches. Whereas 2-DE led to the identification of proteins within a molecular weight range of 16,000 to 125,000 and a pI range of 5 to 11, LC-MS was successful in the identification of proteins in the molecular weight range of 8,000 to 114,000 and in the pI range of 4 to 12. Especially the broader pI range led to the identification of distinct proteins exclusively within the LC-MS approach. Several 14-3-3 proteins, which pI ranges from 4.5 to 4.8, were detected only by LC-MS, whereas none of them were found with 2-DE. Further general statements about possible differences between the proteins detected solely in one of the applied methods could not be drawn.

4.2.3. Assessment of stress-related processes in correlation to mesophyll tissue by Western blot analyses

Several proteins detected in barley leaf epidermis tissue are considered to be involved in defence processes against abiotic and biotic stress factors. A more detailed analysis of some of the stress-related components was performed in comparison to leaf tissue for one biological experiment by Western blotting using antisera against ADH, APX, PAL, PR-Q, STINT, and SOD (Cu/Zn). Expression patterns obtained using immunoblotting differed for the analysed proteins (Figure 17).

A higher expression in the mesophyll was observed for ADH. PAL and APX, both occurring in 2 bands, were detected nearly to the same extent in epidermis and mesophyll. Immunodetection of SOD led to 4 bands showing differences in their expression patterns between mesophyll and epidermis, at which the first two bands were slightly higher expressed in the mesophyll and the third and fourth band in epidermis. A higher expression in epidermis tissue was observed for STINT and PR-Q, whereas the latter occurred in three bands.

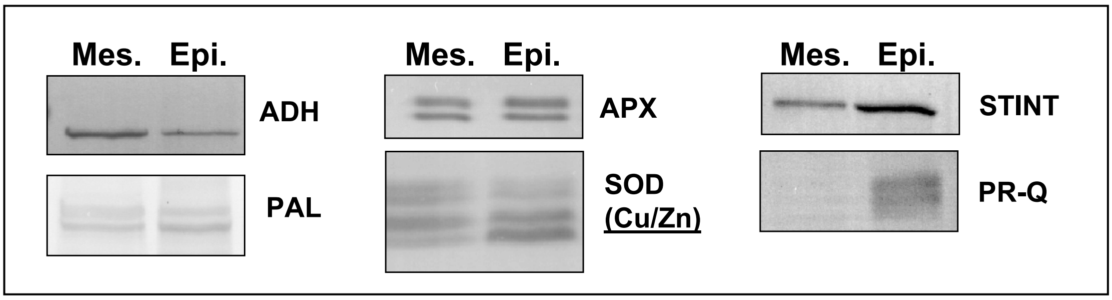


Figure 17: Western blot analysis of selected proteins with antisera against alcohol dehydrogenase (ADH), phenylalanine ammonia-lyase (PAL), ascorbate peroxidase (APX), superoxide dismutase (SOD), stress-inducible protein in *Nicotiana tabacum* L. (STINT), and a pathogen-related protein (PR-Q) for a comparison of mesophyll (Mes.) and epidermis (Epi.) tissue.

4.2.4. Analyses of metabolites in the leaf epidermis using GC-MS

Gas chromatographic separation coupled to MS detection (GC-MS) was applied to investigate the function of barley epidermis tissue on metabolite level. Quantification of metabolites was performed in correlation to the remaining mesophyll tissue based on equal fresh weight for both tissues. After derivatization, extracted metabolites were separated and analysed on a GC-MS system as described in Material and Methods section 3.4.3. Visual inspection of the chromatograms revealed a higher complexity for mesophyll tissue compared to epidermis also denoted by the number of detectable peaks (55 *vs.* 41, respectively). Corresponding typical total ion chromatograms (TIC) are shown in Figure 18. Metabolites out of three biological harvests were measured. Data were acquired for three extractions per harvest and two GC-MS runs per extraction leading to 18 GC-MS runs per tissue type.

Complete data sets were included into a PCA, which was accomplished with the parameters described in Materials and Methods (section 3.4.3). Calculated clusters correlated strongly with the two different tissue types revealing intense differences on metabolite level between the two target tissues (Figure 19). In total 26 compounds could be identified, among them 12 amino acids. A comparative analysis of the relative metabolite amounts was performed between mesophyll and epidermis tissue based on mass peak intensities of compound-specific MS fragments (Figure 20).

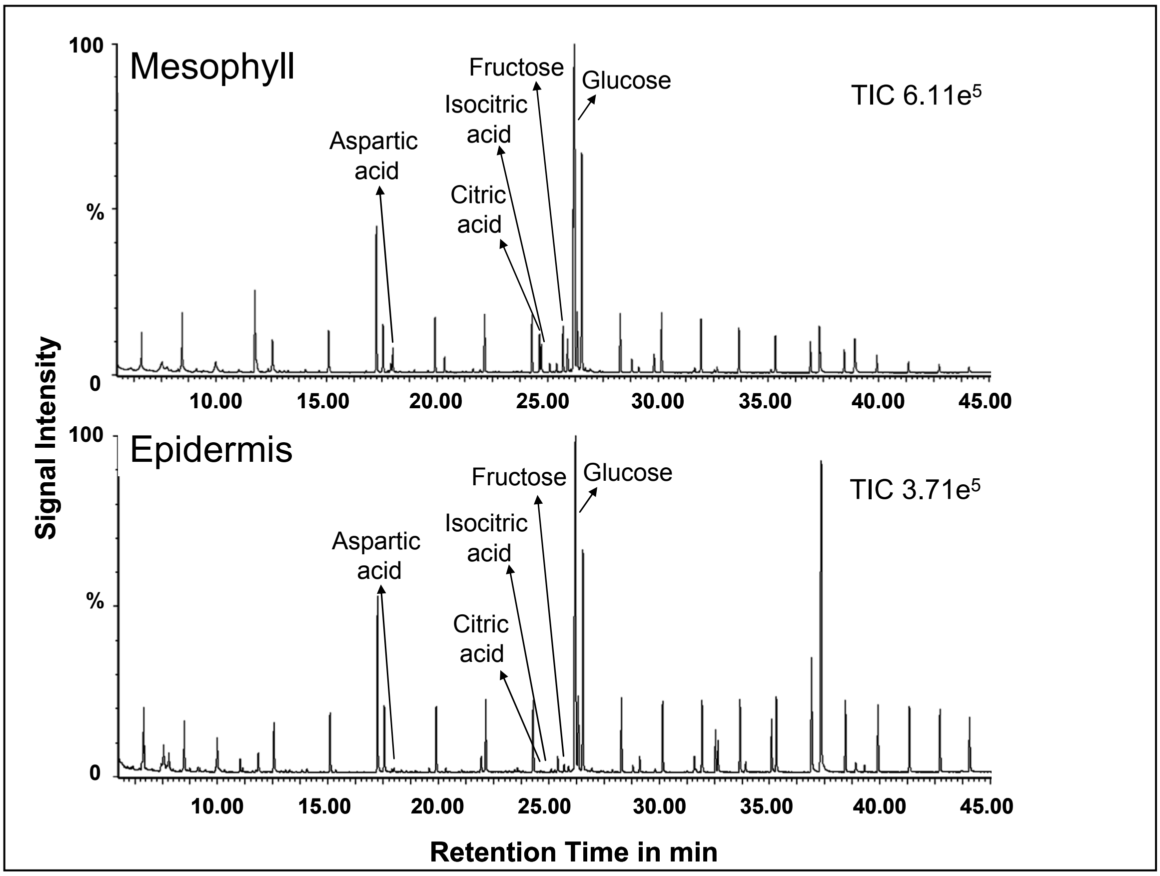


Figure 18: Representative total ion chromatograms (TIC) of GC-MS analysis of metabolites extracted out of barley mesophyll (upper part) and epidermis (lower part) tissue. Metabolites were separated using gas chromatography and detection was done on a TOF mass spectrometer (GCT Premier, Waters). Same fresh weight was used for both tissues for metabolite extraction (50 mg). Some detected metabolites are assigned as examples.

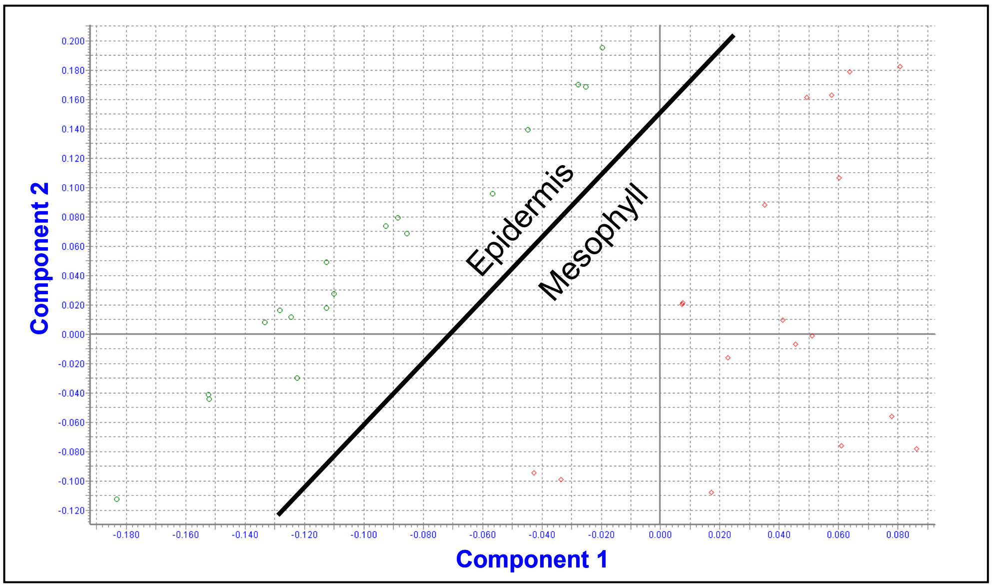


Figure 19: PCA plot for metabolite analyses of barley leaf epidermis (green) and mesophyll tissue (red). Principal component 1 is plotted against principal component 2. Data sets out of 18 GC-MS runs per tissue type (three independent harvests, three extractions per harvest and two injections per sample) were included into the analysis. Separation between both tissue types is visible and was marked by a black line.

Significant differences in metabolite profiles of barley leaf epidermis and mesophyll were monitored. Highest signal intensities in mesophyll tissue were detected for citric acid, fructose, glucose, sucrose, l-alanine, isocitric acid, aspartic acid, serine, and 4-hydroxyproline (Figure 20A). Lower signal intensities were detected for valine, isoleucine, proline, glycine, threonine, β-alanine, aminoisobutyric acid, methionine, fumarate, malate, inositol, arabinose, glutamine, asparagine, putrescine, and succinic acid (Figure 20B). Most measured metabolites, besides β-alanine, were significantly higher in mesophyll tissue compared to epidermis tissue. Corresponding P-values are indicated in Figure 20. Major differences were determined for citric acid, isocitric acid, aspartic acid, fructose, and sucrose. Sucrose, methionine, isoleucine, and isocitric acid could not be detected in epidermis tissue. Fumarate and malate, both involved in the cellular respiration within the tricarboxylic acid cycle, were amongst the five highest expressed metabolites in epidermis tissue. A high number of enzymes involved in this pathway were detected in barley leaf epidermis tissue using proteomic profiling (pyruvate dehydrogenase, isocitrate dehydrogenase, fumarate dehydrogenase, malate dehydrogenase). Only late products of the citrate cycle were detected in epidermis tissue, whereas citric acid and isocitric acid could be detected in relatively high amounts in mesophyll tissue.

Even though GC-MS analysis revealed first information about tissue-specific distribution of metabolites in barley leaf tissue, low signal intensities close to the detection limit were observed for several metabolites. The enlarged view into the low intensity range of the TIC for epidermis and mesophyll clearly showed low signal intensities for different metabolites (Figure 21). Especially some of the amino acids, like asparagine, but also β-alanine, methionine, and glutamine were detected with low intensities close to the detection limit. Thus, a targeted extraction and separation of these compounds was necessitated.

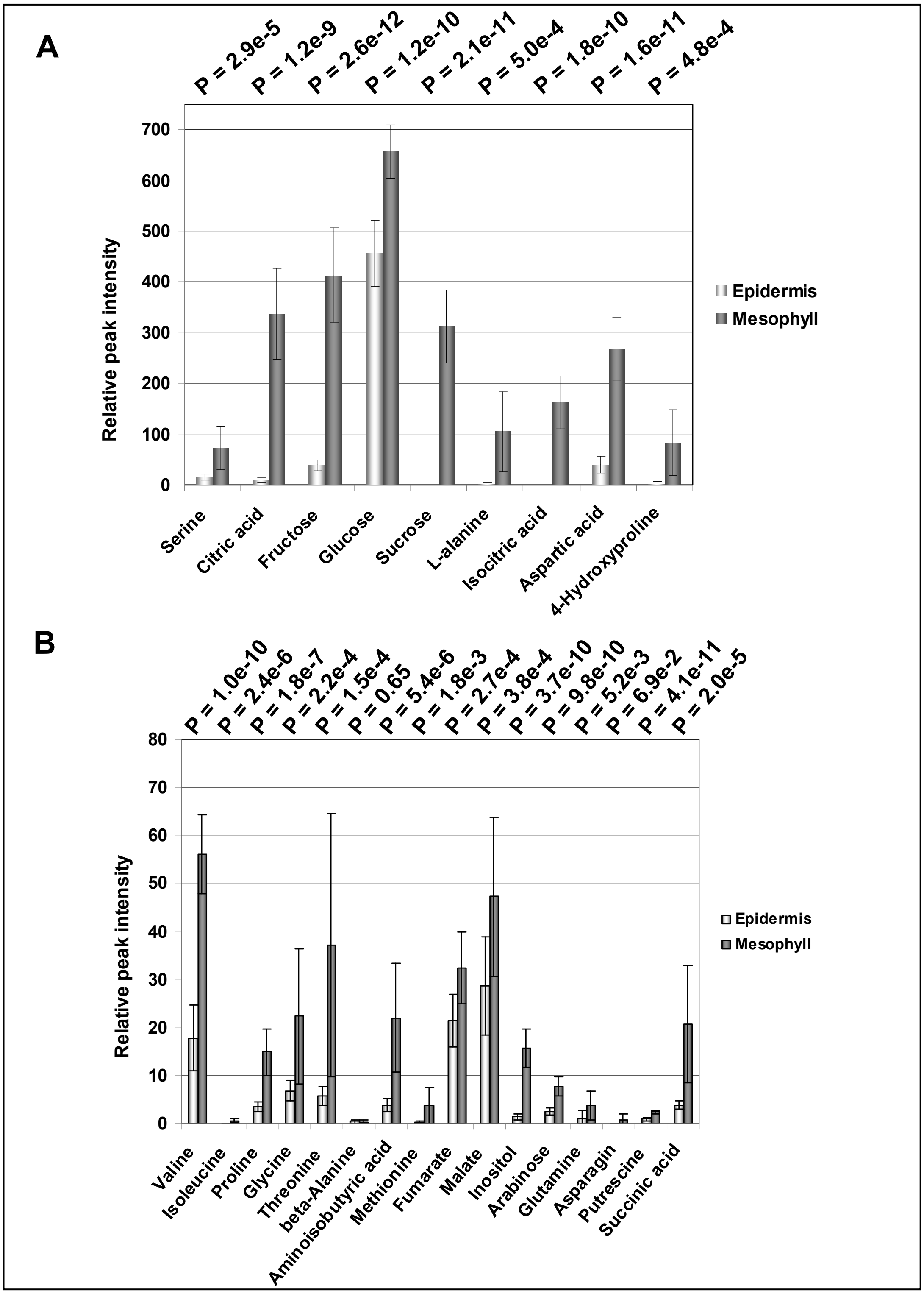


Figure 20: Results of the relative comparison of metabolites detected and identified using GC-MS analysis between epidermis and mesophyll tissue. Metabolite extraction was done using same fresh weight for both tissues (50 mg). Correlation was performed based on the MS peak intensities of compound specific fragments. Comparison of compounds with higher signal intensities (A) as well as close-ups of metabolites detected in only small relative amounts (B) are shown. P-values derived from the conducted t-test (Microsoft Excel) are given in the upper parts of the diagrams to display the significance of differences in relative peak intensity between epidermis and mesophyll tissue.

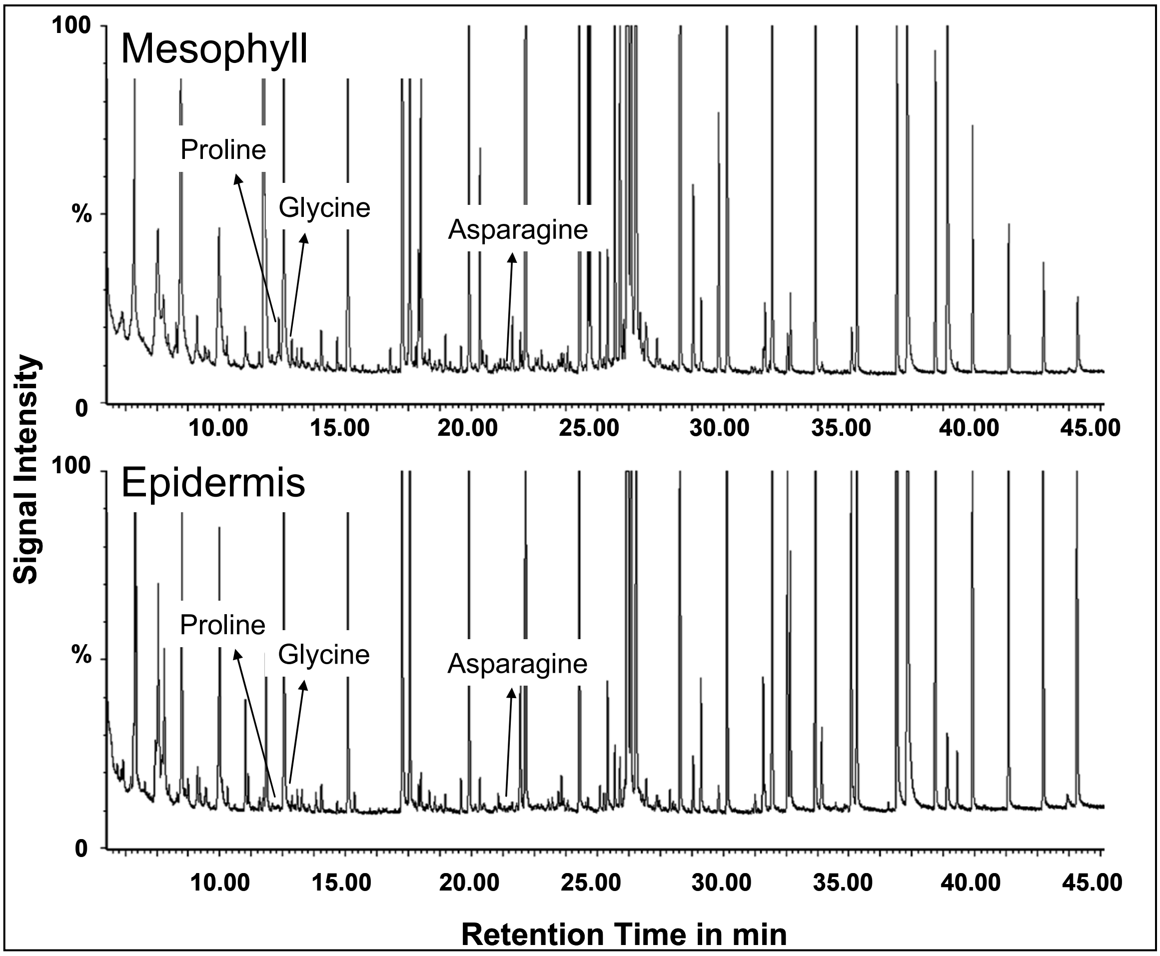


Figure 21: Representative total ion chromatograms (TIC) of GC-MS analysis of metabolites extracted out of barley mesophyll (upper part) and epidermis (lower part) tissue. Picture shows enlarged region of the low intensity signals. Metabolites were separated using gas chromatography and detection was done on a TOF mass spectrometer GCT Premier (Waters). Same fresh weight was used for both tissues for metabolite extraction (50 mg). Some detected metabolites are assigned as examples.

4.2.5. Analyses of amino acids using HPLC/Fluorescence detection

Differences between epidermis and mesophyll tissue emerged within the identified amino acids in the GC-MS approach (Figure 20). As the detected amounts for amino acids were relatively low, HPLC separation coupled to fluorescence detection was additionally applied for the analyses of barley leaf epidermis and mesophyll tissue (Material and Method section 3.4.2). Data were acquired in three biological replicates and three injections per replicate both for mesophyll and epidermis tissue. Mean values were used to reveal differences and equalities between both tissue types. A significantly higher content in mesophyll tissue compared to epidermis tissue was observed for most of the detected amino acids (Figure 22). The corresponding P-values are indicated in Figure 22. Proline contents revealed no significant difference between both target tissues. Also histidine, serine, tyrosine, methionine, and isoleucine were found to occur in a nearly comparable extent in both tissue types contradictory to the results gained out of GC-MS analyses. Glycine was the only amino acid detected in significantly higher amounts in epidermis compared to mesophyll tissue. Methionine and isoleucine were detected in relatively low amounts (< 100 fmol/mg fresh weight) in both tissue types comparable to GC-MS analysis.

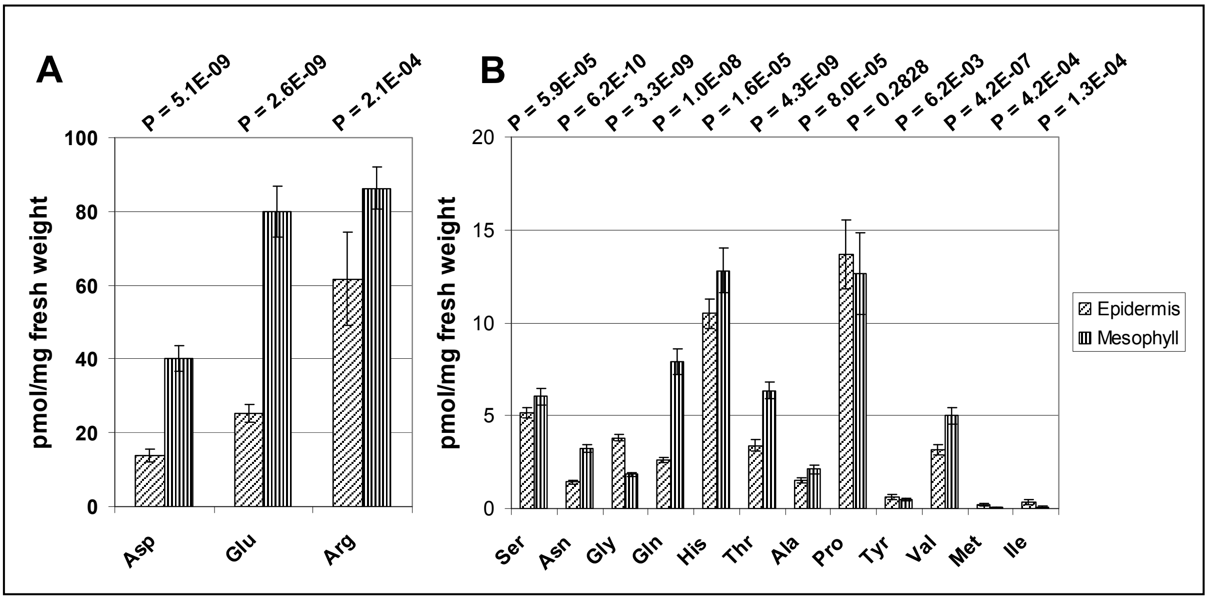


Figure 22: Determination of the content of amino acids in barley leaf epidermis and mesophyll using HPLC coupled to fluorescence detection. Amino acids were separated on a AccQ.Tag, 3.6 mm x 150 mm column using an acetonitrile gradient ranging from 0–18% within 45 min. Shown are the mean values of the total amount in pmol/mg fresh weight of three biological replicates and three injections per replicate, together with the standard deviation separately for high abundant (A) as well as lower abundant (B) amino acids. P-values displaying significance of differences in the relative peak intensities between epidermis and mesophyll tissue are given.

The targeted approach using HPLC-separation coupled to fluorescence detection revealed contradictory results for some amino acids compared to GC-MS analysis, e.g. glycine. A detailed consideration of possible reasons for the method-specific differences can be found in the discussion (section 5.2)

4.3. Proteome analyses of developing barley grains

This chapter deals with the qualitative and quantitative protein profiling to investigate temporal distribution patterns during barley (cv. Barke) grain development. Five different time points ranging from early to late developmental stages were included in the analyses (3, 5, 7, 10, and 16 DAF, see Figure 23). Comparative protein profiling was performed using a label-free LC-MS approach (chapter 4.3.1.). One major aspect of grain development is the nutrient transfer from maternal to filial tissue, which is accomplished by the NP and the ETC. It was aimed to obtain a closer insight into the composition of both tissue types on proteome level as both cell types influence the influx of metabolites into the developing grain. For this purpose laser-micro-dissected tissues were analysed.

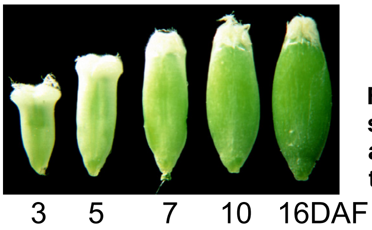


Figure 23: Barley (cv. Barke) grains from five different developmental stages (3, 5, 7, 10, and 16 days after flowering (DAF)) used for the analyses of temporal protein distribution patterns are displayed (picture taken from W. Weschke, IPK Gatersleben).

4.3.1. Temporal protein expression patterns during barley grain development

Analyses of changes in protein expression patterns during barley grain development were performed in two independent experiments using gel-free LC-based separation coupled to label-free mass spectrometric detection (as described in Material and Methods, section 3.2.1). Optimized sample preparation, as well as verified separation and detection methods were applied as described in section 4.1.

Equal protein amounts (experiment 1: 0.15 µg, experiment 2: 0.5 µg) of the five different time points were used for LC-based separation for each experiment and samples were analysed in triplicates. Chromatograms of the samples were consistent over all injections, whereas strong variation between the different developmental stages could already be monitored in the corresponding BPI chromatograms of the low energy trace from the different LC runs (Figure 24).

Data were recorded using label-free multiplexed MS detection. The suitability of this method for protein expression analyses has already been verified (see section 4.1 in the results part). The data out of high and low energy trace were clustered among the different developmental stages and including the technical replicates of one time point according to their m/z values and retention times (EMRTs). A schematic overview about the data clustering throughout the complete sample set is shown in Figure 25.

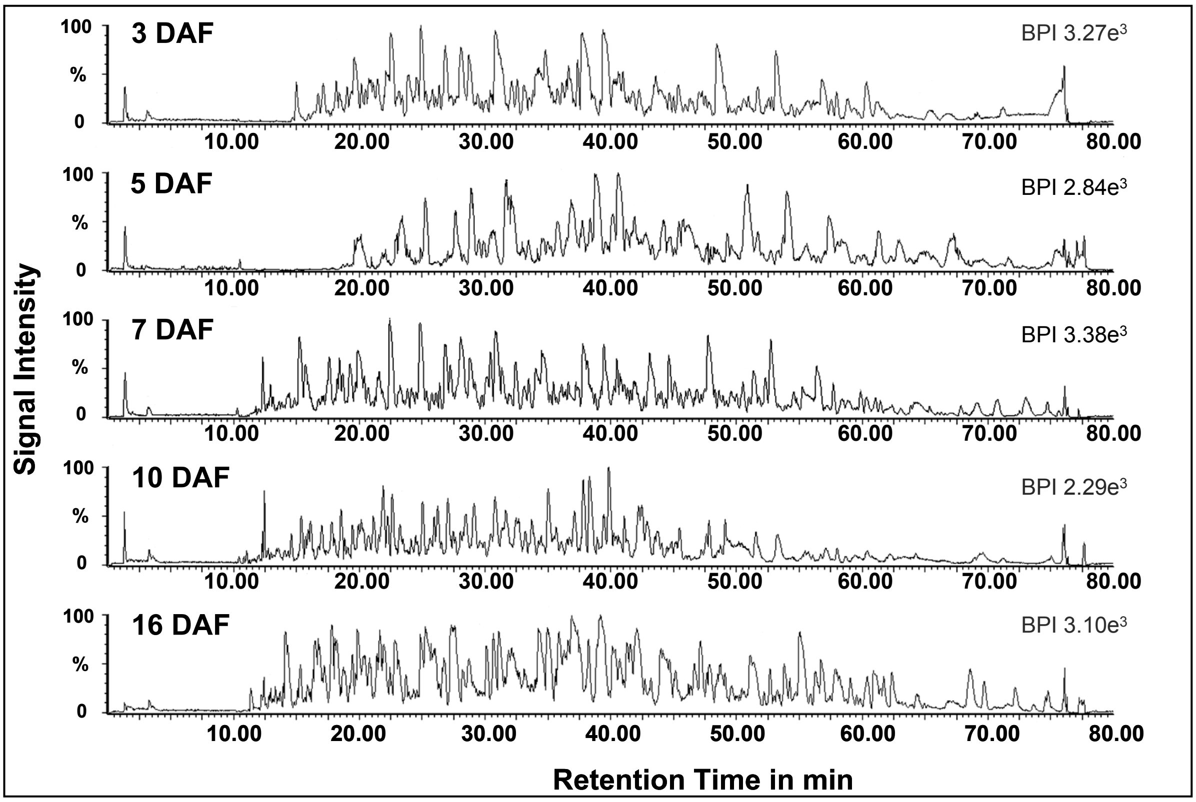


Figure 24: Base peak intensity (BPI) chromatograms of the low energy trace from protein expression analyses of barley grain development. Equal amounts of protein (0.15 or 0.5 µg) for each of the measured time points (3, 5, 7, 10, and 16 DAF) were loaded onto a nanoLC-column and separated using an acetonitrile gradient ranging from 0-33% and detected using multiplexed LC-MS mode. The present data was derived from the second experiment.

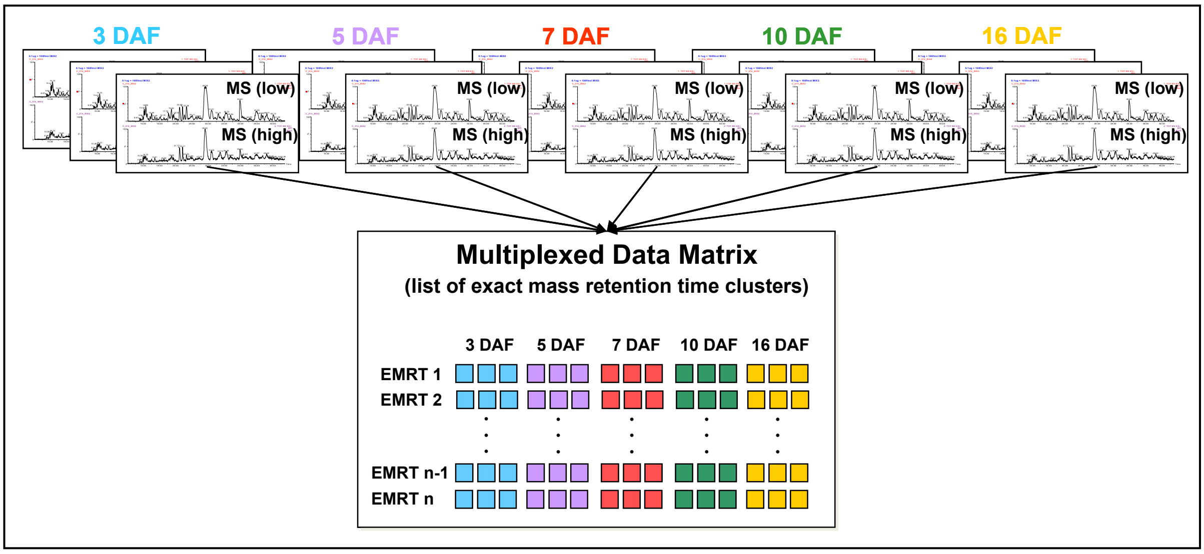


Figure 25: Overview about multiplexed data processing of the analyses of barley grain development from one experiment. Three technical replicates were conducted per time point. Corresponding data was clustered among the different samples and within the technical replicates according to m/z values and retention time to EMRT pairs.

Results were composed of a list containing information about mass signal intensities and retention times for all three replicates of each included time point. In total, 15 LC runs (five time points, three injections per time point) and around 60,000 EMRTs for each of the two conducted biological experiments had to be compared for elucidation of kinetic proteins patterns during barley grain development.

In summary, 51,098 EMRTs were detected in the first experiment and 78,530 EMRTs in the second. The single runs per sample were highly similar, as the measured precursor signal intensities of the replicate injections showed almost no variation for all time points. The results for the developmental stage at 3 DAF are shown as an example for both experiments (Figure 26, A). A 45° diagonal line was obtained displaying almost no variation between the two injections throughout the detected range. Some EMRTs are located directly either on the x- or y-axis, meaning that they were found only in one of the runs. Nevertheless, the vast majority of features were reproducibly detected throughout the multiple injections. For both experiments all of the detected EMRTs showed a relative standard deviation of <5% of their ion intensity (Figure 26, B). As a high stability of replicate runs and ion intensities was also achieved for the remaining time points in both experiments, the recorded data sets were found to be reliable for further in-depth investigations.

Whilst the replicate runs of one sample showed a high similarity, the measurements between the time points differed. A comparison of logarithmic normalised signal intensities of gained EMRTs between different time points can be used to roughly display differences in the intensity of single peptides between different time points. These data already revealed that variations were larger when comparing early and late developmental stages. For example the differences of logarithmic normalized signal intensities between 3 DAF and 5 DAF were quite complex, but they were still smaller than those between samples from 3 DAF and 16 DAF (Figure 27).

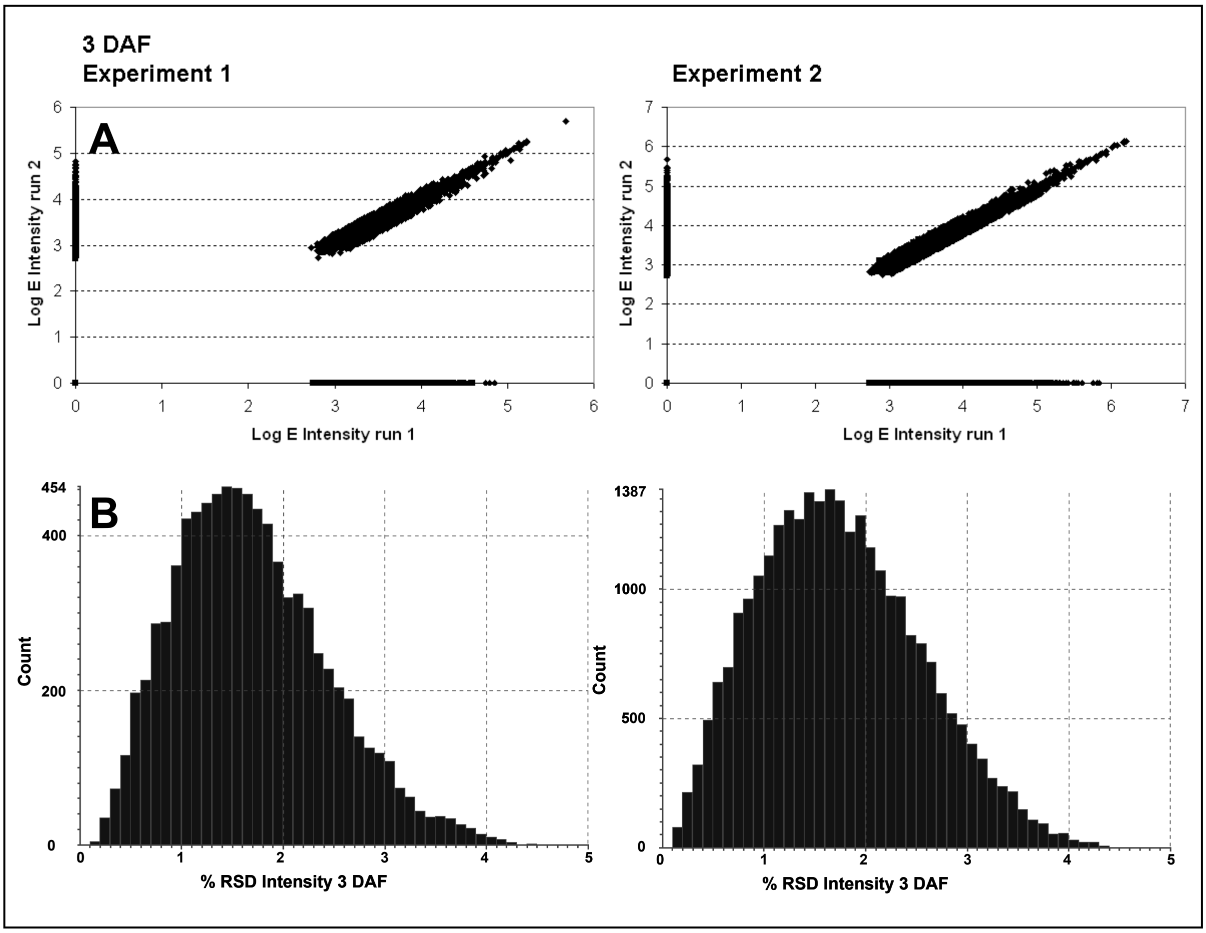


Figure 26: Evaluation of the data quality for the LC-MS analyses of developing barley grains. (A) Displayed are the logarithmic signal intensities of 2 independent LC runs (run 1 and 2) recorded for the developmental stage of 3 days after flowering (DAF) for both conducted experiments. (B) The relative standard deviation (RSD) in % of the ion intensities are shown for one time point (3 DAF) for both experiments. All of the detected EMRTs showed a RSD of <5% of their ion intensity for both experiments.

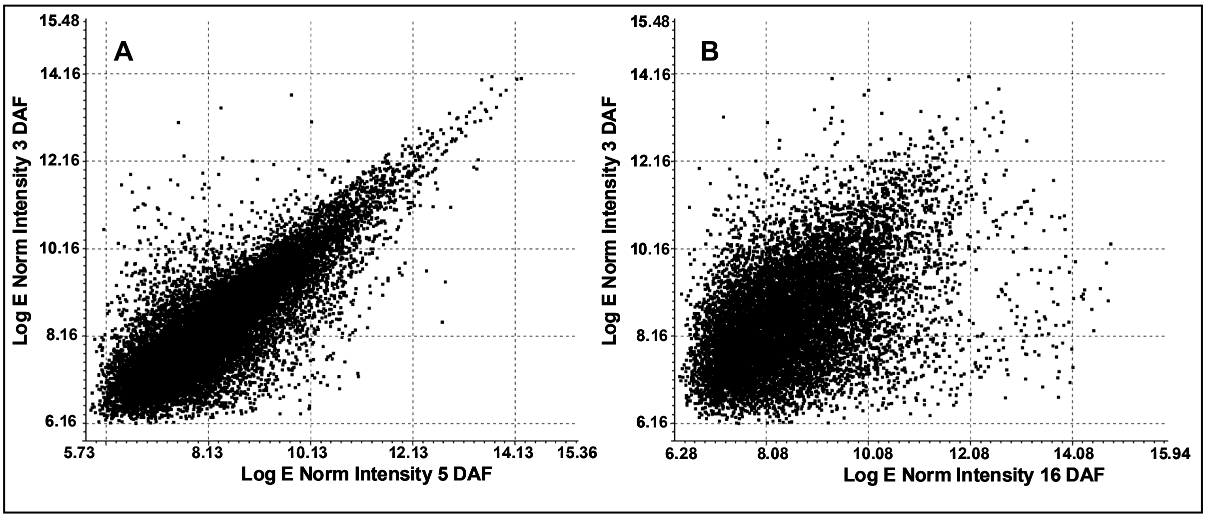


Figure 27: Log plots of detected EMRTs displaying differences between analysed developmental stages. Comparisons of logarithmic scales of normalized signal intensity for 3 DAF versus 5 DAF (A) and 3 DAF versus 16 DAF (B) are shown. A clear increase in differentially expressed EMRTs with increasing distance in the developmental stage can be detected.

Kinetic patterns elucidated using multivariate statistics

Due to the high complexity of the obtained multiplexed LC-MS data sets and large changes on proteome level during the developmental phases, multivariate statistics was applied to elucidate statistically significant and objective kinetic patterns. Raw data were processed as described before and lists of EMRTs were exported for further data analyses. Prior to data evaluation, data pre-processing and initial visualization was performed as described in Materials and Methods (section 3.2.4) to ensure data quality. EMRT data were clustered separately for each of the two conducted experiments according to their behaviour during the developmental stages using Neural Gas clustering. In the course of the application of this algorithm the number of clusters was initially set to ten according to some preliminary investigation of the data set. Each of the ten individual clusters formed by Neural Gas represented a prototypic temporal gradient of the underlying peptide abundances (Figure 28). As the unsupervised clustering process was performed separately for both experiments, results were only dependent on expression patterns of the EMRTs in the individual experiment. Despite this separate treatment of both experiments, an overlapping behaviour between the ten assigned groups could be detected. A correlation of the groups between the two experiments was successfully performed on the basis of the signal intensities and the number of included EMRTs in single classes as well as the corresponding developmental behaviour within these classes.

The ten classes differed in the developmental time-course, but also in the signal intensities. Within both experiments the first class consisted of the highest number of EMRTs (experiment 1: 45,236, experiment 2: 70,983) with relatively low signal intensities compared to the other classes. The peptides underneath these EMRTs and thus also the corresponding proteins were low abundant. The classes 1 to 7 had a common feature as they showed highest signal intensities in the middle phase of development (5-7 DAF), but they differed in the signal intensities. EMRTs grouped into class 7 had highest signal intensities, but only a small number of EMRTs could be assigned towards this class for both experiments (experiment 1: 39, experiment 2: 36). The highest expression in the latest stage of the analysed developmental phase was detected for EMRTs grouped into the classes 8-10. These classes also differed in their intensities, in which the lowest number of EMRTs could be assigned towards the class 8 (experiment 1: 54, experiment 2: 52). This class included EMRTs with highest signal intensities within the classes showing highest expression at 16 DAF.

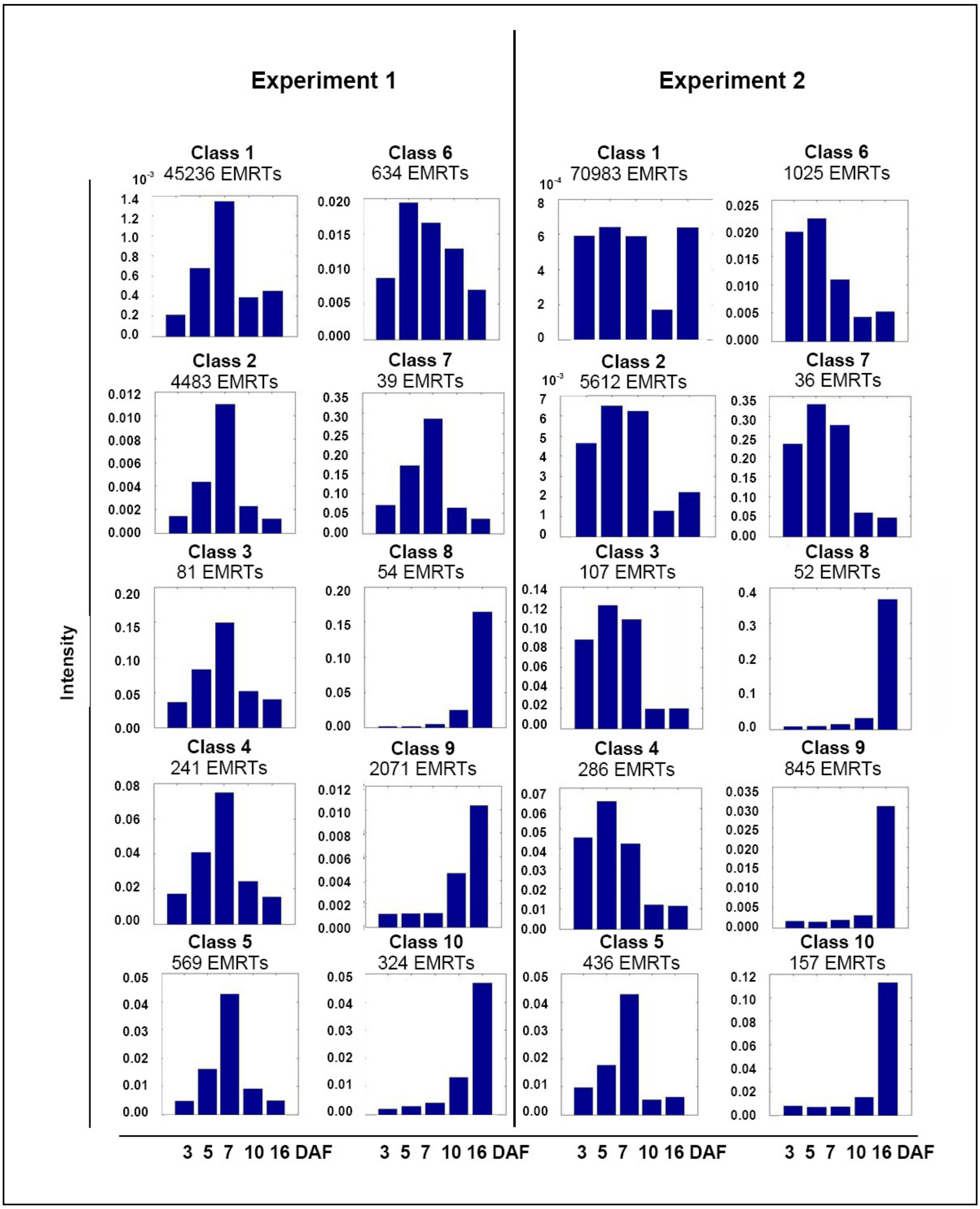


Figure 28: Neural Gas clustering of results obtained out of the protein profiling approach of barley grain development led to the assignment of ten classes differing in their developmental behaviour. Prototypes of the classes representing their virtual centre and the number of EMRTs belonging to each class for each experiment are shown.

It was expected, that peptides derived from high abundant proteins also were high abundant in the overall mass spectra, and vice versa for low abundant proteins. As these peptides should in general have comparable signal intensities and should also show the same developmental behaviour, data clustering and identification was performed separately for each of the classes for each harvest. Only proteins represented by at least two peptides within one class were used for further investigations. For some of the detected proteins peptides occurred in two or more different classes and thus overlapping features between the classes were observed. For example, proteins were detected among those overlapping features with peptides occurring in two or more classes with the same developmental pattern. A calreticulin like protein (35_14693) was detected in class 1 and 5 in the first experiment, and in the classes 1, 2, 4, and 5 in the second experiment. The overall expression pattern throughout the grain development did not differ for the single peptides but variations in intensity occurred. Also proteins with peptides grouped into classes with contrary behaviour were detected. Osr40g2 (35_268) could be identified among the latter proteins and corresponding peptides were found in the classes 4 and 9 for the first experiment and in the classes 2 and 9 for the second experiment. Thus, the assumption, that peptides accounting for one protein show the same developmental behaviour and signal intensity, could not be affirmed completely. As a consequence the grouping setup was changed to get a clearer picture about developmental changes on proteome level. The ten classes were further grouped according to their overlap in developmental behaviour into three different groups (Figure 29). The first group (Group I) showed a transiently high expression in the early and middle phase of development (class 1 to 7), whereas the second group (Group II) included proteins with an increase in expression during development (class 8 to 10). The third group (mixed pattern) consisted of proteins, whose peptides were detected in the first and the second group and therefore showed a mixed pattern related to the developmental behaviour. Also proteins with a different behaviour between the two experiments were assigned to the latter group.

Examples of proteins belonging to the three groups are shown in Table 7. Proteins with a mixed pattern in only one of the conducted experiments (lipoxygenase 2, formate dehydrogenase) or for both experiments (aspartate aminotransferase) were detected within the group having a mixed pattern. Additionally, one protein, named adenosylhomocysteinase (35_14558), showing a contrary developmental behaviour throughout the two experiments is listed. All peptides connected to this protein showed highest expression at later stages of development in the first experiment, whereas for the second experiment highest expression in the middle phase was observed. In some cases identical peptides were detected with different expression patterns between the two conducted experiments. Such behaviour was observed for lipoxygenase 2 in several peptides (e.g. ALVDGIIPAIR, TITLDNVPGR, LGVPGAIIVK, and GDDQQGPYLDHDR). A more detailed consideration of this aspect can be found in the discussion (section 5.3).

Proteins were identified within these three assigned groups instead of single classes, meaning that all proteins identified with at least two peptides within one of the groups were taken into account for further investigations.

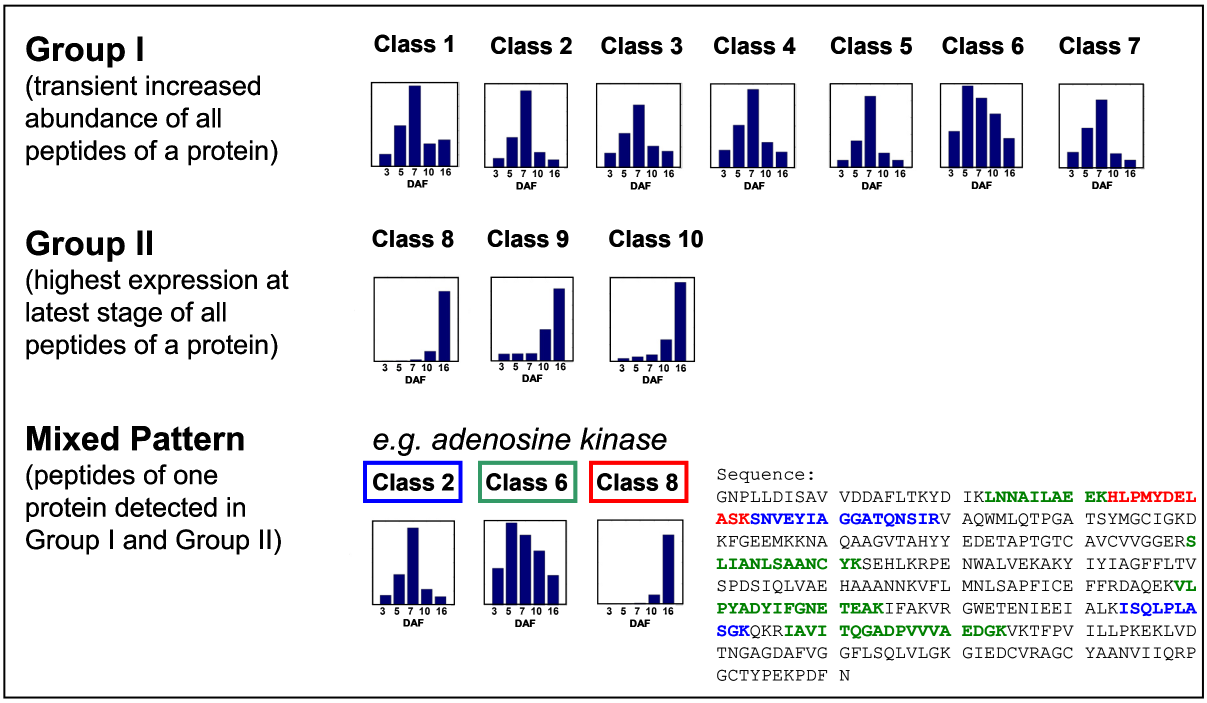


Figure 29: Grouping of Neural Gas clustering results from the protein profiling approach of barley grain development. The assigned ten classes were grouped together according to their developmental behaviour. Group I includes classes showing highest expression in the middle phase and Group II at the later phase of development. The third group showed a mixed pattern containing proteins with peptides detected in the first and second group.

Table 7: Examples of proteins out of the barley grain development profiling assigned to the different groups. The identified protein, as well as the detected peptides and the groups they were assigned to, are shown for the two performed experiments. A complete list of identified proteins is provided in Table 9.

Protein/ Accession number	**Experiment 1**		**Experiment 2**	
	Peptides Group I	*Peptides Group II*	*Peptides Group I*	*Peptides Group II*
Group I				
40S ribosomal protein S6 (*A. thaliana*)/ 35_14411	LVTPLTLQR/ ISQEVVGDLLGEEFK/ LNIANPTTGCQK		LVTPLTLQR/ LNIANPTTGCQK/ KGENDLPGLTDTEKPR	
Group II				
Alpha amylase inhibitor BMAI (H. vulgare)/ P16968		SQCAGGQVVESIQK/ ELGVALADDK		SQCAGGQVVESIQK/ ELGVALADDK/ ATVAEVFPGCR
Proteins with mixed pattern				
Lipoxygenase 2 (*H. vulgare*)/ 35_14192	STVYTPASTGVEAWIWQLAK/ GVTCQLISSTNVR/ LEGIEK/ YDVYNDLGDSR/ QVVAMNSDPQLK/ GVTCQLISSTNVDHNNGGR/ STLDPSK	ALVDGIIPAIR/ TITLDNVPGR/ LGVPGAIIVK/ LPNIPALEEVR/ GDDQQGPYLDHDR/ GMAVEDASSPHK/ QLSVTHPVYK/ GVTCQLISSTNVDHNNGGR/ SLEGLTVQQALAGNR	ALVDGIIPAIR/ NRNGPVHFPYMLLYPNTSDHTGK/ FAVTFDWSVDK/ DTMNINAR/ EVGHGDLKDAAWWPK/ RGMAVEDASSPHK/ EMLAGVNPMMIK/ YDVYNDLGDSR/ SLEGLTVQQALAGNR/ RPMPVQGSEEYAELER/ DAAWWPK/ FPYMLLYPNTSDHTGQAEGLTAR/ GMAVEDASSPHK/ DPEK/ HWNFTEQALPADLIK/ VQGSEEYAELER/ QVVAMNSDPQLK/ LGVPGAIIVK/ TITLDNVPGR/ TYVDLSPGEFDSFADILK/ VGAEANLEQWLLPTNLPFITTGENK/ AWMTDEEFAR/ GMAVEDASSPHK/ LGVGGIVSDLTGGIR/ GVTCQLISSTNVDHNNGGR/ GDDQQGPYLDHDR/ GDGTLAPVAIELSSPLIQGELTTAK/ YNRVFFANDTYLPHQMPAALKPYR/ HSSDEVYLGQHDTPAWTSDAK	
Aspartate aminotransferase (*O. sativa*)/ 35_14619	AEQMLIHNESR	TVPHLADAIHAAVTK	ISMAGLSSR/ NMGLYGERVGALSIVGSADIAVK/ SYRYYDPATR	TVPHLADAIHAAVTK
Formate dehydrogenase (*H. vulgare*)/ Q9ZRI8		GEEFPVENYIVK CDVVVINTPLTEK	CDVVVINTPLTEK/ EGELASQYK/ NFLPGYQQVVK/ GEWNVAGIAHR	NFLPGYQQVVK/ CDVVVINTPLTEK/ GEEFPVENYIVK/ LQINPELEK/ FEEDLDAMLPK
Adenosylhomocysteinase 1 (*A. thaliana*)/ 35_14558		VAVVCGYGDVGK VPDPESTDNPEFK	VPDPESTDNPEFK/ LVGVSEETTTGVK/ VAVVCGYGDVGK/ IAASSLSPLLAR	

Protein identification using mass spectrometry data

After evaluation of the data set using multivariate statistics, protein identification was performed using two different manually assembled databases as described in Material and

Methods section 3.2.4 separately for both experiments. An example for the quantification and identification process based on the obtained raw data and the subsequent data visualisation is shown in Figure 30. Peptides eluting from the nanoLC system were detected in a low energy and high energy mode (Figure 30 A). Extracted ion chromatograms of defined m/z signals revealed first information about quantitative changes throughout the barley grain development (B). The m/z signal information was used for quantification process. Corresponding peptides were clustered into distinct classes according to the changes in relative quantities during grain development (C). Subsequent identification was performed based on the fragment information out of the high energy trace (D). Typically more than one peptide was detected for a protein.

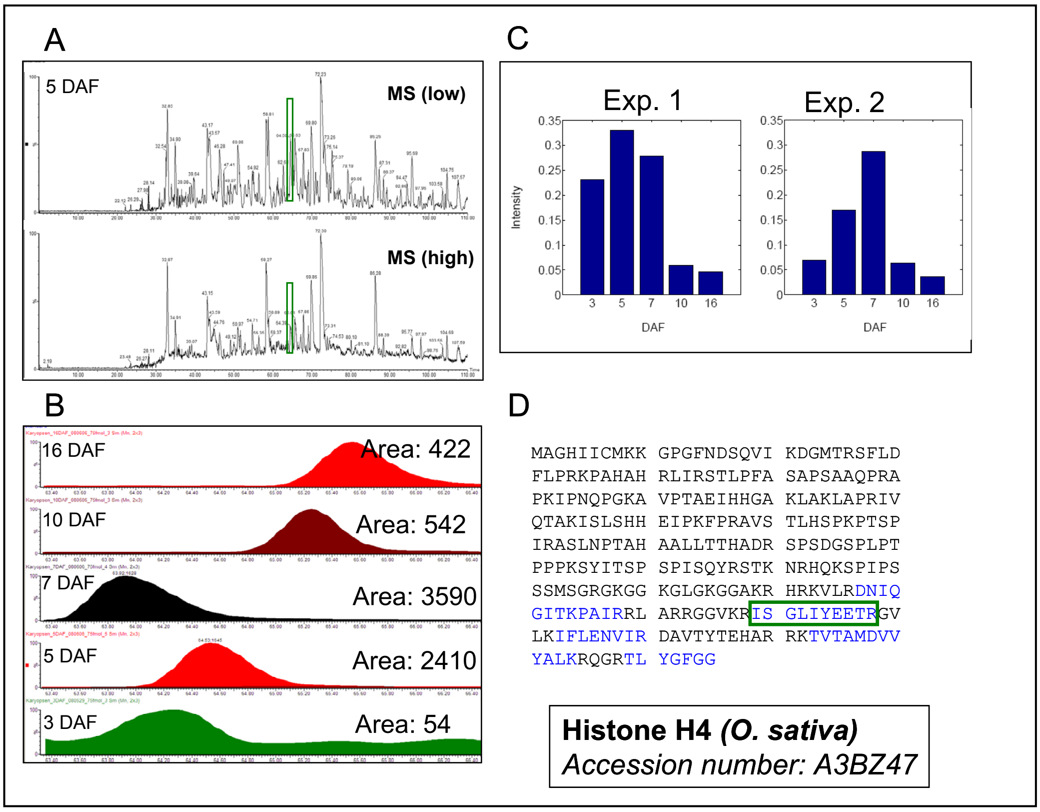
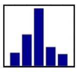
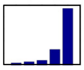


Figure 30: Workflow of quantification and identification process for the analyses of temporal protein distribution patterns during barley grain development. Data acquisition was performed in an alternating mode between low (upper panel) and high (lower panel) energy trace (A). Quantitative information of a single peptide (shown: m/z 1180.32, RT 64.50 min) based on the peak areas obtained out of the extracted ion chromatograms revealed first insight into developmental changes (B). Data was clustered according to the developmental behaviour using multivariate statistics separately for the two experiments (C, shown are the clusters representing the virtual centre of the classes). Protein identification was performed by searching against two manually assembled databases. Shown EMRT cluster led to the identification of Histone H4 and corresponding peptide is marked green. Further peptides, which were additionally found, are marked blue (D). Base peak chromatograms, extracted ion chromatograms, and identification are shown for the second experiment.

Final results contained proteins found with at least two peptides per protein in both experiments. The number of EMRTs, identified peptides and proteins found in each single experiment and the overlapping proteins for each group are shown in Table 8.

Table 8: Results of protein profiling of barley grain development using LC-based approach. Results were grouped according to the developmental behavior into three different groups, one showing a transient increased abundance (Group I), the other showing highest expression of proteins in latest stage of development (Group II) and one containing proteins, which peptides were detected in Group I and Group II (proteins with mixed patterns). The number of detected EMRTs, identified peptides and resultant proteins for each group and the individual experiments as well as the number of proteins detected in both experiments are shown. Protein identification was performed using PLGS software by searching against a translated HarvEST database and a manually assembled UniProt reference database combining entries from *Oryza sativa* and *Hordeum vulgare*.

	Experiment 1	**Experiment 2**	**In Exp. 1 and 2**
Number of EMRTs:	51098	78530	
Identified Peptides:	2284	4027	
Identified Proteins:	498	680	
Proteins in Group I **(transient increased abundance)** 	379	585	**147**
Proteins in Group II **(highest at latest stage)** 	49	45	**19**
Proteins with mixed patterns	70	50	**55**

Results revealed differences in the number of detected EMRTs between the first and the second experiment caused by slight changes in the experimental setup (see Table 1). A higher number of EMRTs could be detected if separation was performed on a shorter column when higher protein amounts were loaded onto the column. Thus higher signal intensities could be achieved and therefore more low abundant signals can be detected. Consequential, the number of identified peptides and proteins also differed and were higher for the second experiment.

Due to yet incomplete databases the number of identified peptides was very low in comparison to the detected features for both experiments as only 5% of the EMRTs could be successfully identified. Thus, also a relatively low number of proteins were detected. The total number of proteins found within the three assigned groups differed. One hundred and forty-seven proteins were found in Group I in both experiments. The number of identified proteins in Group II was generally lower and 19 proteins showed an overlap between both experiments. In total, 55 proteins were allocated towards the group with a mixed pattern. Two hundred and twenty-two proteins were identified in both conducted experiments with average sequence coverage of 27% and a PLGS-score of 460. The average number of peptides detected for single proteins differed between the assigned groups. Whereas an average of 10 peptides per protein was detected for Group I and II, generally around 14 peptides per protein were identified in the group with mixed patterns. As proteins found in two independent experiments revealed a higher confidence of monitored changes in the temporal expression pattern, those were used for further evaluation. The complete list of identified EMRTs is provided in appendix (Table A 3).

Functional classification of proteins expressed during barley grain development

Identified proteins were classified according to their function using a previous described assignment scheme (Bevan *et al.* 1998). Classification was done separately for each of the groups (Figure 31). Various identified proteins were connected to disease and defence processes, energy metabolism, metabolism, protein destination, and protein synthesis, whereas cell wall, DNA binding, transport, and transcription were covered only by a low number of proteins. All proteins identified within the assigned groups are given in Table 9.

Most of the proteins, showing a high expression in the middle phase of development (Group I), have no presumed function (“Unclassified”). Also proteins from the second and the third group fell into this category. The second largest category of identified proteins annotated to Group I could be correlated to the function of disease and defence. Proteins in the third largest category are involved in protein destination and storage, followed by protein synthesis. Low numbers of proteins fell into the categories of energy metabolism, metabolism, DNA binding, and transport and only few proteins could be found connected to the functions transcription and cell wall synthesis. Most of the proteins showing highest expression level in the latest phase of development (Group II) were assigned to disease and defence processes, followed by proteins involved in protein destination and storage. No protein connected to the functional groups of cell wall synthesis, DNA binding, protein synthesis, transcription, and transport could be detected. Those proteins, which corresponding peptides could be found in Group I and Group II and therefore showing a mixed pattern, could be mainly allocated to general metabolism. Furthermore, a high number of proteins belonging to energy metabolism and protein synthesis were identified. Only few proteins were connected to the functions disease/defence, protein destination and storage, transport, and unclassified, whereas no protein was found to be connected to cell wall synthesis, DNA binding, and transcription. A high number of proteins were still unclassified within the complete data set. The complete set of proteins together with their functional classification can be found in Table 9.

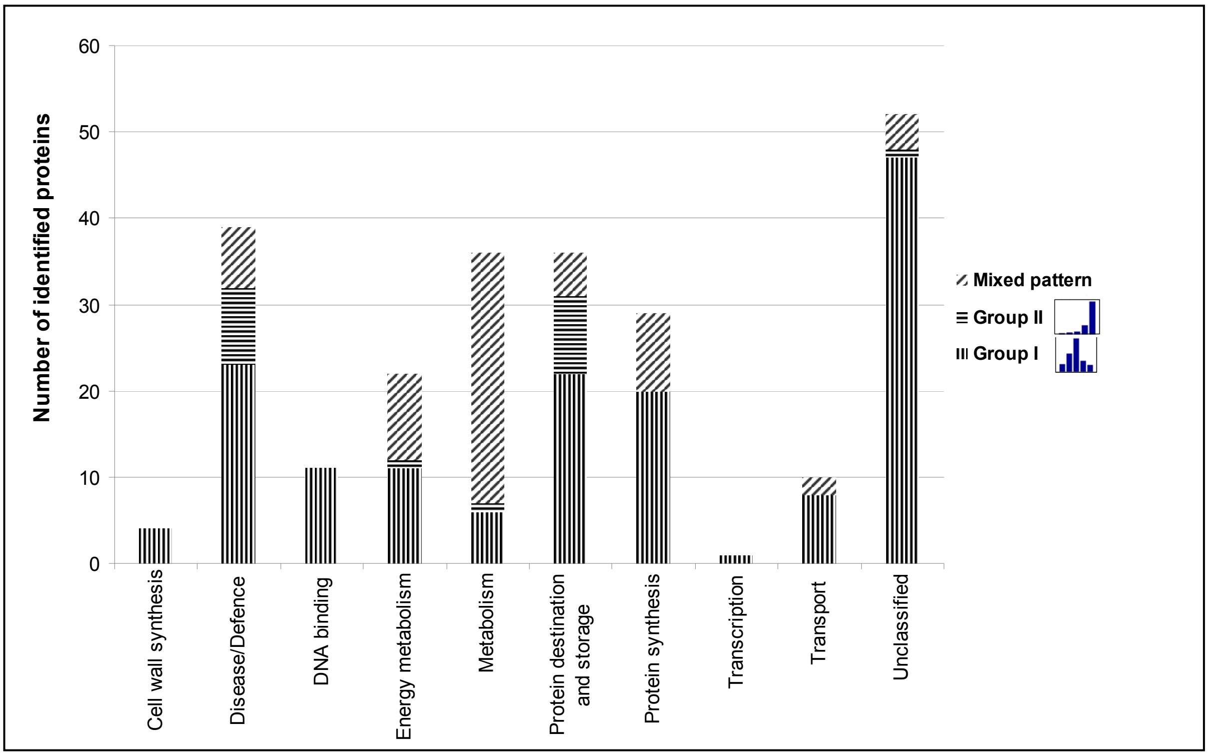


Figure 31: Functional classification of proteins found during barley grain development (according to Bevan *et al.* 1998). The total numbers of proteins according to the corresponding function for each of the found groups are shown.

In conclusion, proteins identified in the three different groups revealed distinct functions related to the respective developmental process. Proteins in the first group were characterized by functional categories displaying a complex metabolic activity of the grain. Proteins with highest expression at later stages (Group II) were mainly connected to seed storage and plant defence. The main function covered by proteins in the group with mixed pattern was general metabolism. Most of the proteins assigned to the latter group were detected with a high number of peptides (e.g. phosphoglycerate kinase: 6 peptides in experiment 1/17 peptides in experiment 2, lipoxygenase 2: 15/32).

Table 9: Proteins identified in the analysis of barley grain development using a label-free LC-MS approach. All proteins with their accession number (Acc. number) together with the used database (^{1}HarvEST, ^{2}Uniref), the number of identified peptides for both experiments as well as the presumed function, are given separately for the three assigned groups (Group I, II, and proteins with mixed patterns).

Protein	Acc. number	Number peptides Exp 1/2	Function
GROUP I			
Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272^1	2/9	Cell wall synthesis
Actin *(P. salicina)*	A9UAM8^2	5/4	Cell wall synthesis
Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85^1	4/6	Cell wall synthesis
Tubulin alpha 2 alpha 4 chain *(A. thaliana*)	P29510^2	3/5	Cell wall synthesis
Glutaredoxin (*T. aestivum*)	35_1143^1	5/8	Disease/Defence
Salt tolerant protein (*T. aestivum*)	35_788^1	3/9	Disease/Defence
Ascorbate peroxidase (*H. vulgare*)	O23983^2	3/10	Disease/Defence
Heat shock protein 90 (*O. sativa*)	Q5Z9N8^2	5/5	Disease/Defence / Protein destination and storage
Heat shock 70 kDa protein (*O. sativa*)	35_1230^1	5/11	Disease/Defence / Protein destination and storage
Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137^1	2/6	Disease/Defence / Protein destination and storage
Cu Zn superoxide dismutase (*T. aestivum*)	35_15373^1	2/4	Disease/Defence
RAD23 protein (*O. sativa*)	35_15614^1	4/11	Disease/Defence
FAM10 family protein At4g22670 (*A. thaliana*)	35_1653^1	5/14	Disease/Defence
Peroxiredoxin (*O. sativa*)	35_35528^1	2/7	Disease/Defence
Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432^1	2/11	Disease/Defence / Protein destination and storage
CAA303712 1 protein (*O. sativa*)	35_759^1	3/10	Disease/Defence
Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189^2	2/10	Disease/Defence / Protein destination and storage
Luminal binding protein 2 precursor (*Z. mays*)	P24067^2	13/9	Disease/Defence
Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629^2	4/12	Disease/Defence / Protein destination and storage
14 3 3 like protein A (*H. vulgare*)	P29305^2	3/16	Disease/Defence
Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41^2	3/5	Disease/Defence / Protein destination and storage
OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5^2	9/11	Disease/Defence
Ascorbate peroxidase (*H. vulgare*)	Q945R5^2	2/10	Disease/Defence
GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6^2	3/3	Disease/Defence
Putative disulfide isomerase (*O. sativa*)	35_15052^1	3/24	Disease/Defence
Histone H2A 2 1 (*T. aestivum*)	35_30953^1	3/4	DNA binding
Histone H2B 5 (*O. sativa*)	A2WKT4^2	3/3	DNA binding
Probable histone H2AXb (*O. sativa*)	A2ZL69^2	3/3	DNA binding
Histone H4 (*O. sativa*)	A3BZ47^2	6/9	DNA binding
Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20^2	3/2	DNA binding
Methyl binding domain protein MBD109 (*Z. mays*)	35_15492^1	3/27	DNA binding
Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627^1	4/14	DNA binding
HMG I Y protein HMGa (*T. aestivum*)	35_2226^1	3/9	DNA binding
Histone H2B 3 (*Z. mays*)	35_50103^1	3/4	DNA binding
Histone H4 (*A. thaliana*)	P59259^2	3/7	DNA binding
Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20^2	4/2	DNA binding
Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635^1	2/9	Energy metabolism
Oxygen evolving complex (*T. aestivum*)	35_14958^1	5/3	Energy metabolism

Protein	**Acc. number**	**Number peptides Exp 1/2**	**Function**
Os03g0129300 protein (*O. sativa*)	35_435[1]	2/3	Energy metabolism
Phosphoglycerate kinase (*O. sativa*)	A2Y650[2]	5/5	Energy metabolism
Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93[2]	15/17	Energy metabolism
Putative transaldolase (*O. sativa*)	35_14408[1]	6/8	Energy metabolism
Putative plastidic aldolase (*O. sativa*)	35_15473[1]	3/3	Energy metabolism
Enolase 2 (*Z. mays*)	P42895[2]	5/13	Energy metabolism
Nucleoside diphosphate kinase (*L. perenne*)	35_610[1]	2/4	Energy metabolism
Fructose bisphosphate aldolase (*O. sativa*)	35_1410[1]0	2/13	Energy metabolism
Putative enoyl ACP reductase (*O. sativa*)	35_1359[1]	2/2	Metabolism
Enoyl ACP reductase precursor (*O. sativa*)	35_1360[1]	2/6	Metabolism
S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443[1]	3/4	Metabolism
GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581[1]	13/18	Metabolism
Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835[2]	6/13	Metabolism
Putative sex determination protein tasselseed 2 (*O. sativa*)	Q7XAN5[2]	2/2	Metabolism
Putative 20 kDa chaperonin (*O. sativa*)	35_1423[1]	3/5	Protein destination and storage
Putative chaperonin 21 (*O. sativa*)	35_1424[1]	4/5	Protein destination and storage
Calreticulin like protein (*T. aestivum*)	35_14693[1]	5/19	Protein destination and storage
Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703[1]	3/6	Protein destination and storage
Putative uncharacterized protein (*O. sativa*)	A2Y2Y4[2]	2/9	Protein destination and storage
Putative uncharacterized protein (*O. sativa*)	A3ATH4[2]	7/5	Protein destination and storage
Calreticulin family protein (*O. sativa*)	Q10BR5[2]	5/3	Protein destination and storage
Cystatin Hv CPI8 (*H. vulgare*)	Q1ENF0[2]	4/4	Protein destination and storage
Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27[2]	3/3	Protein destination and storage
QM (*T. aestivum*)	Q7X9L9[2]	2/3	Protein destination and storage
OSJNBb0012E08 10 protein (*O. sativa*)	35_14268[1]	4/5	Protein destination and storage
Putative cysteine proteinase (*O. sativa*)	35_16147[1]	4/4	Protein destination and storage
Putative chaperone GrpE type 2 (*O. sativa*)	35_17646[1]	3/4	Protein destination and storage
Putative chaperonin 21 (O. sativa)	35_1799[1]	3/9	Protein destination and storage
Phytepsin precursor (*H. vulgare*)	35_280[1]	3/4	Protein destination and storage
Putative CDR1 (*O. sativa*)	35_3551[1]	2/8	Protein destination and storage
Putative uncharacterized protein (*O. sativa*)	A2XF40[2]	5/2	Protein destination and storage
EEA1 (*H. vulgare*)	O22491[2]	4/3	Protein destination and storage
Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529[2]	8/4	Protein destination and storage
Endoplasmin homolog precursor (*H. vulgare*)	P36183[2]	7/13	Protein destination and storage
Probable ubiquitin fold modifier 1 precursor (*O. sativa*)	Q94DM8[2]	2/2	Protein destination and storage
OSJNBb0006N15 8 protein (*O. sativa*)	35_13701[1]	3/3	Protein synthesis
40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411[1]	3/3	Protein synthesis
40S ribosomal protein S4 (*Z. mays*)	35_14431[1]	5/10	Protein synthesis
Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477[1]	5/7	Protein synthesis
Ribosomal protein L11 (*T. aestivum*)	35_14636[1]	3/6	Protein synthesis
Ribosomal protein L10A (*T. aestivum*)	35_14911[1]	2/5	Protein synthesis
Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967[1]	5/6	Protein synthesis
60S ribosomal protein L13 (*A. thaliana*)	35_15048[1]	4/2	Protein synthesis
Eukaryotic initiation factor (*T. aestivum*)	35_15745[1]	3/8	Protein synthesis
Putative uncharacterized protein (*O. sativa*)	A2XMW9[2]	4/11	Protein synthesis
60S ribosomal protein L8 (*S. lycopersicum*)	35_14319[1]	2/5	Protein synthesis
40S ribosomal protein S19 (*O. sativa*)	35_14825[1]	6/6	Protein synthesis
Elongation factor 1 beta (*T. aestivum*)	35_41584[1]	5/2	Protein synthesis
60S acidic ribosomal protein P2B (*Z. mays*)	35_49914[1]	3/7	Protein synthesis
40S ribosomal protein (*O. sativa*)	35_685[1]	5/7	Protein synthesis

Protein	Acc. number	Number peptides Exp 1/2	Function
Putative uncharacterized protein (*O. sativa*)	A2XHR6[2]	2/3	Protein synthesis
Putative uncharacterized protein (*O. sativa*)	A3BQX7[2]	4/6	Protein synthesis
60S ribosomal protein (*P. armeniaca*)	O50003[2]	3/4	Protein synthesis
Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8[2]	4/10	Protein synthesis
BTF3b like transcription factor (*M. acuminata*)	35_15306[1]	6/5	Transcription
Nuclear transport factor 2 (*O. sativa*)	35_15374[1]	6/3	Transport
Plastidial ADP glucose transporter (*H. vulgare*)	35_17753[1]	4/4	Transport
Ferredoxin, chloroplast precursor (*T. aestivum*)	P00228[2]	2/2	Transport
Type 1 non specific lipid transfer protein precursor (*T. aestivum*)	Q2PCD1[2]	3/2	Transport
Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756[1]	4/8	Transport
Putative uncharacterized protein (*O. sativa*)	A2YSB2[2]	2/2	Transport
ATP synthase subunit (*Z. mays*)	35_14757[1]	2/11	Transport
OsS5a (*O. sativa*)	35_120[1]	2/4	Unclassified
Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470[1]	5/11	Unclassified
Putative cytochrome b5 (*O. sativa*)	35_14940[1]	3/3	Unclassified
Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515[1]	2/3	Unclassified
Putative stress related like protein interactor (*O. sativa*)	35_1563[1]	2/13	Unclassified
Ankyrin domain protein (*N. tabacum*)	35_15734[1]	2/8	Unclassified
Putative p23 co chaperone (*O. sativa*)	35_15864[1]	3/4	Unclassified
Putative plastid protein (*O. sativa*)	35_15958[1]	2/2	Unclassified
Putative nucleic acid binding protein (*O. sativa*)	35_16721[1]	3/7	Unclassified
Putative Hsp70 binding protein (*O. sativa*)	35_16911[1]	4/8	Unclassified
Ubiquitin family protein (*O. sativa*)	35_1872[1]	2/3	Unclassified
KH domain containing protein NOVA like (*O. sativa*)	35_2063[1]	4/4	Unclassified
Luminal binding protein 3 (*Z. mays*)	35_47882[1]	6/3	Unclassified
Os02g0131700 (*O. sativa*)	35_698[1]	2/4	Unclassified
Os05g0373700 protein (*O. sativa*)	35_836[1]	3/4	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2X7R0[2]	5/4	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2XZH4[2]	2/2	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2YZ92[2]	2/8	Unclassified
Putative uncharacterized protein (*O. sativa*)	A3A7Q0[2]	2/6	Unclassified
Putative uncharacterized protein (*O. sativa*)	A3B7Q6[2]	2/4	Unclassified
Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3[2]	5/7	Unclassified
Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3[2]	4/2	Unclassified
Os07g0173500 protein (*O. sativa*)	35_14252[1]	2/4	Unclassified
Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299[1]	4/2	Unclassified
Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404[1]	2/12	Unclassified
Putative steroid membrane binding protein (*T. aestivum*)	35_15441[1]	3/4	Unclassified
Putative nuclear RNA binding protein A (*O. sativa*)	35_16328[1]	4/12	Unclassified
Os09g0125100 protein (*O. sativa*)	35_16653[1]	2/3	Unclassified
Os05g0373700 protein (*O. sativa*)	35_16909[1]	2/12	Unclassified
Putative nuclear RNA binding protein A (*O. sativa*)	35_2103[1]	6/9	Unclassified
Dehydroascorbate reductase (*T. aestivum*)	35_861[1]	2/8	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2WW49[2]	4/4	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2X180[2]	2/2	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2XLB7[2]	4/3	Unclassified
Histone H2A (*O. sativa*)	A2XLW3[2]	3/2	Unclassified
40S ribosomal protein S12 (*O. sativa*)	A2YI73[2]	3/2	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2YLI4[2]	3/3	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2ZJS3[2]	4/5	Unclassified
Putative uncharacterized protein (*O. sativa*)	A3C065[2]	6/5	Unclassified
Cp31BHv (*H. vulgare*)	O81988[2]	2/3	Unclassified
Os07g0173500 protein (*O. sativa*)	Q0D8A3[2]	2/2	Unclassified

Protein	**Acc. number**	**Number peptides Exp 1/2**	**Function**
Dehydroascorbate reductase (*O. sativa*)	Q65XA0[2]	5/3	Unclassified
OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8[2]	4/7	Unclassified
Putative translational inhibitor protein (*O. sativa*)	Q8H4B9[2]	3/7	Unclassified
Putative stress induced protein sti1 (*O. sativa*)	35_15495[1]	7/29	Unclassified
Putative stress induced protein sti1 (*O. sativa*)	Q6H660[2]	3/12	Unclassified
P0402A09 25 protein (*O. sativa*)	35_1149[1]	4/3	Unclassified
GROUP II			
Hordoindoline b (*H. vulgare*)	35_50624[1]	3/3	Disease/Defence
Trypsin inhibitor CMe precursor (*H. vulgare*)	P01086[2]	2/3	Disease/Defence
Purothionin II (*H. vulgare*)	P01545[2]	3/6	Disease/Defence
Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691[2]	7/8	Disease/Defence
Alpha amylase inhibitor BMAI 1 precursor (*H. vulgare*)	P16968[2]	2/3	Disease/Defence
Beta hordothionin, Acidic protein (*H. vulgare*)	P21742[2]	2/2	Disease/Defence
Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041[2]	3/3	Disease/Defence
Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9[2]	2/5	Disease/Defence
Serpin Z4 (*H. vulgare*)	P06293[2]	7/4	Disease/Defence
Thiamine biosynthetic enzyme (*O. sativa*)	35_320[1]	7/14	Energy metabolism
Alanine aminotransferase 2 (*H. vulgare*)	P52894[2]	6/11	Metabolism
Putative avenin like (*A. cylindrica*)	35_14422[1]	2/4	Protein destination and storage
BTI CMe4 protein precursor (*H. vulgare*)	O49863[2]	2/2	Protein destination and storage
Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596[2]	3/6	Protein destination and storage
Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643[2]	6/7	Protein destination and storage
Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936[2]	2/7	Protein destination and storage
Gamma hordein 3 (*H. vulgare*)	P80198[2]	2/2	Protein destination and storage
Gamma hordein 1 precursor (*H. vulgare*)	35_69[1]	3/6	Protein destination and storage
Grain softness protein (*H. vulgare*)	Q0GIL0[2]	2/3	Unclassified
Proteins with mixed pattern			
Protein Z (*H. vulgare*)	35_14790[1]	3/7	Disease/Defence
Auxin induced protein PCNT115 (*O. sativa*)	35_2241[1]	3/16	Disease/Defence
Subtilisin chymotrypsin inhibitor CI 1A (*H. vulgare*)	P16062[2]	2/3	Disease/Defence
1 Cys peroxiredoxin (*H. vulgare*)	P52572[2]	4/17	Disease/Defence
Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8[2]	2/9	Disease/Defence
Protein disulfide isomerase precursor (*T. aestivum*)	35_14571[1]	15/27	Disease/Defence
Fructose bisphosphate aldolase (*O. sativa*)	35_14090[1]	2/3	Energy metabolism
Malate dehydrogenase (*O. sativa*)	35_14420[1]	6/4	Energy metabolism
Phosphoglycerate kinase (*T. aestivum*)	35_19[1]	6/17	Energy metabolism
Orthophosphate dikinase precursor (*O. sativa*)	O24612[2]	3/8	Energy metabolism
Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477[2]	5/11	Energy metabolism
Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136[1]	4/2	Energy metabolism
Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042[2]	3/7	Energy metabolism
Protein disulfide isomerase precursor (*T. aestivum*)	P52589[2]	18/22	Disease/Defence
Phosphoglycerate kinase (*T. aestivum*)	P12783[2]	19/23	Energy metabolism
Enolase (*O. sativa*)	A3AG33[2]	4/2	Energy metabolism
Lactoylglutathione lyase (*O. sativa*)	35_118[1]	4/5	Metabolism
Lipoxygenase 2 (*H. vulgare*)	35_14193[1]	7/3	Metabolism
Sucrose synthase 1 (*O. sativa*)	35_14479[1]	2/11	Metabolism

Protein	Acc. number	Number peptides Exp 1/2	Function
Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558[1]	2/4	Metabolism
Adenosine kinase (*Z. mays*)	35_14937[1]	8/10	Metabolism
Phosphoglucomutase (*B. inermis*)	35_15040[1]	11/25	Metabolism
Thiamine biosynthetic enzyme (*O. sativa)*	35_50571[1]	3/6	Metabolism
Putative ketol acid reductoisomerase (*O. sativa*)	35_730[1]	2/2	Metabolism
Putative uncharacterized protein (*O. sativa*)	A2XUU7[2]	6/5	Metabolism
Sucrose synthase 2 (*O. sativa*)	P31924[2]	2/12	Metabolism
Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72[2]	6/4	Metabolism
Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466[2]	5/8	Metabolism
Cytosolic glyceraldehyde 3 phosphate dehydrogenase	Q9M4V4[2]	2/10	Metabolism
Beta amylase (*H. vulgare*)	35_14441[1]	5/12	Metabolism
Sucrose synthase 1 (*O. sativa*)	P30298[2]	15/14	Metabolism
Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523[2]	5/20	Metabolism
Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare)*	P30524[2]	14/30	Metabolism
Sucrose synthase 2 (*H. vulgare*)	P31923[2]	6/14	Metabolism
Aspartate aminotransferase (*O. sativa*)	P37833[2]	3/15	Metabolism
Lipoxygenase 2 (*H. vulgare*)	Q42847[2]	15/32	Metabolism
UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772[2]	9/15	Metabolism
Beta amylase (*H. vulgare*)	P16098[2]	6/5	Metabolism
Alpha amylase trypsin inhibitor CMb (*H. vulgare*)	35_111[1]	2/2	Protein destination and storage
Putative legumin (*O. sativa*)	35_1242[1]	4/3	Protein destination and storage
Os01g0663400 protein (*O. sativa*)	35_15471[1]	9/25	Protein destination and storage
Embryo globulin *(H. vulgare*)	Q03678[2]	8/7	Protein destination and storage
Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6[2]	3/9	Protein destination and storage
Elongation factor 1 alpha (*A. thaliana*)	35_13730[1]	2/3	Protein synthesis
60S acidic ribosomal protein (*O. sativa*)	35_14696[1]	3/4	Protein synthesis
Elongation factor 2 (*B. vulgaris*)	35_373[1]	4/20	Protein synthesis
Ribosomal protein L25 (*Z. mays*)	O81229[2]	5/9	Protein synthesis
Cytoplasmatic ribosomal protein S13 (*T. aestivum*)	Q5XUU9[2]	2/2	Protein synthesis
Elongation factor 1 alpha (*A. thaliana*)	35_13677[1]	7/3	Protein synthesis
Elongation factor 1 gamma 3 (*O. sativa*)	35_593[1]	4/16	Protein synthesis
ATP synthase subunit beta (*Z. mays*)	35_14758[1]	2/4	Transport
Non specific lipid transfer protein (*H. vulgare*)	Q42848[2]	5/3	Transport
Osr40g2 protein (*O. sativa*)	35_268[1]	2/5	Unclassified
RNA binding protein Rp120 (*O. sativa*)	35_617[1]	4/10	Unclassified
Putative uncharacterized protein (*O. sativa*)	A2Z2G4[2]	4/6	Unclassified

Validation of selected kinetic protein expression patterns using enzyme assays

Subsequent to the analyses of protein expression patterns during barley grain development, activities for two of the detected enzymes were measured to confirm the results gained by the proteome analysis. Protein extracts of all five developmental stages were prepared as described in Materials and Methods (section 3.3.1) for the analyses of fructose-bisphosphate aldolase and alanine aminotransferase activity. Information about the extract dilutions required to run enzyme assays at optimal conditions were determined in previous experiments (see Material and Methods, section 3.3.2). Measured enzyme activities were correlated to corresponding protein concentrations of each time point, as those values differed heavily between the developmental stages. Enzyme activity measurements were performed for one harvest, which was not included into the proteome profiling approach, in two technical replicates and four measurements per replicate. The results showed an increase in the specific enzyme activity for alanine aminotransferase throughout the development. The specific enzyme activity for fructose-bisphosphate aldolase showed highest activity in the middle phase of development (7 DAF, Figure 32).

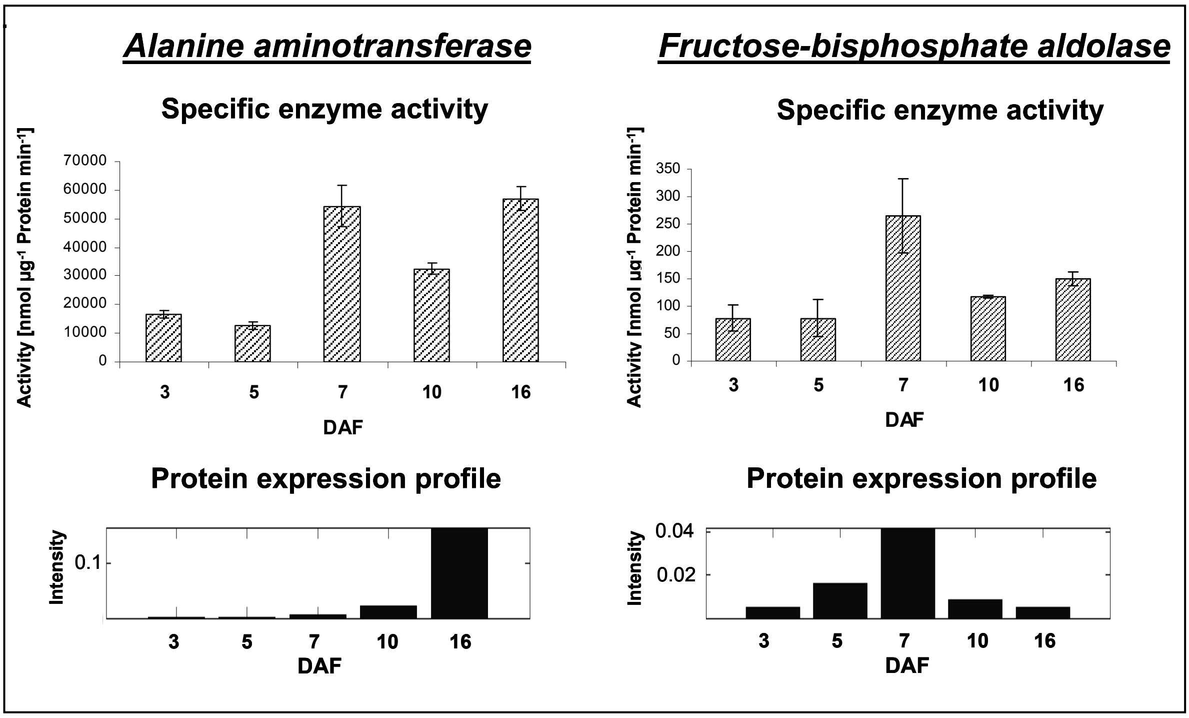


Figure 32: Results for specific enzyme activities determined in developing barley grains. Enzyme activities were measured for alanine aminotransferase and fructose-bisphosphate aldolase during five different developmental stages (3, 5, 7, 10, and 16 DAF). Activities correspond to the amount of protein in each extract (µg). Expression profiles, representing the virtual centre of the corresponding classes, are given and correlated highly to the gained enzyme activity results.

Results of enzyme activity measurements were in agreement with the data gained out of the proteome analyses approach of kinetic patterns during barley grain development even though samples for protein expression analyses and enzyme activity measurement originate from different harvests.

4.3.2. Proteome analyses of dissected material to unravel spatial protein distribution patterns

Besides the analyses of temporal expression patterns, spatial distribution of proteins plays an important role due to the functional organisation of barley grain tissues (Gubatz *et al.* 2007). For this purpose laser-micro-dissected material of NP and ETC was analysed as they are important tissues for nutrient transfer from maternal to filial tissues and thus play a crucial role for endosperm growth and development (Thiel *et al.* 2008).

Sample preparation and LC-MS analysis of laser-micro-dissected endosperm transfer cells and nucellar projection

Method optimization revealed feasibility of nanoLC-based separation coupled to MS detection for the analyses of small sample amounts (section 4.1.3). ETC become functional in barley grains at 6 DAF, and therefore grain material at middle phase of development (8 DAF) was used. ETC and NP were cut out of cryosections using LMD. Cross sections of barley grain material were placed on a glass slide. The region of interest was first separated from the surrounding tissue with the aid of a completely closed cutting line, and then carried away by a number of laser shots and catapulted into the lid of an adhesive cap. A schematic overview about LMD process is shown in Figure 33.

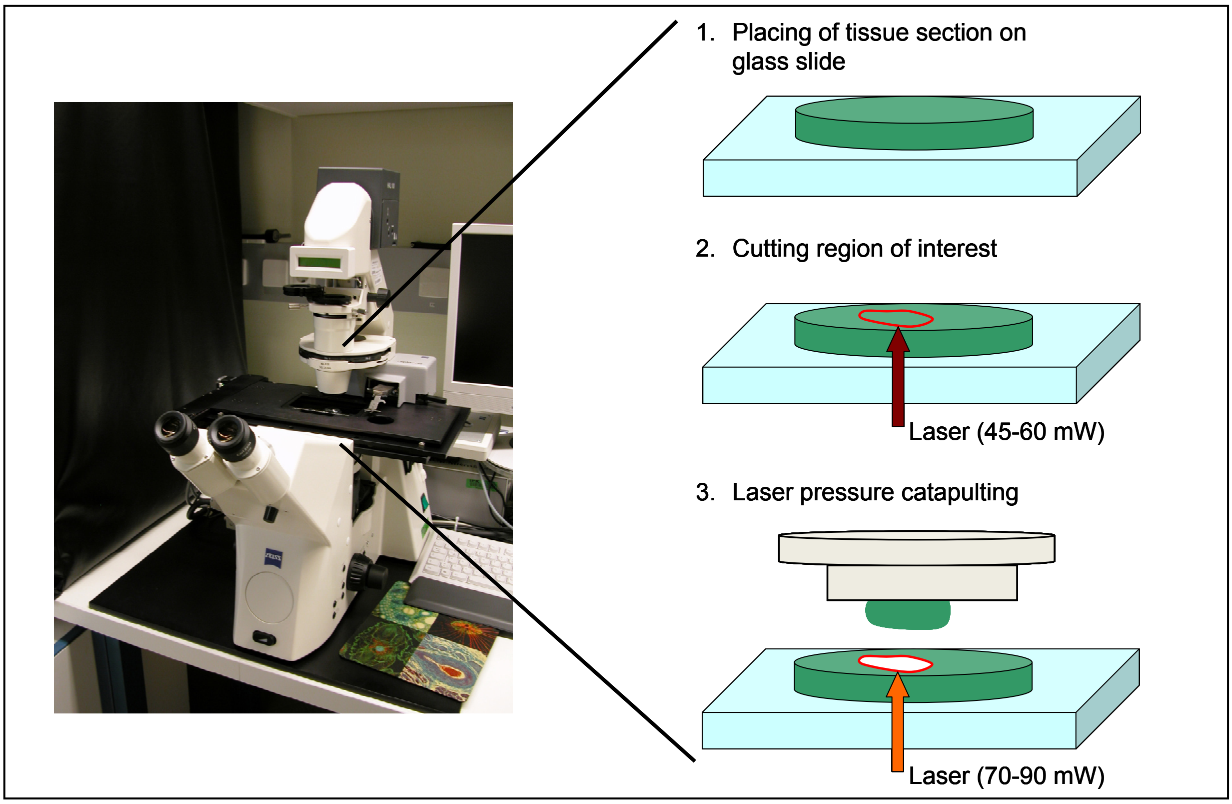


Figure 33: Schematic overview of the laser-micro-dissection workflow. First the tissue section is placed on a glass slide (1). The region of interest is cut using a laser (power 45-60 mW, 2) and afterward this region is catapulted into a lid of a special cap using higher laser power (70-90 mW, 3).

For the analyses of laser-micro-dissected material, typically, between 70 and 75 sections were processed per experiment for dissection of ETC referring to about 4,500,00 μm^2 of section area. For dissection of NP, about 40 sections were processed per experiment, which corresponds to about 2,500,000 μm^2 section area. Protein extraction, separation, and detection of tryptic peptides was performed as described in Material and Methods section 3.2.1. For each tissue type three individual preparations were made. Two µl of the peptide mixture of each sample, which were diluted to a concentration of 100,000 µm^2/µl, were injected and measured in triplicates per preparation. Data acquisition was done using label-free LC-MS approach as described in Material and Methods section 3.2.4. The complete workflow for the analyses of laser-micro-dissected barley grain material is shown in Figure 34.

The BPI chromatograms gained out of the three different sample preparations were similar to one another, both for NP and ETC (Figure 35). Visual inspection of the BPI chromatograms displayed a higher complexity of the ETC profile compared to NP, reflected by a higher number of detectable peaks (ETC: 17,043 EMRTs, NP: 13,958 EMRTs). The replicate injections of the individual samples were reproducible in ETC and NP (see Figure A 4).

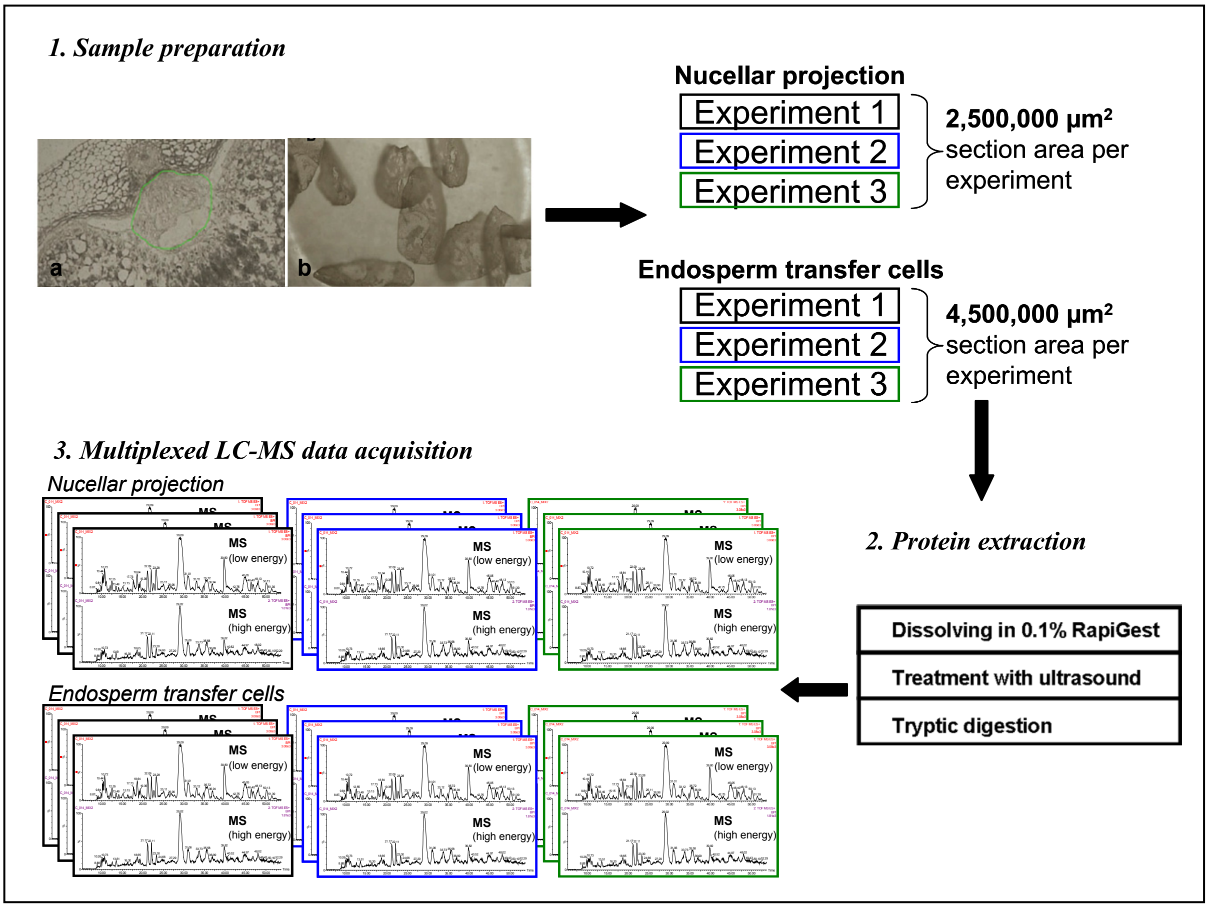


Figure 34: Workflow for the analyses of laser-micro-dissected barley grain material. (1) Sample were prepared by dissecting target tissues from barley grain cross sections (8 DAF) using a PALM lasermicrobeam instrument. The region of interest was marked (a), cut (b) and catapulted into the lid of a PALM adhesive cap. For the preparation of both, nucellar projection and endosperm transfer cells, three independent experiments were performed. Typically, around 2,500,000 µm^2 of section area per experiment were collected for the nucellar projection and 4,500,000 µm^2 of section area for endosperm transfer cells. (2) Proteins were extracted in 0.1% RapiGest^{TM} SF/50 mM ammonium bicarbonate, and digested with trypsin. (3) Data were acquired by a multiplexed LC-MS experiment using a nanoLC-ESI-Q-TOF MS instrument in alternating high and low energy acquisition mode. Samples of each experiment were injected in triplicate.

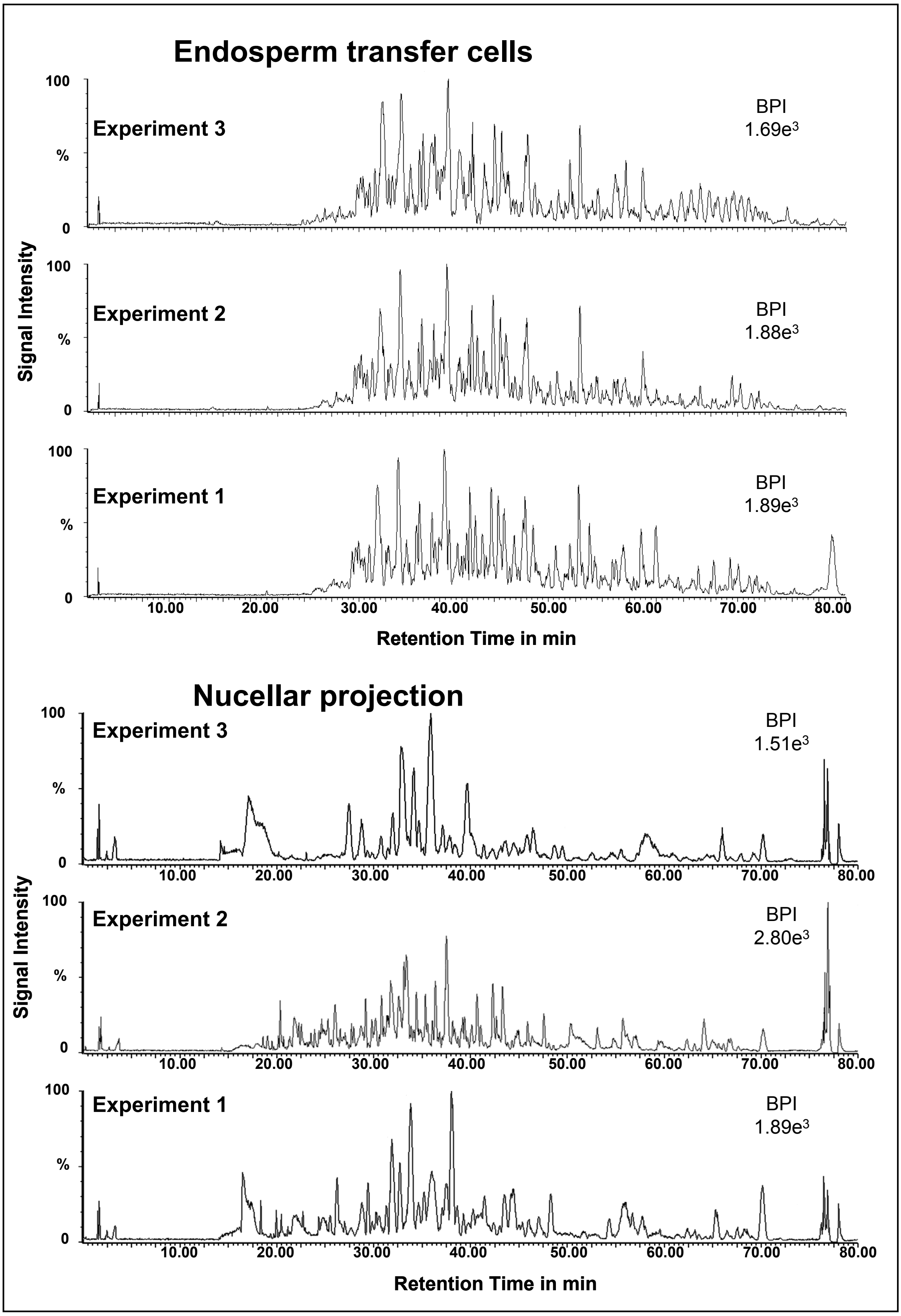


Figure 35: Base peak intensity (BPI) chromatograms of the low energy trace for the LC-based separation of peptides from laser-micro-dissected endosperm transfer cells and nucellar projection. Two µl of protein extract were directly loaded onto the column and peptides were detected using multiplexed LC-MS approach. Gradient ran from 0-33% acetonitrile in 80 min. Chromatograms showed a similar pattern between the three independent extractions (Experiment 1, 2, and 3).

Protein identification and comparative proteome analyses of micro-dissected endosperm transfer cells and nucellar projection

As described before, the number of detected EMRTs was higher for ETC compared to NP. Thus the subsequent protein identification by searches against two manually assembled databases (UniProt reference database and HarvEST) led to a higher number of identified peptides and proteins for ETC as for NP cells. Due to incomplete databases only around 5% of the detected features could be identified. The identification efficiency found in these analyses conformed to the detection of protein expression profiles during barley grain development (section 4.3.1).

A total of 137 proteins were significantly found in the ETC, whereas only 44 proteins could be identified in the NP. A summary displaying the total numbers of EMRTs, identified peptides and proteins in both tissues is shown in Table 10.

Table 10: Results of protein profiling of barley grain endosperm transfer cells and nucellar projection using LC-MS. The number of detected exact mass and retention time (EMRT) clusters, as well as the number of peptides and proteins identified using manually assembled UniProt reference and HarvEST database.

	Endosperm transfer cells	Nucellar projection
Number of EMRTs	17,043	13,958
Identified peptides	1,086	650
Identified proteins	137	44

Among the identified proteins 31 were present in both, NP and ETC (Figure 36). The complete list of identified proteins within each tissue type can be found in the Tables A 4 and A 5, which also details their presumed functional annotations, number of peptides, PLGS score, and sequence coverage.

The functional annotation of the corresponding proteins was performed according to an assignment scheme previously described for plant gene products (Figure 37). The proteins were sorted according to their function and numbers are given in relative (percentages) terms. Most proteins (30, 24%) of the ETC could be allocated to protein synthesis, whereas such proteins were lacking in the NP. The second largest group of ETC proteins belonged to energy metabolism and a third group consists of yet non-classified proteins. There was no protein detected with transcriptional activity in the ETC. Only few proteins fell into the categories cell wall synthesis, disease/defence, DNA binding, metabolism, and transport.

Most of the proteins found in NP have no presumed function. Second, third and fourth group contained proteins involved in protein destination and storage, energy metabolism as well as disease/defence. Additionally, a few proteins belonged to DNA-binding, metabolism, and transport. None of the NP proteins were associated with cell wall synthesis, protein synthesis or transcription.

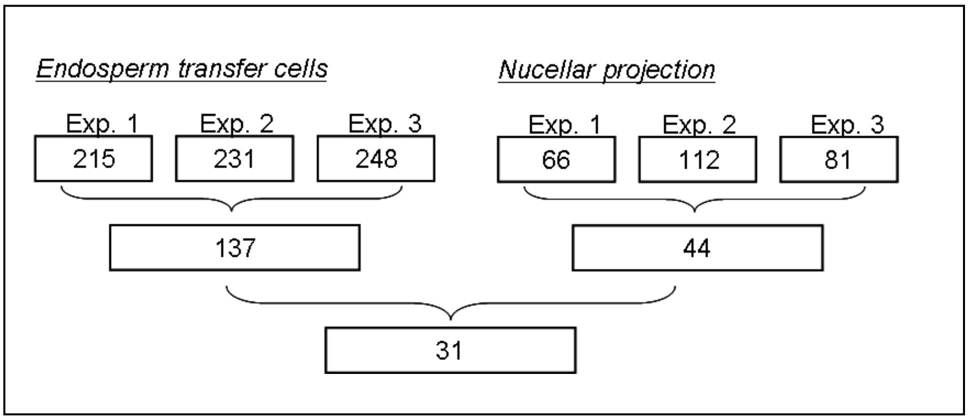


Figure 36: Proteome analysis of endosperm transfer cells and nucellar projection using nanoLC ESI-Q-TOF MS. The number of proteins identified in each of the three experiments (Exp. 1, Exp. 2, Exp. 3) is shown, together with number of proteins overlapping in at least 2 out of 3 experiments within one tissue type. Additionally, the number of proteins common for both tissue types is given.

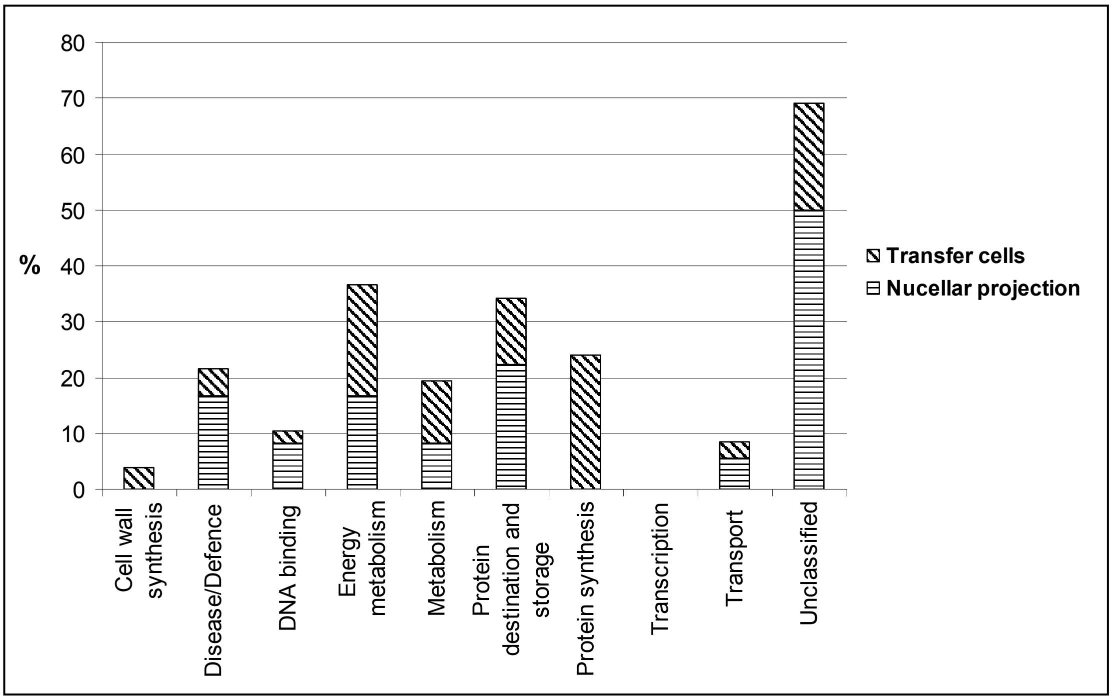


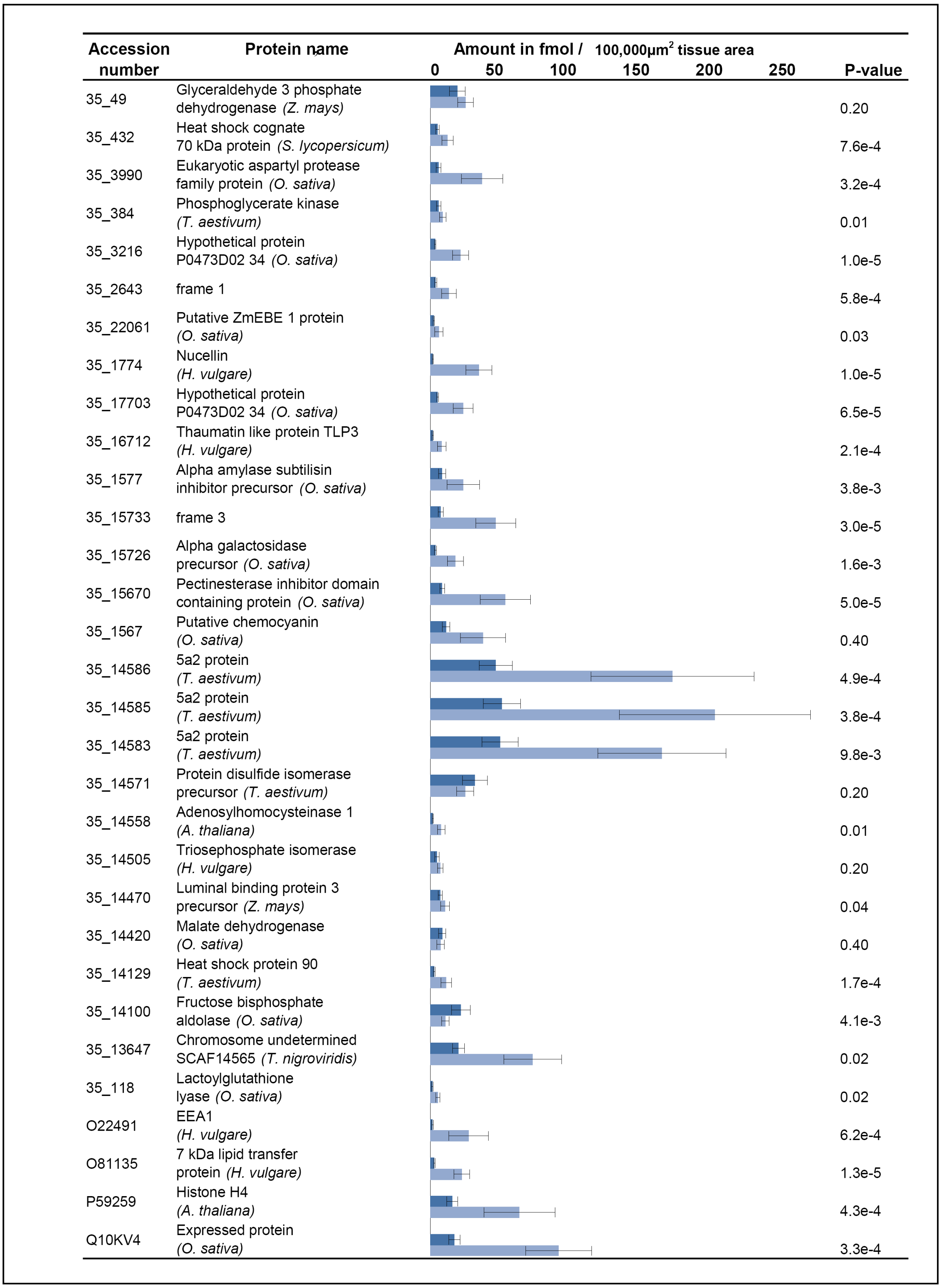
Figure 37: Functional classification of proteins found in the analyses of laser-micro-dissected nucellar projection, endosperm transfer cells and the overlap between both tissue types. Classification was performed according to a previous described assignment scheme (Bevan *et al.* 1998). Functional distribution is given in percentage.

The major differences between ETC and NP protein profiles were adherent with cell wall and protein synthesis, present only in ETC, and disease/defence, showing a higher coverage in NP. Of the 13 NP-specific proteins, two grain peroxidases (35_13648, 35_36536), and one protein involved in protein amino acid glycosylation (LGC1, 35_2002) were detected. The presumed function of five other proteins is not known. Additionally, proteins involved in glycolysis (35_119, P34937), protein folding and/or stress response (heat shock cognate 70kDa protein, P22954) as well as a probable histone H2AXb (Q2QPG9) were specific to the NP. Among the 106 proteins only detected in the ETC, 22 ribosomal proteins were found, and nine proteins were involved in carbohydrate degradation, e.g. sucrose synthase 1 (35_14484) and 2 (35_14483). Proteins involved in amino acid biosynthesis (e.g. alanine aminotransferase 2, 35_27721) and degradation, as well as protein destination related proteins (e.g. elongation factor 1, 35_41584) were also represented among the ETC-specific proteins, as was the 14-3-3 protein (35_14382).

An absolute quantification based on the mass signal intensities was performed to gain a clearer picture about differences and possible specializations in the molecular functions of NP and ETC. Amounts have been determined for those proteins common to both target tissues, and have been calculated for comparative purposes as fmol protein/100,000 µm^2 tissue area (Figure 38).

Most of the proteins detected in both tissues differed significantly in their amount ($P \leq 0.05$), tending to have higher amounts in NP compared to ETC. Five proteins were detected in similar amounts, among them three proteins involved in the glycolysis pathway (glyceraldehyde-3-phosphate dehydrogenase [35_49]; triosephosphate isomerase [35_14505]; malate dehydrogenase [35_14420]). Nucellin (35_1774), a protein supposed to be potentially localized in the NP, was also present in ETC, but with a lesser extend (34 fmol *vs.* 1.8 fmol per 100,000 µm^2). The embryo sac/basal endosperm transfer layer/embryo surrounding region protein (ZmEBE 1 protein, 35_22061) was detected in the NP and ETC, although at low level in both target tissues (NP: 6.0 / ETC: 2.4 fmol / 100,000 µm^2). Additionally, proteins related to proteolysis were common to both tissues; including an early embryogenesis gene EEA1 (O22491) and a eukaryotic aspartyl protease family protein (35_3990).

In general a higher number of proteins were found in the ETC compared to the NP. Most of these proteins are involved in degradation processes of carbohydrates and also translation processes. Proteins detected in the NP on the other hand showed less complexity but were mostly higher abundant (per 100,000 µm^2) compared to the ETC.



Accession number	Protein name	P-value
35_49	Glyceraldehyde 3 phosphate dehydrogenase *(Z. mays)*	0.20
35_432	Heat shock cognate 70 kDa protein *(S. lycopersicum)*	7.6e-4
35_3990	Eukaryotic aspartyl protease family protein *(O. sativa)*	3.2e-4
35_384	Phosphoglycerate kinase *(T. aestivum)*	0.01
35_3216	Hypothetical protein P0473D02 34 *(O. sativa)*	1.0e-5
35_2643	frame 1	5.8e-4
35_22061	Putative ZmEBE 1 protein *(O. sativa)*	0.03
35_1774	Nucellin *(H. vulgare)*	1.0e-5
35_17703	Hypothetical protein P0473D02 34 *(O. sativa)*	6.5e-5
35_16712	Thaumatin like protein TLP3 *(H. vulgare)*	2.1e-4
35_1577	Alpha amylase subtilisin inhibitor precursor *(O. sativa)*	3.8e-3
35_15733	frame 3	3.0e-5
35_15726	Alpha galactosidase precursor *(O. sativa)*	1.6e-3
35_15670	Pectinesterase inhibitor domain containing protein *(O. sativa)*	5.0e-5
35_1567	Putative chemocyanin *(O. sativa)*	0.40
35_14586	5a2 protein *(T. aestivum)*	4.9e-4
35_14585	5a2 protein *(T. aestivum)*	3.8e-4
35_14583	5a2 protein *(T. aestivum)*	9.8e-3
35_14571	Protein disulfide isomerase precursor *(T. aestivum)*	0.20
35_14558	Adenosylhomocysteinase 1 *(A. thaliana)*	0.01
35_14505	Triosephosphate isomerase *(H. vulgare)*	0.20
35_14470	Luminal binding protein 3 precursor *(Z. mays)*	0.04
35_14420	Malate dehydrogenase *(O. sativa)*	0.40
35_14129	Heat shock protein 90 *(T. aestivum)*	1.7e-4
35_14100	Fructose bisphosphate aldolase *(O. sativa)*	4.1e-3
35_13647	Chromosome undetermined SCAF14565 *(T. nigroviridis)*	0.02
35_118	Lactoylglutathione lyase *(O. sativa)*	0.02
O22491	EEA1 *(H. vulgare)*	6.2e-4
O81135	7 kDa lipid transfer protein *(H. vulgare)*	1.3e-5
P59259	Histone H4 *(A. thaliana)*	4.3e-4
Q10KV4	Expressed protein *(O. sativa)*	3.3e-4

Figure 38: Absolute quantification of proteins found in nucellar projection (light blue) and endosperm transfer cells (dark blue). Amounts were calculated in correlation to the amount of yeast enolase, which was spiked as a reference protein in a known concentration. Results showing the average amount in fmol/100,000 µm² gained out of three replicates and the corresponding standard deviation are displayed.

4.3.3. Correlation of spatial and temporal protein patterns during barley grain development

Results gained out of the analyses of barley grain development revealed a number of proteins showing distinct temporal distribution patterns. These results were compared with proteins identified during the analyses of NP and ETC providing initial information about spatial distribution patterns in correlation to the temporal expression profiles. In total, 34 proteins were found in developing grains as well as in the protein profiles of the NP and the ETC. Nine of the proteins were detected in both, NP and ETC. Most of these proteins were related to energy metabolism and protein destination. In total, 25 of the proteins detected within the analyses of spatial as well as temporal distribution patterns were exclusively found in ETC, whereas all of the proteins detected in NP were also found in ETC (Table 11). As described before, a high number of ribosomal proteins were detected in ETC and five of these proteins were also found during the analyses of spatial distribution patterns. None of the proteins known to be specifically expressed in NP and ETC (Nucellin, ZmEBE) could be detected during the analyses of temporal distribution patterns. All of the proteins, found in the analyses of spatial and temporal distribution patterns, belonged either to the Group I (highest expression in the middle phase of development) or to the group with mixed patterns. None of the detected proteins showed highest expression in the late phase of development as for the detection of spatial distribution patterns sample material from grains harvested 8 DAF was used.

Table 11: Summary of proteins found in the analyses of developing barley grains and in microdissected ETC and NP. Analyses were performed using LC-based separation coupled to MS detection. Presented are the protein names, accession numbers together with the used database ([1]HarvEST, [2]Uniref), experiment in which protein was detected and the functional classification, which was performed according to a previous described assignment scheme (Bevan *et al.* 1998). Additionally, the group out of the grain development protein profiling approach (as explained in Figure 29) is provided.

Protein name	Accession number	Grain development	Transfer cells	Nucellar projection	Function	Group
Lactoylglutathione lyase *(O. sativa)*	35_118[1]	x	x	x	Unclassified	mixed pattern
Fructose-bisphosphate aldolase *(O. sativa)*	35_14100[1]	x	x	x	Energy metabolism	mixed pattern
Malate dehydrogenase *(O. sativa)*	35_14420[1]	x	x	x	Energy metabolism	mixed pattern
Luminal-binding protein 3 *(Z. mays)*	35_14470[1]	x	x	x	Protein destination	I
Adenosylhomocysteinase 1 *(A. thaliana)*	35_14558[1]	x	x	x	Metabolism	mixed pattern
Protein disulfide-isomerase *(T. aestivum)*	35_14571[1]	x	x	x	Protein destination	mixed pattern
Hypothetical protein P0473D02 34 *(O. sativa)*	35_17703[1]	x	x	x	Unclassified	I
Phosphoglycerate kinase *(T. aestivum)*	35_384[1]	x	x	x	Energy metabolism	mixed pattern
Heat shock cognate 70 kDa protein 2 *(S. lycopersicum)*	35_432[1]	x	x	x	Protein destination	I
111P0402A09 25 protein *(O. sativa)*	35_1149[1]	x	x		Unclassified	I
40S ribosomal protein S4 *(Z. mays)*	35_14431[1]	x	x		Protein synthesis	I
Enolase 2 *(Z. mays)*	35_14444[1]	x	x		Energy metabolism	I
Sucrose synthase 1 *(O. sativa)*	35_14479[1]	x	x		Metabolism	mixed pattern
Sucrose synthase 2 *(H. vulgare)*	35_14483[1]	x	x		Metabolism	mixed pattern
Aspartate aminotransferase *(O. sativa)*	35_14619[1]	x	x		Metabolism	mixed pattern
60S acidic ribosomal protein P0 *(O. sativa)*	35_14696[1]	x	x		Protein synthesis	mixed pattern
ATP synthase subunit beta *(Z. mays)*	35_14758[1]	x	x		Transport	mixed pattern
40S ribosomal protein S19 *(O. sativa)*	35_14825[1]	x	x		Protein synthesis	I
Putative 60S ribosomal protein L1 *(O. sativa)*	35_14967[1]	x	x		Protein synthesis	I

Protein name	**Accession Number**	**Grain development**	**Transfer cells**	**Nucellar projection**	**Function**	**Group**
Phosphoglucomutase *(B. inermis)*	35_15040[1]	x	x		Metabolism	mixed pattern
Osr40g2 protein *(O. sativa)*	35_268[1]	x	x		Unclassified	mixed pattern
Alpha-1,4-glucan-protein synthase *(Z. mays)*	35_272[1]	x	x		Cell wall	I
Elongation factor 1 beta *(T. aestivum)*	35_41584[1]	x	x		Protein synthesis	I
Elongation factor 1 gamma 3 *(O. sativa)*	35_593[1]	x	x		Protein synthesis	mixed pattern
Nucleoside diphosphate kinase *(L. perenne)*	35_610[1]	x	x		Energy metabolism	I
RNA binding protein Rp120 *(O. sativa)*	35_617[1]	x	x		Unclassified	mixed pattern
40S ribosomal protein S3a *(O. sativa)*	35_685[1]	x	x		Protein synthesis	I
Ketol-acid reductoisomerase *(O. sativa)*	35_730[1]	x	x		Metabolism	mixed pattern
UTP-glucose-1-phosphate uridylyltransferase *(H. vulgare)*	35_751[1]	x	x		Metabolism	mixed pattern
Putative reversibly glycosylated polypeptide *(O. sativa)*	35_85[1]	x	x		Cell wall	I
Peptidyl-prolyl cis-trans isomerase *(O. sativa)*	Q1KL27[2]	x	X		Protein destination	I
Cytoplasmatic ribosomal protein S13 *(T. aestivum)*	Q5XUU9[2]	x	x		Metabolism	mixed pattern
QM *(T. aestivum)*	Q7X9L9[2]	x	x		Cell wall	I
Cytosolic glyceraldehyde 3 phosphate dehydrogenase *(T. aestivum)*	Q9M4V4[2]	x	x		Protein destination	mixed pattern

5. Discussion

The presented work was focussed on the protein profiling of various barley tissues, namely on leaf epidermis tissue, barley grains, and barley grain tissues, and included the establishment of micro-scale proteomic approaches.

5.1. Micro-scale proteome analyses are accomplishable using gel-free LC-separation coupled to label-free MS detection

The study presented here aimed at the proteomic profiling of laser-micro-dissected material. Therefore, the development and evaluation of a proteomic approach feasible for the separation and detection of micro-scale samples was necessary. One major drawback of 2-DE is the need for high sample amounts restricting its usefulness for protein analyses of micro-dissected material (Schad *et al.* 2005). Thus, it was aimed to apply nano-scale based liquid chromatography coupled to MS detection for the analyses of micro-scale samples. Quantification of underlying proteins can be either performed using label-based or label-free methods. Label-free MS detection was chosen in this study, as label-based methods feature several limitations, like increased time requirement and complexity of sample preparation, requirement for higher sample concentration, high costs of the reagents and incomplete labelling (Zhu *et al.* 2010). One aim was to show the reliability of the technique for quantification issues and the feasibility for the analyses of small sample amounts. Quantification using ESI-Q-TOF MS can be done based on the intensity of a detected ion, because the signal intensity from electrospray ionization correlates with the ion concentration (Voyksner and Lee 1999). The detected molecular ions are characterized by a defined m/z ratio and the corresponding retention time. The correlation of these species among different samples and replicates can be done using accurate mass and retention time (AMT) tags (Masselon *et al.* 2008), also called EMRT pairs. Thus, the applicability of this technique is strongly dependent on both, retention time and m/z stability. Both parameters were monitored over five independent LC runs in the presented experiments (see Results, section 4.1.2) and showed a high stability as the deviation for retention time was only 1000 ppm (~ 6 s) and for mass accuracy 34 ppm (5 mDa). These results are comparable with previous experiments describing the analysis of four standard peptides spiked into a tryptic digest of cytosolic proteins of *E. coli*. Li and colleagues (2009) found a mass accuracy of within 10 ppm for peptides assigned to the corresponding proteins and a retention time difference of around 8 s. Additionally, the accuracy for relative quantification in a complex biological background could be shown in the present work. Quantification was done using a data-independent multiplexed MS mode, in which all peptide precursors eluting from the LC-system are simultaneously fragmented regardless of their intensity (Cheng *et al.* 2009).

Alternating scans of low and high collision energy were recorded revealing information used for protein quantification and identification in a single experiment. The experimentally obtained ratios of four proteins spiked into a protein extract of barley leaf epidermis correlated strongly with the theoretical values (Table 4). Thus, a high stability and accuracy related to the quantification efficiency could be verified for the multiplexed LC-MS method. Besides, the applicability for small sample amounts originating from micro-dissected material was confirmed in the presented study. NanoLC-based separation coupled to multiplexed MS detection was able to reproducibly identify about 260 proteins from five barley grain sections, which represented a total section area of around 417,000 µm^2 (see Results, section 4.1.3). Thus, the method was applicable for comparative proteome analyses of LMPC obtained barley grain tissues. A previous study investigating vascular bundles prepared out of *A. thaliana* stems displayed that the high sample amount required for 2-DE clearly restricts the usefulness of this method and favours LC-MS (Schad *et al.* 2005). The obtained results underlay the appropriateness of the nanoLC-based separation method coupled to multiplexed MS detection for quantitative proteomic approaches, especially for the analysis of limited sample amounts as it is performed in the study presented here.

5.2. Biochemical profiling of barley leaf epidermis tissue points toward a protective function

Proteome analyses revealed expression of a variety of stress-related proteins in epidermis tissue

The molecular characterization of the barley leaf epidermis through protein profiling by 2-DE as well as LC-MS technique was aimed (see Results, section 4.2.2). Both methods are based on different separation strategies. Whereas 2-DE implies the separation of proteins, LC-based separation is done on the peptide level. The application of gel-based and gel-free methodologies to enlarge the number of identified proteins and thus to gain a more comprehensive data set has already been emphasized (Wolff *et al.* 2006). The complementary character of both methods could be shown in the analysis presented here, as 387 proteins were identified by 2-DE, 230 proteins by LC-MS, and only 75 proteins were detected by both approaches. These results support the application of both methods, when sufficient sample material is available, to get the most entire insight into the proteome of complete tissues.

Several proteins were detected in multiple spots on 2-D gels. The occurrence of multiple spots for single proteins using 2-DE can amongst others be caused by the existence of multiple isoforms. The study of barley leaf epidermis tissue using proteomic tools led to the identification of several proteins known to exist in different isoforms, such as tubulin α and ß

(Eun and Wick 1998) and 14-3-3 proteins (Testerink *et al.* 1999). Furthermore, post-translational modifications, like phosphorylation and acetylation can lead to the detection of multiple spots. Degradation creates additional protein spots detectable in the lower molecular weight range.

S-adenosylmethionine synthase 1 was detected in six different spots, with the same molecular weight but different pI (see Results, Figure 13 D). This enzyme is involved in the methionine cycle. Methionine synthase as well as adenosyl-homocysteine hydrolase, further enzymes participating in this pathway, were also detected within the mapping approach. S-adenosylmethionine synthase catalyses the reaction of an adenosyl group from ATP with a sulphur atom of methionine. The end product is S-adenosylmethionine (SAM), which is involved in the methylation of nucleic acids, proteins, carbohydrates, membrane lipids, cell wall lignification, and other processes (Wienkoop *et al.* 2004). Besides its function as universal methyl donor, SAM is a precursor for ethylene, a plant hormone. Amino-cyclopropane carboxylic acid (ACC) oxidase is involved in the conversion of SAM into ethylene and was detected in the protein profiling of epidermis tissue. ACC synthase (ACS), a further enzyme important for ethylene synthesis, could not be detected using stated techniques. ACS is known to be an unstable protein present only in low amounts in plant tissues, as for example gene transcript was undetectable or at very low levels under control conditions in tomato leaves. Signals corresponding to this enzyme were only detected after induction with UV-B treatment (An *et al.* 2006). Methionine, as a precursor of SAM, was only found in relatively low amounts (<100 fmol) in epidermis tissue (see Results, Figure 22). It is known that ACS catalyses the formation of 5-methylthioadenosine out of SAM, which can further be used for the synthesis of new methionine. Thus, low amounts of methionine detected in the analyses presented here are not limiting the ethylene biosynthesis (Lin *et al.* 2009). Ethylene itself is known to be responsive to various stresses, such as wounding, low or high temperature, ozone exposure, water stress, UV-B radiation (An *et al.* 2006), but also regulates important aspects of plant life cycle, e.g. seed germination, root initiation, root hair development, and flower development (Lin *et al.* 2009). As ACC was detected in epidermis tissue the production of this hormone may be accomplished by the tissue itself, rather than being dependent on supply mechanisms from the mesophyll. To further support this hypothesis investigations should also include the measurement of ethylene in epidermis tissue.

The total number of secondary metabolism-related proteins, among them proteins involved in flavonoid synthesis, was relatively low (see Results, Figure 16). This was an unexpected result as secondary metabolites, especially flavonoids, are known to be produced and highly accumulated in barley epidermis leaf tissue (Schmelzer *et al.* 1988). However, key enzymes required for the synthesis of flavonoids (i.e. PAL, chalcone synthase, and chalcone isomerase), starting from phenylalanine, could be identified (Figure 39). Therefore, the activity of this pathway in epidermis tissue and not a transport related accumulation of flavonoids during plant growth and stress events can be assumed from proteomics results. Immunodetection of PAL was performed with comparison to the remaining leaf and detected 2 bands of comparable expression values in both tissue types (Figure 17). Protein profiling led to the detection of PAL 1 (35_14236) and PAL 2 (35_14228) in epidermis tissue, at which isoform-specific peptides were only detected for PAL 1 (DLLLTIDR and LAMFEQELR). Remaining peptides could be allocated towards both isoforms. As also 2 bands were detected in the immunodetection approach, probably both isoforms are expressed in the epidermis. Southern analysis of barley genomic DNA conducted by Kervinen and colleagues (1997) revealed at least five different members of the PAL gene family. Three cDNA clones were fully sequenced (hpal 2, 3, and 7). Peptides detected in the presented study correlate in most cases to the translated sequences of hpal 2 and 7, whereas peptides specific to PAL 1 were only found in hpal 2. Two peptides were found in the translated sequence of all three genes (SPQWLGPQIEVIR and NPSLDYGFK). Nevertheless, no peptides exclusive for the hpal 3, a gene observed to be specifically expressed in the mesophyll (Kervinen *et al.* 1998), were detected. PAL is known to be an inducible enzyme, and the *de novo* synthesis of its isoforms is induced by abiotic and biotic stress (MacDonald and D'Cunha 2007). Thus, even though detected levels of PAL may not differ under control conditions between epidermis and mesophyll tissue, expression patterns after application of different stressors need to be determined in future experiments. Additional enzyme activity measurements might further verify the presence and activity of secondary metabolite-related enzymes in leaf epidermis tissue.

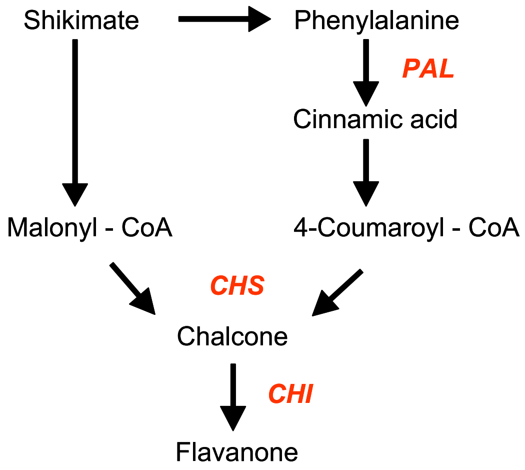


Figure 39: Schematic overview of flavonoid synthesis pathway in barley (adopted according to Jendestrid (1993)). The enzymes detected in barley leaf epidermis using proteomic approaches are displayed in red (PAL: phenylalanine ammonia-lyase, CHS: chalcone synthase, CHI: chalcone isomerase / chalcone flavanone isomerase).

One major functional category covered by a high number of proteins detected in barley leaf epidermis tissue was disease/defence. Several proteins related to the antioxidative system were detected in this group; e.g. SOD, peroxiredoxin, dehyrdoascorbate reductase, and several peroxidases (e.g. peroxidase 10, peroxidase 3, APX), displaying a high activity of redox-reduction-related processes. Immunodetection of SOD isoforms revealed slight differences in expression patterns within the 4 detected bands and no obvious difference for the two bands of APX. ROS are continuously produced in plants as biproducts of many metabolic reactions, such as photosynthesis, photorespiration, and respiration (Ahmad *et al.* 2008). Detoxification of these species by ROS scavenging enzymes is important for all cellular components and thus comparable levels of SOD and APX were detected in the epidermis and the mesophyll. Expression of several isoforms of SOD and APX has already been described in barley root and shoot tissue. Kim and colleagues (2005) described the expression of at least 5 SOD- and 2 APX-isoforms differing in their expression upon salt-treatment. Isoform-specific differences of epidermis and mesophyll tissue towards stress factors will provide valuable information about the tissue-specific regulation, but have not been determined yet.

One putative stress-induced protein was detected based on sequence homology to *O. sativa*. Homologues of this protein are known in tobacco *(N. tabacum)* and *A. thaliana*. Western blot analyses revealed a higher abundance in barley epidermis tissue compared to mesophyll (Figure 17). Previous experiments showed higher expression of this protein in *N. tabacum* trichomes compared to leaf material and together with further stress-related proteins detected predominantly in trichomes their possible function connected to disease/defence was presumed (Amme *et al.* 2005). Immunodetection has additionally been performed for the PR-Q protein, which belongs to the acidic chitinases (Heitz *et al.* 1994), and showed higher expression in the epidermis compared to mesophyll in all three detectable bands. Chitinases are ubiquitous proteins occurring in all plants in multiple isoforms and are supposed to function in pathogen defence (Graham and Sticklen 1994). Epidermal cells provide protection of underlying tissues due to their location as outermost cell layer, and thus protection against pathogens is an important function. Therefore, the high expression of chitinases in the epidermis is plausible and has already been observed in epidermal cells of potato (Ancillo *et al.* 2003).

ADH has been detected with higher signal intensities in mesophyll compared to epidermis tissue. ADH is known to be regulated by several environmental stresses, including low oxygen, dehydration, and low temperature (Dolferus *et al.* 1994), whereas its biochemical role is correlated to low-oxygen conditions. ADH expression in leaves was detected by Kato-Noguchi (2001) under control conditions in maize and lettuce plants together with an increase in activity caused by wounding. The results indicated that wounding may have induced ADH through increasing level of abscisic acid. Induction of ADH by abscisic acid has already been described in *A. thaliana* roots (deBruxelles *et al.* 1996). Nevertheless, the biochemical role of ADH under wounding stress conditions is still unknown. One further study focussing on proteome changes in leaves from grapevine transformed for ADH activity (sense and antisense transformants) showed alterations in the one-carbon metabolism-associated proteins (Sauvage *et al.* 2007). Thus, ADH may have additional functions in leaf tissues, which have not yet been analysed in more detail.

Besides the detection of different proteins somewhat connected to stress and disease-related processes also proteins involved in general metabolism were identified, including several carbohydrate metabolism-related enzymes (e.g. beta-D-glucan exohydrolase, fructokinase, phosphoglucomutase). Sugars are centrally embedded in general metabolism as they serve as primary energy source to generate adenosine triphosphate and redox energy (Lalonde *et al.* 2004). Therefore, the activity of the carbohydrate metabolic pathway is important to sustain the different biological functions realized by the epidermis. Further proteins involved in the general metabolism were related to amino acid biosynthesis. Amino acids play a central role as they are on the one hand the organic transport form of nitrogen and on the other hand the main units for protein synthesis.

Metabolite analyses point toward stress- as well as accumulation-related processes in epidermis tissue

Determination of metabolites in epidermis tissue was performed in correlation to the mesophyll, as differences between both tissue types may point towards a possible molecular function of the epidermis. Therefore, GC-MS analysis was applied as an untargeted approach, as well as HPLC separation coupled to fluorescence detection for targeted amino acid detection.

GC-MS led to successful identification of 26 metabolites in epidermis and mesophyll tissue (see Results, Figure 20). As GC-MS is an untargeted approach a higher number of metabolites were expected. However, identification is reliant on available databases and it is known that a high number of detected metabolites are still uncharacterized. Additionally, the method discriminates against thermolabile and large compounds exceeding about 500 Da (Enot *et al.* 2007). Even though only a relatively small data set could be achieved, the identified metabolites revealed first information about tissue specific differences. Most metabolites were detected in higher relative amounts in mesophyll compared to epidermis tissue. Interestingly, sucrose could not be detected in epidermis tissue, whereas fructose and glucose were found at lower concentrations as in mesophyll tissue. Sucrose is the major product of photosynthesis and mesophyll cells are known to synthesize and accumulate sucrose. The tissue-specific distribution of sucrose has been already detected in barley mesophyll and epidermis protoplasts (Dietz *et al.* 1994) as well as in the sap extracted from individual epidermal and mesophyll cells of barley leaves (Koroleva *et al.* 1997). Authors found that from 5-15% of the leaf's glucose and fructose was stored in the epidermis and thus considerable proportions of these compounds were located in the epidermis, irrespective of the actual metabolite levels of the leaves. The detected differences in the level of various sugars in the two tissue types led to the assumption that the epidermis holds a storage function, which is selective and discriminates against sucrose. Nevertheless, it is interesting that sucrose could not be detected in the barley leaf epidermis tissue, as it is the most important energy source and transport form in plants (Lalonde *et al.* 2004). Glucose occurs as intermediate of invertase-driven sucrose degradation, as a product in the starch metabolism, and in further metabolic reactions. High levels of this metabolite are known to be stored in the vacuoles (Deuschle *et al.* 2006). As the barley leaf epidermis cells are occupied by vacuoles to 99% (Winter *et al.* 1993) they hold a high potential to accumulate glucose. Malate and fumarate were detected in relatively high amounts in the epidermis when compared to mesophyll tissue. Both metabolites are by-products of the tricarboxylic cycle, whereas malate is a secondary product of fumarate. Here, several enzymes involved in this pathway were detected using proteomic profiling (i.e. pyruvate dehydrogenase, isocitrate dehydrogenase, fumarate dehydrogenase, malate dehydrogenase) displaying a correlation between proteomics and metabolomics data as well as the high importance of this pathway in epidermis tissue. Nevertheless, only late products of the citrate cycle were detected in epidermis tissue, whereas citric acid and isocitric acid could be detected in relatively high amounts only in mesophyll tissue, indicating differences in the activity between both tissue types. Whether this is caused by transport-related processes of precursors from the mesophyll or by a high rate of conversion remains to be examined in studies with labelled precursors.

Tissue-specific differences were also detected within the identified amino acids. As the detected amounts for amino acids were relatively low with the untargeted GC-MS method, a targeted method for extraction and separation was used in addition. HPLC separation coupled to fluorescence detection led to the finding that most amino acids occurred in a higher relative abundance in mesophyll compared to epidermis tissue (see Results, Figure 22), which is consistent with the GC-MS results. Amino acids are used to generate a wide variety of products, like proteins, enzyme co-factors, and hormones. The dominant organ in amino acid synthesis and distribution in most crop plants is the leaf using the energy and carbon skeletons produced by photosynthesis to assimilate nitrogen into primary amino acid products (Noctor *et al.* 2002). Even though several amino acids are synthesized principally or exclusively in the chloroplast, studies already showed that the major part of the amino acids are stored in the vacuole and cytosol. Leidreiter *et al.* (1995) showed that around 50% of the amino acids in potato leaves were located in the chloroplast, whereas the remaining amount was distributed between the cytosol (30%) and the vacuole (20%). By applying GC-MS none of the amino acids revealed a higher or equal relative abundance in epidermis tissue compared to mesophyll. However, HPLC separation led to the detection of higher relative amounts for glycine in epidermis tissue and no significant difference between epidermis and mesophyll for proline. Differences in the detection efficiency of GC-MS and HPLC coupled to fluorescence detection for amino acid analysis have been observed before by Noctor *et al.* (2007). They clearly showed an underestimation of amino acids in *A. thaliana* leaves by GC-MS, probably caused by difficulties in volatilization out of complex extracts. Nevertheless, Noctor and colleagues denoted the applicability of GC-MS to produce biologically meaningful data for the majority of detected compounds as the occurring problems were potentially related to the chemical structures of amino acids, which may interact with the sample matrix. Proline has long time been known to act as a compatible osmolyte. Recently, several studies highlight its additional function in stress adaptation, recovery and signalling (Szabados and Savoure 2009). Numerous studies have shown that the proline content increases under environmental stresses, such as drought stress (Choudhary *et al.* 2005), high salinity (Yoshiba *et al.* 1995), UV irradiation (Saradhi *et al.* 1995), oxidative stress (Yang *et al.* 2009), and in response to biotic stresses (Fabro *et al.* 2004). Therefore, the relatively high levels in epidermis tissue may point towards the multiple functions of proline especially in disease/defence-related processes. Within the proteome profiling approach none of the proteins detected in epidermis tissue were connected with proline biosynthesis. Transporters specialized for proline are known in plants (Kishor *et al.* 2005), but could not be detected in the presented analyses. Gene expression analysis of single epidermal cells of *A. thaliana* showed an extremely high accumulation of transcripts from a putative amino acid transporter (Lieckfeldt *et al.* 2007). Nevertheless, proline transporter-specific transcripts were not yet detected in epidermis tissue. Thus, further analyses are necessary to determine whether the high amount of proline is caused by transport-related processes from the mesophyll or by the synthesis in the epidermis itself.

Glycine was detected in significantly higher relative amounts in epidermis tissue. Both, serine and glycine, can be produced via photorespiratory pathway or via a non-phosphorylated pathway out of phosphoglycerate (Ho *et al.* 1998). Enzymes important for both pathways were detected in the epidermis tissue (namely phosphoserine aminotransferase, serine hydroxymethyltransferase, glycolate oxidase) and therefore no preference could be ascertained. Glycine is important for the biosynthesis of purines, as source of one-carbon units (Walton and Woolhouse 1986), and as the substrate for the glycine decarboxylase:serine hydroxymethyltransferase complex synthesizing serine, ammonia, and carbon dioxide (Di Martino *et al.* 2003). The expression of higher amounts of glycine in epidermis tissue compared to mesophyll has not yet been described or discussed. As glycine can be stored in vacuoles one could also speculate a storage function of the epidermis as suggested by Dietz *et al.* (1994). Authors found lower glycine levels in the epidermis compared to mesophyll. The reason for this discrepancy to the present work might be age- and sample-dependent differences. While 5 day old seedlings were analysed in the present work, Dietz and colleagues investigated epidermal protoplasts from 10 day old seedlings. Besides the possible role as storage compound, glycine is a precursor of glycine betaine, an important osmolyte synthesized upon abiotic stresses (Bhuiyan *et al.* 2007). Both, proline and glycine betaine, are osmolytes that accumulate in a variety of plant species in response to several abiotic stresses like drought, salinity, extreme temperatures, UV-radiation, and heavy metals (Ashraf and Foolad 2007). Thus, apart from storage processes, a possible function of both metabolites with regard to abiotic stress in leaf epidermis tissue can be hypothesised.

In summary, the work presented here gives a broad overview about possible molecular functions of leaf epidermis tissue for the first time. Basic findings are summarized in Figure 40. In general, proteome and metabolome profiling of epidermis tissue revealed enhanced expression of proteins and metabolites correlated to stress-related processes. Enzymes involved in ethylene and secondary metabolite production, as well as scavenging of reactive-oxygen species (ROS) were detected. This supports the proposed function of the epidermis as a protective barrier. Additionally, the relatively high amounts of proline and glycine point toward a guarding function of the epidermis. These results reflect the importance of the epidermis to protect underlying tissues from pathogen attacks and abiotic stress impacts. Multiple proteins involved in general metabolism, like carbohydrate metabolism and amino acid synthesis, were detected. Thus, the epidermis is able to synthesize essential metabolites rather than being dependent on the supply from the mesophyll. Besides the preformed protective function, also the presumed function for glucose and fructose accumulation could be strengthened in the analyses presented here.

Transcript studies would provide additional information about molecular functions of the leaf epidermis tissue and have already been initiated. The combination of transcriptome, proteome, and metabolome data will lead to a comprehensive overview giving correlative evidences about its functional specificities. Also, the importance of the epidermis in stress defence-related processes needs to be further confirmed in additional studies identifying tissue-specific reaction towards biotic and abiotic stresses between the epidermis and the remaining leaf. By monitoring the response of barley seedling to a wide range of abiotic stresses using a stress dedicated cDNA microarray, Atienza and colleagues found (2004) stress-specific regulation patterns as well as genes commonly induced by different stress conditions. Comparable experiments applied to analyse the reaction of epidermis tissue separately would help to further decipher stress responses in barley and the importance of the epidermis in those processes. First analyses included the responses of both tissues upon UV-B radiation and revealed main reaction in the epidermis on proteome and flavonoid level protecting the mesophyll against this harmful radiation (Kaspar *et al.* 2010). Analysis of membrane proteins would address transport-related processes to determine compounds, which are transported into the epidermis rather than being produced by this tissue itself. Furthermore, enzyme assays will provide information about the actual activity of detected enzymes. Thus, for example the secondary metabolite pathway could be investigated in more detail in comparison to mesophyll tissue.

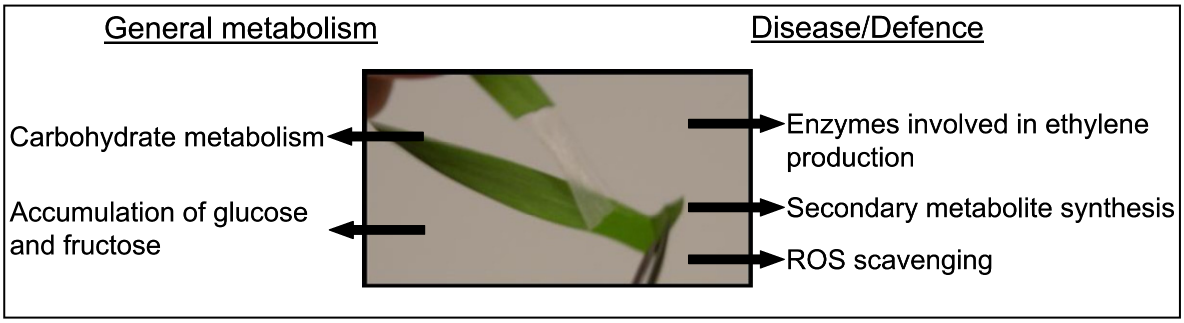


Figure 40: Basic molecular functions of barley leaf epidermis as detected by proteome and metabolite profiling approaches. An assortment of functional groups highly present in barley leaf epidermis is shown. Besides a high coverage of disease/defence-related processes, also several general metabolism-related proteins and metabolites were detected.

5.3. Proteome analyses of barley grain development reveal distinct patterns related to developmental processes

The present study aimed at the qualitative and quantitative protein profiling to monitor changes during barley grain development. The applicability of nanoLC-based separation coupled to MS detection for protein expression analyses could be shown (see Discussion, section 5.1) and thus was applied. Results revealed complex changes of the proteome and showed differences between the two performed experiments with regard to the number of detected EMRTs, identified peptides, and proteins. Mainly these differences were caused by the appliance of different experimental set-ups (see Material and Methods, section 3.2.4). Whereas the first data set was recorded on longer LC-columns (150 mm *vs.* 100 mm) with a longer gradient (110 min *vs.* 80 min), a higher total protein amount was injected on column for the second data set (0.15 µg *vs.* 0.5 µg, see Material and Methods, section 3.2.4). As a higher number of proteins could be detected within the second experiment, the quantity of detected features seems to be more dependent on the total protein amount on column rather than on column parameters. Thus, to increase the number of identified proteins and therefore data quality, experimental parameters used for the second experiment should be applied for future analyses. Only around 5% of the detected features were identified in each experiment. As the multiplexed approach is known to be beneficial for protein identification due to a higher sequence coverage compared to data-dependent methods including precursor ion selection (Blackburn *et al.* 2010), the low identification rate derives from the yet still incomplete plant protein databases. Future database improvements will therefore increase the information obtained by the presented data set.

The complex experimental setup necessary to compare 5 developmental stages throughout barley grain development demanded the usage of multivariate statistics for proper data evaluation. First, results were clustered on the basis of their temporal protein expression into 10 classes using Neural Gas clustering. A strict grouping of all identified peptides derived from one protein to a single class was not possible. Therefore, the data set was further clustered into three groups according to their developmental expression patterns with proteins showing highest abundance in the middle phase of development (7 DAF, group I), at later stages of development (16 DAF, group II), or with a mixed pattern. These distinct patterns correlate to the different developmental stages known for barley grain development. The early developmental pre-storage phase is followed by an intermediate or transition phase (at around 7 DAF), which is then followed by the storage phase (10 to 16 DAF).

The transition phase of grain development is characterized by high metabolic activity with regard to protein synthesis and cell cycle regulation

Proteins of the first group contained the highest number of detected proteins underlining intense changes in the transition phase. Previous transcript analyses of developing barley grains already discovered massive re-programming of gene expression during the transition phase (Sreenivasulu *et al*. 2004). A high number of proteins with yet no presumed function were detected within this group, which can not be used to define metabolic processes in the barley grain at the moment. Among the proteins having a defined function disease/defence-related, as well as protein destination and protein synthesis-related proteins were highly present. Mostly ROS-scavenging enzymes, like APX, SOD, and GPX, were detected as disease/defence-related proteins. All of the peptides assigned to the latter proteins showed highest expression during the transition phase of development (Figure 41). Thus, abundance of those proteins indicates a reduced necessity of the grain to detoxify ROS between 10 to 16 DAF and therefore within the storage phase. Down-regulation of ROS-scavenging enzyme RNAs from 8 DAF onwards has already been described in barley caryopses (Sreenivasulu *et al.* 2004), in aleurone layers, as well as gibberellic acid-treated barley aleurone protoplasts (Bethke and Jones 2001, Fath *et al.* 2001). It is speculated that down-regulation of transcript levels is connected to the programmed cell death (PCD) of the pericarp. Additionally, high expression of cysteine protease, a protein involved in the PCD of the aleurone layer (Bethke *et al.* 1998), was found in the present study in the middle phase of development followed by down-regulation during later developmental phases. These findings support the idea of PCD-related processes in the barley grain throughout the development also on proteome level. A decrease in the expression of ROS-scavenging enzymes has been described in the phases from barley grain filling until maturation on proteome level (Bonsager *et al.* 2007). The presented study demonstrates the high expression of ROS-scavenging enzymes already at early development, followed by a decrease from 8 DAF onwards.

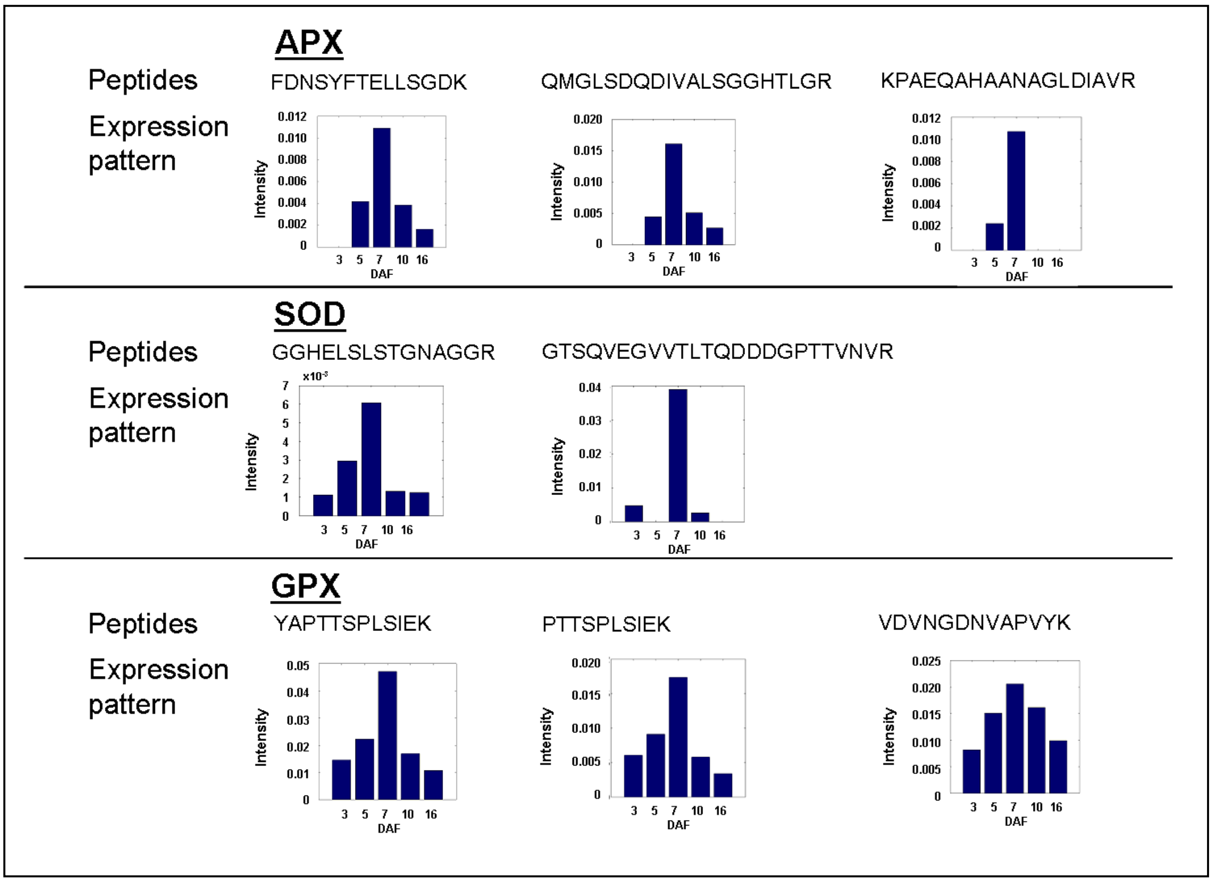


Figure 41: Expression patterns of single peptides belonging to the ROS-scavenging enzymes ascorbate peroxidase (APX), superoxide dismutase (SOD), and glutathione peroxidase (GPX) detected during the analysis of protein profiles in developing barley grains. Each peptide together with its average intensity at the five developmental stages is provided. Data is shown for the first experiment.

A putative stress-induced protein 1 (Sti1; 35_15495), already observed in the barley leaf epidermis as presented in this thesis (see Discussion, section 5.2), was detected with a relatively high number of peptides (7 peptides in experiment 1, 28 peptides in experiment 2). Sti1 has been described in *Saccharomyces cerevisiae* to be induced under different temperature regimes (Nicolet and Craig 1989). Even though Sti1 is known to be a co-chaperone that mediates the interaction between Hsp70 and Hsp90 (Webb *et al.* 2001), only little information, especially on the possible molecular functions of this protein, exists in plants. Recently, a homologue of the stress-induced protein was detected in tobacco leaf trichomes in comparison to the remaining leaf tissue and a possible involvement in protective functions was assumed (Amme *et al.* 2005). Based on the observed regulation in the present study, a possible developmental stage-dependent regulation with highest expression in the middle phase of the development of barley grains has been shown. But further investigations supporting the idea of a time-dependent expression of Sti1 are needed.

Concomitant with disease/defence-related proteins, also proteins involved in protein synthesis were predominately expressed at around 8 DAF. Several ribosomal proteins were detected (e.g. 40S ribosomal protein, 60S ribosomal protein, ribosomal protein L11 and L10A). The detection of high numbers of protein synthesis-related proteins was expected as the reprogramming from cell division towards storage protein accumulation during the transition phase necessitates intense protein synthesis.

Additionally, several histones (histone H2A 2 1, H2B 5, H2AXb, H4, and H2B 3) showed highest expression at 7 DAF followed by a decrease in the later developmental stages. Histones play a key role in cell cycle regulation and the decrease in their protein expression patterns correlates to the transition from cell division towards storage starch accumulation. Spiker and colleagues (1987) observed the same developmental appearance in wheat grains. Whereas expression of histones in barley grains was observed in NP displaying its mitotic activity (Thiel *et al.* 2008), studies showing the development-dependent regulation were missing till now.

Proteins connected towards storage protein accumulation and protection of storage reserves are up-regulated at later developmental stages

The number of proteins detected in the second group (with highest expression at later developmental stages, i.e. at the storage phase (around 16 DAF)), was lower in comparison to the first group. The storage phase is determined by storage product synthesis and accumulation. Therefore, the detection of storage proteins was expected within the second group and could be verified by proteomic approaches. Two hordeins and a hordein precursor were identified in the present study (B3 hordein [P06471], gamma hordein 3 [P801989], gamma hordein 1 precursor [35_69]). Hordeins account for the main protein fraction in barley endosperm and they can be used for barley variety identification (Salplachta and Bobalova 2009). One additional seed storage protein was detected (serpin Z4 [P06293]). Besides these four no further storage proteins were detected, possibly due to the applied extraction method. The biochemical properties of soluble proteins measured in the presented study differ from those of storage proteins. Hence, storage proteins are underrepresented in the presented data set.

Several proteins belonging to the protease/α-amylase inhibitor family were detected in the second group. Finnie *et al.* (2002) already observed increasing amounts of α-amylase inhibitors during grain filling and it was supposed that these proteins defend starch reserves of the grain against invading insects and pathogens rather than targeting endogenous barley α-amylases. The higher expression at later stages of development is in conjunction with increasing amounts of starch. In general, these inhibitors of hydrolases may have a role in plant defence and possibly act as insecticidal proteins (Lara *et al.* 2000). The ß-hordothionine (P21742), a protein also involved in the plant defence system against pathogens (Mendez *et al.* 1996), has been detected showing the same expression pattern during grain development as the protease/α-amylase inhibitors.

At the same time the expression of several hordoindolines (purothionin II [P01545], hordoindoline B1 precursor [Q9FSI9]) increased during grain development. Hordoindolines are barley grain protein homologues to wheat puroindolines, and they are known to be associated with grain hardness (Takahashi *et al.* 2010). Grain texture has a high impact on the quality of cereal grains and therefore the ability to influence grain hardness would be of food and feed value. Additional to the latter proteins a grain softness protein (Q0GIL0), which is related to grain hardness, was identified showing the same expression profile as the hordoindolines. Those proteins are all closely linked to a soft grain texture (Turuspekov *et al.* 2008). Textural differences exist between the European barley cultivars and determine their end-use. For example, good-malting cultivars are softer in texture (Brennan *et al.* 1996) and harder textured barley would be desirable for animal feeding (Turuspekov *et al.* 2008). The up-regulation of those proteins reflects a softer grain texture and thus the predominant usage of the used cultivar 'Barke' for malting on proteome level.

Isoforms, post-translational modifications, and biological variance lead to detection of proteins which peptides showed a mixed pattern

The third group contained proteins, whose peptides showed a mixed temporal pattern, either in one experiment, or in both, or between both experiments (see Results Table 7). Several metabolism- and protein synthesis-related proteins were detected in this group. Most of them were identified with relatively high numbers of peptides compared to the first and second group, as can be seen in Table 9. Thus, these proteins seem to be highly present in barley grains throughout the complete developmental process leading to a good fragmentation pattern of underlying peptides in the MS and a high protein sequence coverage during identification. Differential developmental expression patterns of single peptides can be caused by the occurrence of isoforms for distinct proteins. Plants are known to possess multiple isoforms of a high range of proteins. As software solutions available at the moment still have difficulties to distinguish between protein isoforms (Matros *et al.* 2010), peptides assembled to one protein may belong to different proteins having different expression pattern throughout barley grain development. Finnie *et al.* (2006) identified one and the same protein with different appearance patterns during barley grain development using 2-DE. As they were not able to distinguish the sequences between the proteins by peptide mass data, they suggested a different expression of closely related isoforms. Some of the proteins detected by Finnie and colleagues in multiple spots were also identified in our approach, i.e. malate dehydrogenase and protein disulfide isomerase. Sucrose synthase 1 and 2 were detected with a relatively high number of peptides showing a mixed protein pattern. The main function of sucrose synthases in sink organs, such as the endosperm, is the cleavage of sucrose as the first step of the starch biosynthesis pathway. Sucrose is the major carbon transport form in the developing grain and early enzyme activity studies showed high signal intensities in the endosperm suggesting that this is the major site of sucrose degradation (Guerin and Carbonero 1997). The grain developmental process is accompanied by starch accumulation in the endosperm and activity of sucrose-cleaving enzymes is important throughout the complete development. Further enzymes involved in the carbohydrate metabolism were identified, among them proteins involved in glycolysis (e.g. phosphoglycerate kinase), and starch synthesis (e.g. glucose-1-phosphate adenylyltransferase). Additional metabolism-related processes were covered by proteins detected in the group with mixed patterns, such as fatty acid, and amino acid metabolism. As isoforms of several proteins may occur in different cellular compartments with altered developmental abundance, it is inevitable to perform tissue-specific analysis to fully understand the grain developmental processes and its regulation.

Moreover, also post-translational modifications can cause differences in protein expression patterns. Finnie and colleagues (2006) observed the occurrence of 1 cys peroxiredoxin, a protein regulated in response to oxidative stress and abscisic acid, in three spots with different temporal appearance during grain-filling and maturation phase in barley. As this protein is encoded by a single copy gene they suggest that the observed multiple spots differing in their pI must be caused by post-translational modifications. The same protein was also detected in the presented study in the group of proteins with mixed patterns, but evaluation of possible post-translational modifications has not yet been conducted. In those cases were only one peptide showed an opposite regulation, there is a high chance that this altered expression is caused by modifications of this peptide. To further elucidate this assumption, it is necessary to perform targeted analyses for those proteins.

Furthermore, proteins were detected with peptides showing highest expression in later stages of development in one experiment, but highest expression in the middle phase of development in the second conducted experiment (e.g. alpha amylase trypsin inhibitor CMb [35_111]; elongation factor 1 alpha [35_13730]). Those proteins reflect the biological variance within the experiments.

The occurrence of mixed patterns in only one of the two conducted experiments necessitated a closer consideration of the data sets. Lipoxygenase for example was detected in the first experiment with a mixed pattern, whereas the second experiment clearly revealed highest expression of all peptides in the middle phase of development (Table 7). As none of those peptides could be correlated to further isoforms these contradictory expression patterns can not be correlated to isoform-specific differences as described before for sucrose synthase 1 and 2. In the first experiment most of the peptides with contradictory patterns belonged to class 8 having a relatively high intensity compared to the other classes and a defined temporal distribution pattern. On the contrary the same peptides belonged to either the first or the second class in the second experiment and both classes are characterized by relatively low signal intensities (Figure 28). Thus, these observed differences may be caused by biological variances. Additional experiments, including Western blot analyses and the analyses of further biological replicates, are necessary to clarify this observation.

The observations made here clearly showed that the determination of expression patterns on peptide level as performed in the presented study reveals information about the regulation of single peptides which would be missed by global calculation on protein level. Thus, further investigation of peptides regulated in opponent behaviour will provide additional information about isoform-specificities, post-translational modifications, and biological variances.

Energy production in the developing grain is accomplished via photosynthesis

In the study photosynthesis-related proteins were detected either with highest expression in the middle phase of development (oxygen evolving enzyme [35_14635; A5JV93], oxygen evolving complex [35_14958]) or with a mixed expression pattern (orthophosphate dikinase [O24612], ribulose bisphosphate carboxylase large chain precursor [35_136; O03042]). Expression of photosynthesis-related genes has already been observed for grain and seed development in barley (Hansen *et al.* 2009, Sreenivasulu *et al.* 2006) and *A. thaliana* (Ruuska *et al.* 2002). Highest expression of photosynthesis-related proteins was expected in the middle phase of development and not at later stages, as the chlorenchyma, responsible for photosynthesis in barley grains, degenerates throughout development (Rolletschek *et al.* 2004). Proteins with peptides showing a mixed pattern occurred, among them the ribulose bisphosphate carboxylase large chain precursor protein (35_136). Interestingly, only one and the same peptide for both experiments showed highest abundance at later stages of development (FEFEPVDTIDK), whereas the rest of the peptides were highest expressed in the middle phase of development. As there is a clear trend for all the peptides besides one, the latter peptide could possibly be post-translational modified, e.g. phosphorylation on threonine. However, no clear evidence for such kind of modification can be provided and further targeted experiments are necessary. The major function of photosynthesis is fixation of carbon dioxide. Nevertheless, it is postulated for legumes (Rolletschek *et al.* 2002, 2003) and barley (Sreenivasulu *et al.* 2004) that a more important function of seed photosynthesis is to provide oxygen for the filial tissues, that are hypoxic during early grain development. Consequently, the state of the filial tissues is changed to an aerobic one in the intermediate phase and ATP production is favoured (Sreenivasulu *et al.* 2004). Thus, the photosynthesis in barley grains provides energy rather than photoassimilates. In accordance with this, proteins associated with energy production were found to be mainly up-regulated in the middle phase of development (ATP synthase subunit [35_14757] and [P19023]). One ATP synthase subunit showed a mixed pattern (35_14758), whereas most of the corresponding peptides were found with highest expression in the middle phase of development. Only one peptide showed opponent behaviour. As discussed before, this can be caused by possible post-translational modification and further in-depth analyses are necessary to unveil the conflictive behaviour of this peptide. In general, whereas the occurrence of photosynthesis-related transcripts in the middle phase of development has already been described for barley (Hansen *et al.* 2009, Sreenivasulu *et al.* 2004), the present study supports this finding for the first time on the proteome level.

In summary, the findings presented in this study contribute to the understanding of how metabolic networks are regulated at the protein level during grain development. Thereby it could be shown that the middle phase of development, also called transition or intermediate phase, is determined by a high activity of protein synthesis, as well as by the high expression of ROS-scavenging enzymes, and the occurrence of proteins involved in photosynthesis. A high abundance of histones in the middle phase of development could be shown for the first time for barley grain development. On the other hand, proteins involved in the defence against pathogens and the determination the grain texture, as well as storage proteins were higher expressed in the later stages of development. Most of the proteins involved in carbohydrate metabolism showed a mixed pattern, meaning that peptides were found in the first and in the second group, displaying a probable detection of isoforms. Basic findings are summarized in Figure 42.

Even though first detailed insights into barley grain developmental processes were obtained on proteome level, additional in-depth studies, like the analyses of membrane proteins to determine transport processes on proteome level, are necessary to further unveil the complex biochemical processes during barley grain development. Also studies to resolve the spatial distribution patterns of proteins in the barley grain are necessary to investigate possible tissue-dependent regulation patterns of proteins. Additionally, the data set must be re-evaluated when improved databases are released to increase the information available out-put of the performed experiments.

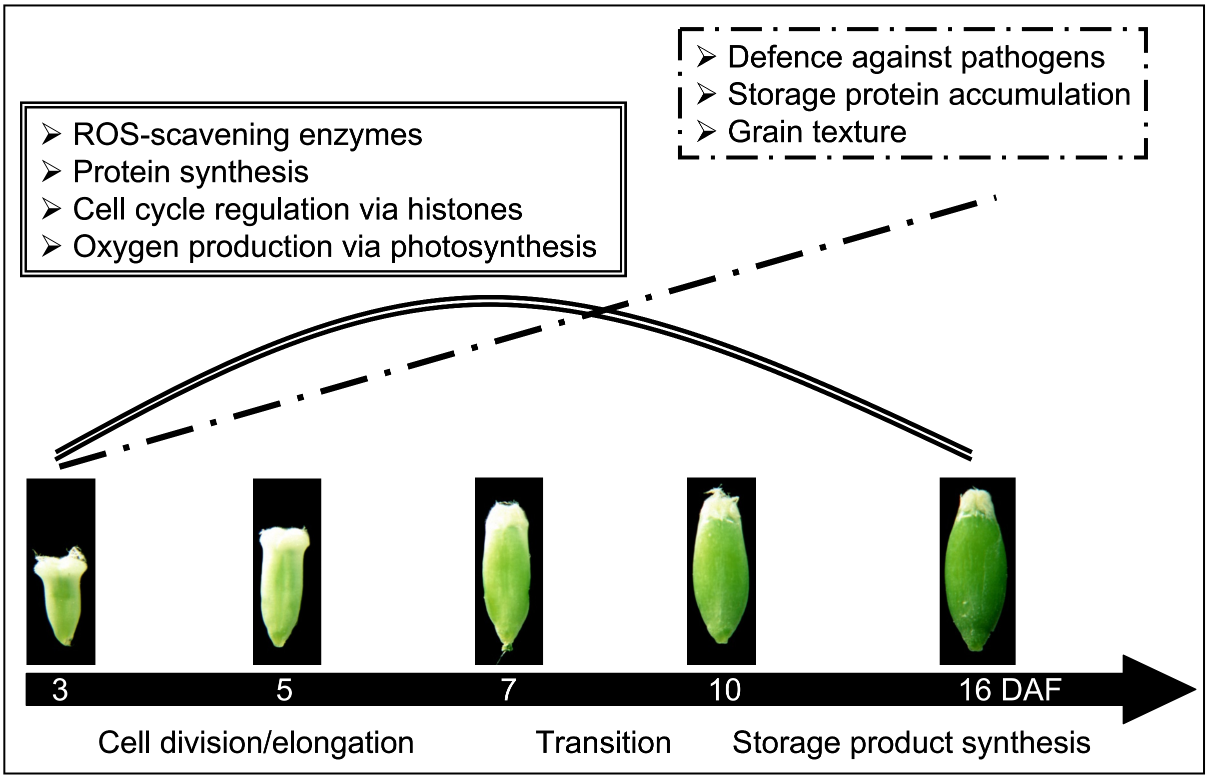


Figure 42: Schematical representation of the basic proteome profiling findings of barley grain development using label-free LC-MS coupled to multivariate statistics. Proteins higher expressed in the middle phase of development were mainly related to ROS-scavenging, protein synthesis, cell cycle regulation, and photosynthesis, whereas proteins higher expressed in the later stages of development were involved in the defence against pathogens, the grain texture and storage product accumulation.

5.4. The analyses of spatial distribution patterns using laser micro-dissection reveal cell-type specific biological functions

The process of barley grain development is not only determined by temporal distribution patterns of proteins, but also by their local arrangement. In the past, the analyses of distinct tissues in the barley grain has been based on manually dissected materials resulting in the fractions maternal pericarp, filial endosperm and embryo (Sreenivasulu *et al.* 2004, Sreenivasulu *et al.* 2006, Sreenivasulu *et al.* 2008) and was restricted to transcripts and metabolites. ETC and NP are both important tissue types involved in the nutrient transfer from maternal to filial tissue. Their analysis should reveal insights into the specificity of their molecular functionality, and provide first information about spatial distribution patterns of proteins within the barley grain. As neither NP nor ETC are accessible by manual dissection, LMPC has been applied, which has already been shown to be suitable for sample preparation and analyses of both tissue types (Thiel *et al.* 2008, 2009).

Proteome profiling points to higher complexity of biochemical processes in ETC compared to NP

The nanoLC-based approach was chosen for protein profiling of barley grain tissues, because 2-DE is not suitable for protein detection of LMPC-derived samples due to its requirement for high sample amounts (Schad *et al.* 2005). The feasibility of the applied methodology was proven before and a higher number of LC-MS features were identified when LMPC-based breast cancer cells were processed using columns of lesser internal diameter (Umar *et al.* 2007). The applicability of nanoLC-based separation coupled to MS detection for the analyses of micro-dissected plant material could be shown in the present study and led to the identification of 137 proteins for ETC and 44 proteins could be identified in the NP. The major differences between the ETC and NP protein profiles concerned cell wall and protein synthesis (in the ETC but not in the NP) and disease response (greater representation in the NP) consistent with previously published transcript analyses (Thiel *et al.* 2008). Here, authors showed that cell wall synthesis genes are more abundant in ETC than in NP. Additionally, NP cells, unlike ETC, characteristically undergo PCD throughout development, and therefore protein degradation tends to be more relevant than protein synthesis in the NP.

Even though both tissue types are known to be important for nutrient supply, only few proteins involved in transport processes were detected. Of these, a 7 kDa lipid transfer protein was present in both tissues. Transporters expressed at transcript level in NP and ETC have shown to be involved in nitrogen remobilization and amino acid transfer on transcript level (Thiel *et al.* 2008). The transport-related gene products detected include a voltage-dependent anion channel 2 gene higher expressed in the NP as in the ETC giving hints for programmed cell death associated processes in NP. On the other hand, proton-coupled co-transporters, like HvSUT1, were expressed at a higher level in the ETC, displaying differences in storage product accumulation activity at the investigated developmental stage. However, the corresponding proteins could not be detected using the applied proteomic tools. Transport proteins are integral membrane components. Particularly the ETC are known to contain many membrane-bound proteins (Offler *et al.* 2003). Although the LC-based separation method coupled to MS detection allows the detection of membrane proteins, the absolute quantity of these proteins present in a complex extract is very low compared to the soluble protein fraction. This raises the necessity to enrich for the hydrophobic protein fraction to enhance the detection of membrane-bound proteins.

Several tissue-specific proteins were detected, that may contribute to the functional differences between NP and ETC. Proteins involved in amino acid biosynthesis and degradation, as well as protein destination-related proteins were represented in the ETC-specific protein set. Interestingly, sucrose synthases 1 and 2, both known to be sucrose cleaving enzymes, were among the ETC-specific proteins. This was an unexpected result, as transcript analyses showed that the expression levels of both enzymes were higher in NP than in ETC (Thiel *et al.* 2008). Those results display the level of divergence between transcript and proteome data and underline the necessity of proteomic approaches to obtain information about gene products. Nevertheless, Ruan and colleagues (1997) already described a role for sucrose synthase in wall ingrowth deposition in coat transfer cells of developing cotton seeds by immunocytochemical evidence, and a lack of normal coat transfer cell development in sucrose anti-sense lines (2003).

Even though the correlation of protein and transcript profiling data is limited, corresponding expression patterns were detected for some proteins. This was the case for the ETC-specific expression of a 14-3-3 protein as earlier reports described the gene induction upon powdery mildew infection exclusively in the ETC (Thiel *et al.* 2008). Thus, despite differences in the full spectrum of genes detected by the protein and the transcript profiling approach, both detected a specific expression of genes related to anti-fungal activity in the ETC. The expression of these genes may be connected to the origin of this tissue type. The ETC originate from the first epidermal row (Olsen *et al.* 2001). This could explain the known up-regulation of genes associated with light-induced protein degradation in the ETC.

Transcripts of several genes predominately or specifically expressed in the ETC (e.g. BETL4) or in the NP (e.g. JEKYLL) have been documented (Thiel *et al.* 2008), but none of the respective proteins were detected in the present experiments. Especially many of the ETC-specific genes encode for low molecular weight cysteine-rich proteins with N-terminal hydrophobic signal peptides (Kovalchuk *et al.* 2009). The technical difficulties in the identification of low molecular weight proteins from a complex mixture are well known and derive from the fact that small proteins contribute only few fragments in complex mixtures and are therefore statistically underrepresented leading to a reduced reproducibility of identification (Klein *et al.* 2007). Further enrichment of complex mixtures with respect to low molecular weight proteins will therefore be necessary to overcome the mentioned bias.

Absolute quantification was performed to gain a clearer picture of the differences and possible specialization of the two target tissues. Most of the proteins differed significantly in amount ($P \leq 0.05$), and tended to be present in greater concentrations in the NP than in the ETC (see Results, section 4.3.2). Interestingly, proteins related to glycolysis were either present to the same amount in the two tissue types or higher in the ETC (fructose bisphosphate aldolase [35_14100]). Thus, a comparable metabolic activity can be expected for both tissue types and the results display that NP and ETC are not only responsible for nutrient transfer but are also involved in metabolic processes. The 5a2 protein was detected in relatively high amounts compared to other proteins in both tissue types with a higher expression in the NP. Although a defined function of this protein is not yet clear, BLAST results revealed a high similarity to the endosperm transfer cell-specific PR60 precursor protein (*T. aestivum*, ACA04813).The expression of the endosperm transfer cell-specific PR60 protein has already been described for wheat and barley. Analyses in wheat demonstrated that the protein interacts with several proteins involved in the regulation of secretion and degradation of signal peptides. Additionally, it is supposed that this protein belongs to the family of lipid-binding proteins and therefore may be involved in the lipid transfer (Kovalchuk *et al.* 2009). Nucellin, a protein supposed to be predominantly or exclusively located in the nucellar cells (Chen and Foolad 1997), was detected in protein extracts of NP and ETC, and absolute quantification clearly depicted the higher protein expression in the NP compared to ETC. The ZmEBE (embryo sac/basal endosperm transfer layer/embryo surrounding region) 1 protein was also identified in both tissue types and absolute quantification showed a slightly higher expression in the NP. Thus, the absolute quantification of proteins detected in both tissue types aided to further access the spatial distribution and expression patterns in the barley grain and therefore the preferentially expression region of underlying proteins can be substantiated.

An overview about main differences with respect to the protein functionality classes is presented in Figure 43.

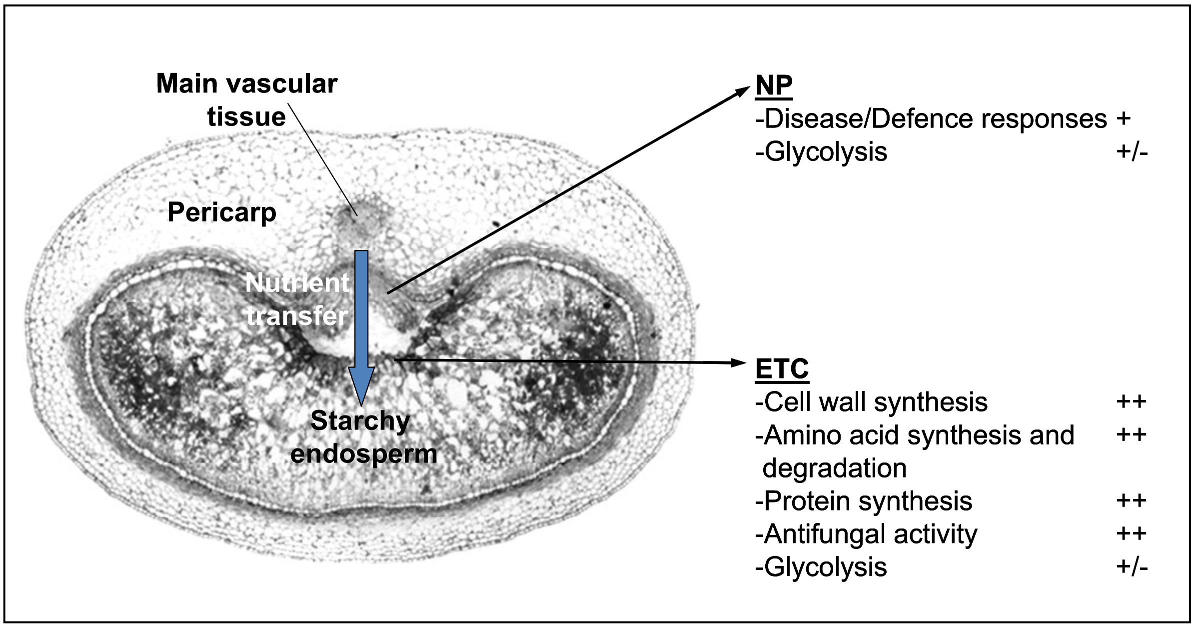


Figure 43: Description next page

Figure 43: Schematical representation of the main findings out of the protein profiling of laser-micro-dissected barley grain material (at 8 DAF). Nucellar projection (NP) and endosperm transfer cells (ETC) were compared and showed main differences with respect to the spectrum of functionality classes. Proteins in distinct functional classes were either detected in only one tissues (denoted by ++), higher expressed in one of the tissues (+), or equally distributed in NP and ETC (+/-).

Proteome profiling of laser-micro-dissected ETC and NP revealed detailed information about spatial distribution patterns

Only 30% and 20% of the proteins identified in the ETC and the NP, respectively, were found previously in the temporal profiling approach (see Results, section 4.3.3). The NP and the ETC represent a relatively small part of the grain and therefore specific proteins are low abundant compared to the proteome of the complete barley grain and may be masked in the analysis of a complete grain extract by high abundant proteins. The findings of the present work clearly underline the necessity of the analyses of dissected material as additional information about low abundant proteins specifically expressed in defined tissue types become accessible.

None of the proteins, detected in the analysis of spatial distribution patterns and the temporal profiling approach, showed highest expression during later developmental stages. Especially NP is known to undergo PCD throughout development to supply assimilates (Thiel *et al.* 2008). Therefore, it is unlikely to find proteins with highest expression patterns in the storage phase within this tissue type. Furthermore, only one time point (8 DAF) was chosen for the analyses of the spatial distribution of proteins and there is a large likelihood that proteins were monitored in the NP and the ETC showing highest expression patterns at the middle phase of development.

Most of the proteins detected in both tissue types and within the temporal profiling approach could be mainly correlated to energy and general metabolism. Proteins detected throughout grain development and in the ETC, but not in the NP, covered a broad spectrum of different biochemical functions, e.g. metabolism, energy metabolism, protein synthesis, protein destination, and cell wall synthesis. This displays a high metabolic activity in the ETC at 8 DAF. All of the proteins found in the NP and during barley grain development were detected in the ETC. Therefore, no tissue specific distribution patterns were observed for the NP.

In summary, analyses of laser-micro-dissected material revealed first insights into the different expression profiles of barley ETC and NP and therefore gave first information about spatial distribution patterns of defined proteins.The analyses clearly illustrated that the two target tissues differ from one another with respect to the spectrum of proteins and protein functionality classes. The number of detected proteins and the complexity of biochemical processes was less in the NP compared to ETC. Differences in the developmental stage, which may occur between both tissue types, were not taken into account. Thus, further studies should include time-course experiments allowing a comparison of the NP and ETC independent of the developmental stage.

MALDI-Imaging MS allows the detection of spatial protein distribution patterns

To gain a more holistic overview about spatial protein distribution patterns it is unavoidable to analyse all tissues and organs within the barley grain. One fairly new method allowing to monitor distribution patterns of proteins/peptides and metabolites in complete intact tissues without prior sample preparation is MALDI-*Imaging* MS. This approach enables the discovery of molecular markers that are either highly localized within specific tissue structures or expressed for only a brief time during development (Cornett *et al.* 2007). Initial experiments to unveil spatial distribution patterns of proteins in developing barley grains using MALDI-*Imaging* MS have been performed and strengthen the applicability of the latter method. Proteins in developing barley grains (8 DAF) were monitored and showed either tissue-specific or co-localized protein expression patterns (Figure 40). One dominant m/z value was detected with a very high intensity in the endosperm (m/z = 4845.2). This m/z value also had the highest intensity in the overall mass spectrum of the complete tissue section displaying a predominance of the underlying molecule in the barley grain.

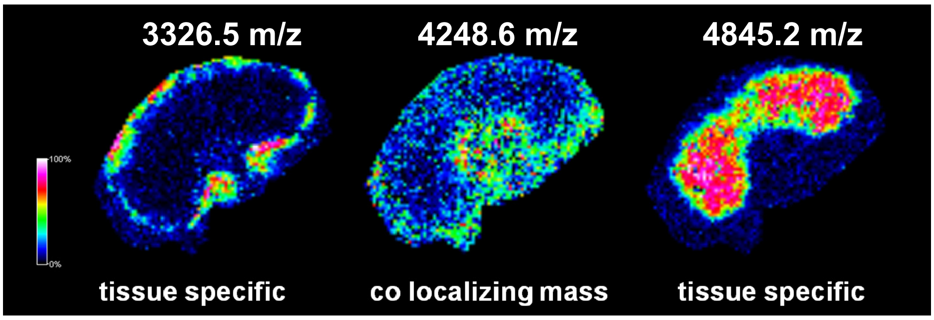


Figure 44: Spatial distribution of selected mass signals gained from MALDI-*Imaging* MS approach is shown for a barley grain cross section. Data evaluation was performed using FlexImaging 2.1 (Bruker). Differences in intensities of mass signals are color-coded.

However, the identity of underlying proteins and / or peptides is still unclear as the method only reveals information about intact molecular ions. The identification process is still challenging and is one drawback of this technology. Strategies to overcome this bias may include direct MS/MS analyses on the tissue, digestion on tissue sections or subsequent targeted analyses of laser-micro-dissected material. At the moment MALDI-*Imaging* MS is a powerful tool to provide a molecular snapshot of abundant molecules, among them proteins, and the mapping of the spatial distribution of those compounds towards special regions in tissue sections (Goodwin *et al.* 2008). Future perspectives to unveil further aspects of barley grain developmental processes should include the MALDI-*Imaging* MS approach to obtain information about the spatial distribution patterns in a time-course experiment throughout different developmental stages as it gives a more comprehensive picture of the spatial distribution pattern of proteins and metabolites in intact tissues.

5.5. Summary: Proteome analyses revealed detailed information about molecular functions and developmental changes of barley tissues

Tissue-specific protein expression profiling is a valuable tool to increase the understanding of developmental processes and biochemical functions. Proteome analyses, including micro-scale proteomic tools, were applied to barley epidermis tissue, as well as to complete grains at different developmental stages and distinct grain tissues.

- The applicability of nanoLC-based separation coupled to label-free MS detection for reproducible and reliable results, especially in micro-scale proteome approaches, could be clearly shown in the present study.
- By the combination of the gel-free LC-MS approach and the 2-DE analysis an overview about the molecular functions of leaf epidermis tissue was obtained and demonstrated a high activity of stress defence-related processes at protein level. Metabolite profiling additionally indicated the activity of stress defence-related processes in barley leaf epidermis. Also, several proteins involved in carbohydrate metabolism and amino acid synthesis were detected displaying the ability of the epidermis to synthesize essential metabolites on its own without dependency on transport related supply from the mesophyll.
- The high complexity of barley grain developmental processes was shown by micro-scale proteomic profiling. Neural Gas clustering was applied to cluster peptides according to their developmental behaviour. Corresponding proteins showed either highest expression in the middle phase of development – in the transition phase – or at later developmental stages – within the storage phase. Whereas proteins highly expressed in the transition phase displayed a high general metabolic activity of the grain with regard to protein synthesis, cell cycle regulation, defence against oxidative stress, and energy production via photosynthesis, proteins up-regulated in the storage phase are related towards storage protein accumulation, and interestingly to the defence of storage reserves against pathogens.
- The regulatory programs underlying barley grain development are conducted in three genetically different organs (maternal tissues, filial endosperm, and filial embryo). However, the barley grain consists of at least 18 different tissue types. Thus, an uneven distribution of protein expression profiles could be expected. Studies of micro-

dissected NP and ETC, both important for nutrient transfer to filial tissues, have been conducted in the present survey. Most of the proteins detected in both tissues were correlated to energy and general metabolism, whereas proteins detected only in the ETC covered a broad spectrum of different biochemical functions. Proteins specific to the NP were not detected. The results showed less complexity of biochemical processes in the NP compared to ETC.

Future prospectives to strengthen the conclusions drawn in the present studies need to address several subjects.

- As proteome and metabolite profiling data are available now for barley leaf epidermis tissue, the connection to transcript profiles would further deepen the information about possible biochemical functions. Accordant analyses have already been initiated and a combined data set consisting of transcript, protein, and metabolite data will give a global overview about processes in barley leaf epidermis tissue. Further studies should include the verification of the stress-defence related function of the epidermis. Thus, reactions towards diverse biotic and abiotic stresses should be compared between epidermis and mesophyll tissues. Enzyme assay measurements could further support findings concerning metabolite synthesis independent of the remaining leaf. Otherwise, detection of membrane proteins using improved methods will help to unveil transport-related processes connected to metabolite supply from the remaining leaf.
- Further studies verifying the detected protein expression profiles in developing barley grains need to be addressed in the future. The detection of ROS enzymes will help to further investigate the reduced necessity of the barley grain to detoxify ROS at later stages of development. Additionally, isoform-specific activities throughout the different developmental stages may play an important role and thus need to be further determined. Therefore, determination of development dependent expression patterns of distinct isoforms using 2-D Western blotting can be performed. Additionally, absolute quantification of isoform-specific peptides by introducing synthetic AQUA peptides into the samples will further help to discriminate differences in protein expression patterns of several isoforms. Further targeted approaches, e.g. analysis of post-translational modifications, have to be included in future studies to depict possible reasons for the detection of proteins with peptides having a mixed pattern in correlation to their developmental behaviour. Additional enzyme activity measurements would also help to support the findings on proteome level.

- As analysis of laser-micro-dissected grain material clearly showed tissue-specific protein distribution patterns and revealed a higher number of proteins not detected in whole grains, spatial protein distributions need to be further monitored. Thus, future analyses have to address the determination of protein expression profiles in additional tissues, e.g. endosperm and pericarp, and should include different developmental stages. The fairly new method MALDI-*Imaging* MS can provide relevant information about spatial protein distribution patterns in intact tissues. Nevertheless, additional studies unveiling the identity of underlying proteins are necessary and need to be developed. Furthermore, methods to enrich low molecular weight proteins could help to detect ETC- and NP-specific proteins. Additionally, extraction of membrane proteins will reveal further information about the nutrient transfer from maternal to filial tissue. Therefore, methods need to be optimized for micro-scale sample amounts.

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7. Abbreviations

2-DE	two-dimensional gel electrophoresis
ACC	aminocyclopropane carboxylic acid
ACS	aminocyclopropane carboxylic acid synthase
ADH	alcohol dehydrogenase
ALA AT	alanine aminotransferase
APX	ascorbate peroxidase
BPI	base peak intensity
BSA	bovine serum albumin
cCBB	colloidal Coomassie Brilliant Blue
CE	collision energy
CHAPS	3-[(3-cholamidopropyl) dimethylamonio]-1-propanesulfonate
CHI	chalcone isomerase
CHS	chalcone synthase
Da	Dalton
DAF	days after flowering
DDA	data-dependent analysis
DTT	dithiothreitol
EMRT	exact mass retention time
ESI	electrospray ionization
EST	expressed sequence tag
ETC	endosperm transfer cells
FBP aldolase	fructose-bisphosphate aldolase
GC	gas chromatography
GPX	glutathione peroxidase
HPLC	high performance liquid chromatography
Hv	Hordeum vulgare
IEF	isoelectric focussing
IPG	immobilized pH gradient
LC	liquid chromatography
LEA	late embryogenesis abundant
LMD	laser micro-dissection
LMPC	laser capture micro-dissection combined with pressure catapulting
MALDI	matrix-assisted laser desorption/ionisation
MS	mass spectrometry
Mw	molecular weight
m/z	mass-to-charge
NP	nucellar projection
PAL	phenylalanine ammonia-lyase
PR-Q	pathogen related protein Q
PCA	principal component analyses
PCD	programmed cell death
pI	isoelectric point
PLGS	Protein Lynx Global Server

PMF	peptide mass fingerprints
Q-TOF	quadrupole time-of-flight
RI	retention time index
ROS	reactive oxygen species
RT	retention time
SAM	S-adenosylmethionine
SDS-Page	sodium dodecyl polyacrylamide gel electrophoresis
SNP	single nucleotide polymorphism
SOD	superoxide dismutase
STINT	stress-inducible protein in *Nicotiana tabacum*
TCA	trichloroacetic acid
TFA	trifluoroacetic acid
TIC	total ion chromatogram
TOF	time-of-flight
x*g*	gravitation force

8. Acknowledgements

At this point I want to thank all colleagues contributing to this dissertation for their support, patience, and guidance.

- First and foremost, I would like to thank my supervisor PD Dr Hans-Peter Mock for giving me the opportunity to carry out my PhD study in his group on such an interesting topic. I am very grateful for his advice and suggestions for the experimental designs and for giving me the opportunity to share the outcome of the analyses with the scientific community at numerousness meetings.

- I am very grateful to Prof Dr Klaus Humbeck at the Martin-Luther-University in Halle and Prof Dr Birte Svensson from the Technical University of Denmark for reviewing my thesis.

- Furthermore, I am thankful to Dr Andrea Matros for her help, support, advice, and suggestions with experimental setups, technical issues, and her contributions of ideas. Especially, I would like to express my thanks for familiarizing me with the nanoLC ESI-Q-TOF MS system and her support during the hard times struggling with diverse facets of “Q-TOF problems”.

- My special thanks go to Prof Dr Birte Svensson and Assoc. Prof Dr Christine Finnie for giving me the opportunity to work in the Enzyme and Protein Chemistry Group at the Technical University of Denmark and for supervising my work during this stay. I am also very grateful to Prof Dr Ole N. Jensen and Dr A. Jimmy Ytterberg for supervising my work during my stay at the Protein Research Group at the Southern University of Denmark.

- I am grateful to all members of the Applied Biochemistry group at the IPK for creating an excellent working environment, and especially for their support with the harvests and preparations of the barley leaf epidermis tissue. I thank Annegret Wolf for her excellent technical assistance. I also want to thank Dr Katja Witzel for fruitful discussions and her help with practical issues whenever they were needed. In regards to the enzyme measurements, I want to thank Kathleen Merx for her help. I am also grateful to Rico Lippmann and Dr Anke Dittbrenner for their support and advice with the GC-MS analyses.

- Part of my work was addressed to the analyses of spatial and temporal protein distribution patterns during barley grain development. Here, I would like to thank Dr. Winfriede Weschke and the Seed Development group at the IPK for providing sample material, and especially Uta Siebert, who helped me with the sample preparation using laser-micro-dissection.

- I would like to express my thanks to Prof Dr Udo Seiffert (IFF Magdeburg) for his help with multivariate statistics and data clustering of the large data sets created by label-free proteomics.

- Additionally, I want to thank Dr AHP America for (Wageningen University) for translation of the HarvEST nucleotide sequence database into protein FASTA format and thus making the database applicable for multiplexed datasets.

- I am thankful to B. Fitig (Université Louis Pasteur, Straßbourg/France), T. Saji (National Institute for Environmental Studies, Tsububa/Jana), and M. Okazaki (Shinshu University, Ueda/Japan) for kindly providing antibodies.

- Financial support from the BMBF (FKZ 0313821A) and the COST organisation (FA0603-05188) is gratefully acknowledged.

- Last but not least, I want to thank my family for their immovable support; my friend, Christof Schönefeld, who has always supported, encouraged and believed in me, especially throughout the busy times at the final phase of this thesis; and my friends for distracting me from work.

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10/2004-03/2005	Trainee	BASF AG Dept. Polymer Research
03/2004	Research Assistant	University of Applied Science Magdeburg-Stendal, Institute of Chemistry/Pharmaceutical Engineering

Education

12/2009	Visit of the laboratory of Prof. Ole N. Jenssen (Protein Research Group, University of Southern Denmark, Odense, Denmark) as recipient of a Short Term Scientific Fellowship by the COST Organisation
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Since 09/2006	PhD thesis “Analysis of Isolated Barley Tissues using Proteomic Approaches” at the Leibniz Institute of Plant Genetics and Crop Plant Research
03/2006-09/2006	Diploma thesis “Chromatographische Untersuchungen zu zellulären Schutzreaktionen gegen UV-Stress bei Gerste“ („Chromatographic analyses of the cellular protective mechanisms against UV-B radiation in barley”) at the Leibniz Institute of Plant Genetics and Crop Plant Research

2002-2006	Study of Analytical Chemistry, University of Applied Science Magdeburg-Stendal, Department of Engineering and Industrial Design
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Publications

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Oral Presentations

Proteome and metabolite analysis of the effect of UV-radiation on barley leaf tissue. IPK Student Conference, Gatersleben/Germany, 29.05. – 01.06.2006

Characterization of the Proteome of Barley Epidermis Tissue and its Responses to UV-B Radiation. PROTEOMLUX, Luxembourg/Luxembourg, 22.10-24.10.2008

Analysis of Temporal and Spatial Protein Patterns during Barley Grain Development. Plant Proteomics in Europe, COST FA0603, Viterbo/Italy, 04.-06.05.2009

Data Mining from Mass Spectrometric and Image Data for Protein Analysis. Triticeace genomics for the advancement of essential European crops, COST FA0604, Viterbo/Italy, 07.-08.05.2009

Targeted protein analyses of barley grains to unveil spatial and temporal distribution patterns. Plant Proteomics in Europe, COST FA0603, Namur/Belgium, 05.-07.05.2010

Poster Presentations

Kaspar, S., S. Peterek, A. Matros & H.-P. Mock: Proteome and metabolite analysis of the effect of UV-radiation on barley leaf tissue. − German Association for Mass Spectrometry (DGMS), 40th Annual Meeting, Bremen/Germany, 11.-14.03.2007.

Kaspar, S., S. Peterek, A. Matros & H.-P. Mock: Proteome analysis of the effect of UV-radiation on barley leaf tissue using a 2-D approach and LC-based separation techniques. − European Summerschool Proteomics, Brixen/Italy, 12.-18.08.2007.

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Kaspar, S., A. Matros, F. Schreiber & H.-P. Mock. Proteome analysis of barley epidermal tissue. – Plant Proteomics in Europe, COST FA0603, Cordoba/Spain, 06.-08.02.2008

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Matros, A., S. Kaspar, U. Seiffert & H.-P. Mock. Adapted workflow for LC-based protein analysis of barley (Hordeum vulgare) grain development. – PROTEOMLUX 2008, Luxembourg/Luxembourg, 22.-25.10.2008.

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Kaspar, S., A. Matros, W. Weschke & H.-P. Mock. LC-MS based Protein Analysis of Microdissected Tissues Revealed Cell-Type Specific Biological Functions in Developing Barley Grains, German Association for Mass Spectrometry (DGMS), 43rd Annual Meeting, Halle (Saale)/Germany, 07.-10.03.2010

Kaspar, S., K. Witzel, B. Schulz, H. Mehlhorn, F. Schreiber & H.-P. Mock. BetaNet: Biochemical Network Analysis for the Identification of Novel Candidates Associated with Increased Sucrose Levels in Sugar Beet, 10th GABI Status Seminar, Potsdam/Germany, 09.-11.03.2010

10. Affirmation

Hereby, I declare that all the work presented in this dissertation is my own, carried out solely with the help of the literature and the aids cited.

Ich erkläre hiermit, dass ich mich mit der vorliegenden wissenschaftlichen Arbeit erstmals um die Erlangung des Doktorgrades bewerbe.
Ich erkläre die Arbeit selbstständig und ohne fremde Hilfe verfasst, nur die von mir angegebenen Quellen und Hilfsmittel benutzt und die den benutzten Werken wörtlich oder inhaltlich entnommenen Stellen als solche kenntlich gemacht habe.

Gatersleben, November 2010

Stephanie Kaspar

Appendix

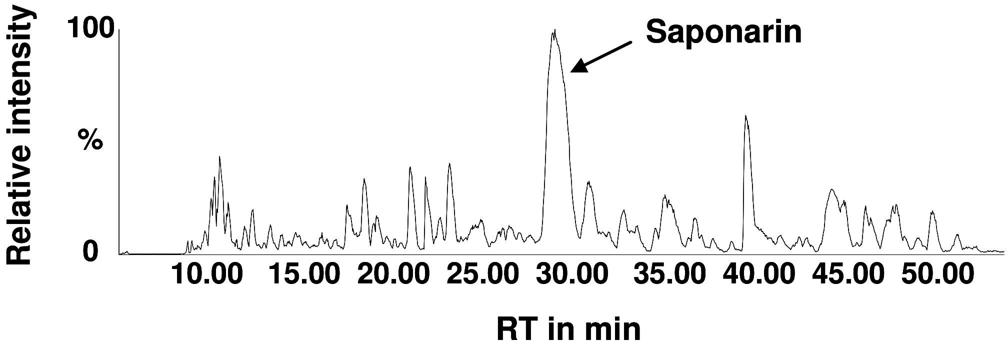

Figure A 1: Base peak intensity chromatogram of LC-based separation of peptides derived from barley leaf epidermis tissue. Proteins were extracted using standard protocol for TCA/Acetone precipitation. Intense peak for saponarin was detectable ([M+H]$^+$ = 595.2*)*.

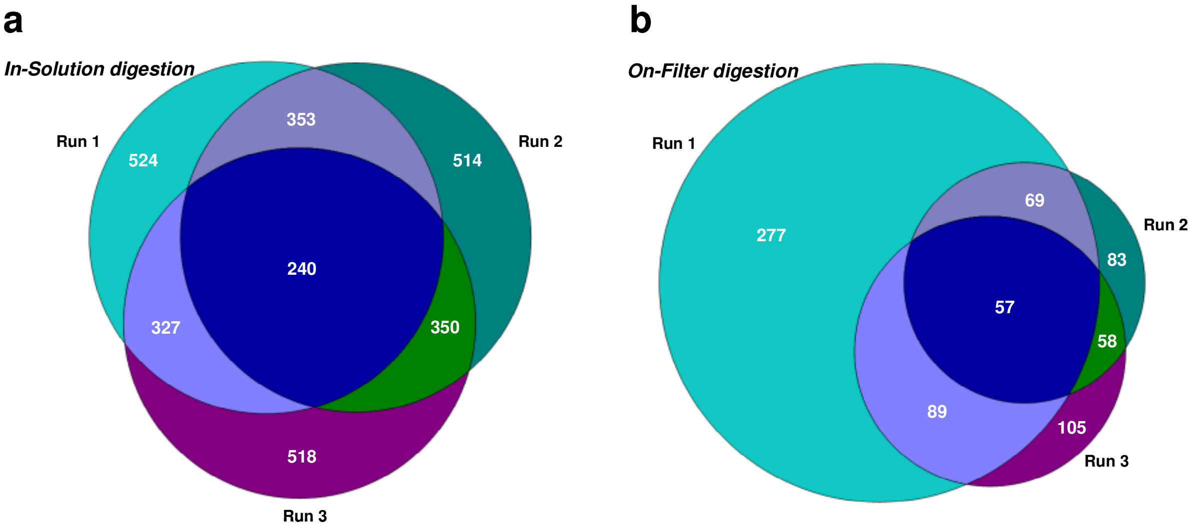

Figure A 2: Venn diagrams displaying the reproducibility of three injections for the analyses of proteins from barley leaf epidermis tissue. Proteins were extracted either using In-Solution digestion (a*)* or On-Filter digestion (b*)*. Number of identified poteins in a single run as well as their overlap between two of the runs and all three runs is displayed.

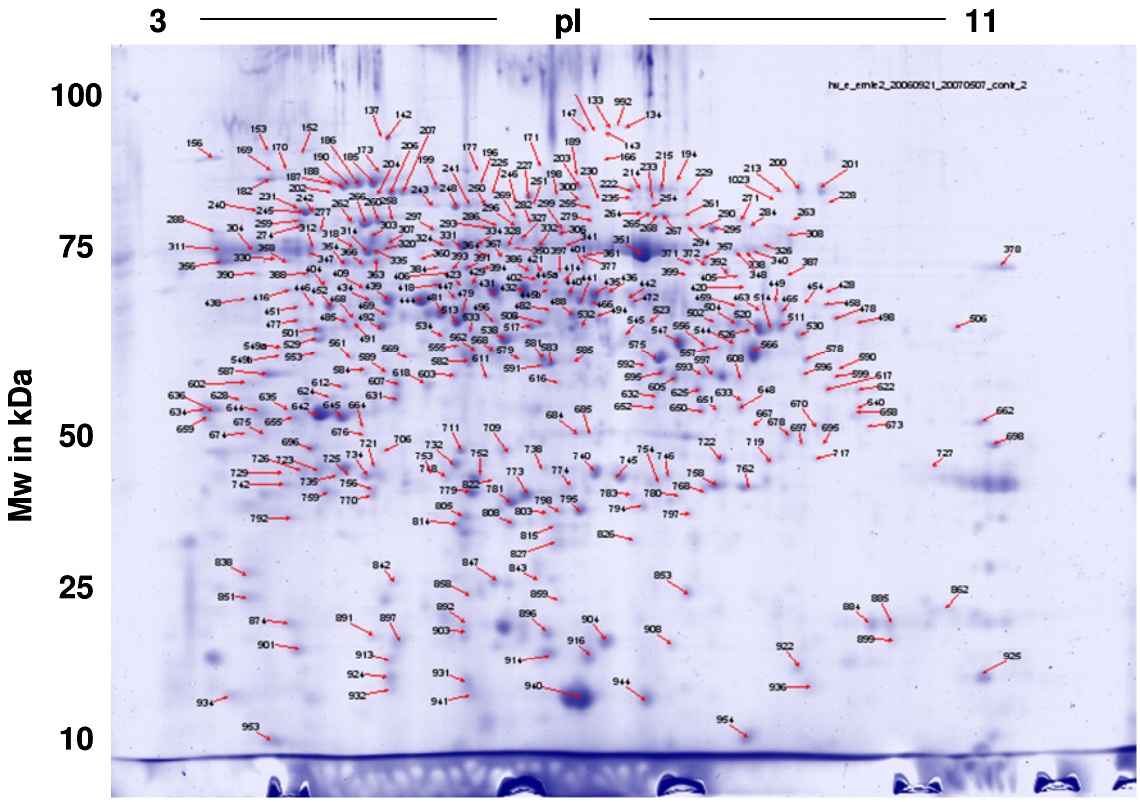

Figure A 3: Representative 2-DE image for the protein profiling of barley leaf epidermis tissue. Water soluble proteins were extracted and subsequently separated using 2-DE (first dimension: non-linear pH gradient from 3-11; second dimension: 11.25% SDS-Page*)*. Proteins were stained with colloidal Coomassie Brilliant Blue. Marked are those spots, which were found in three harvests in at least two technical replicates per harvest and were thus used for the protein reference map.

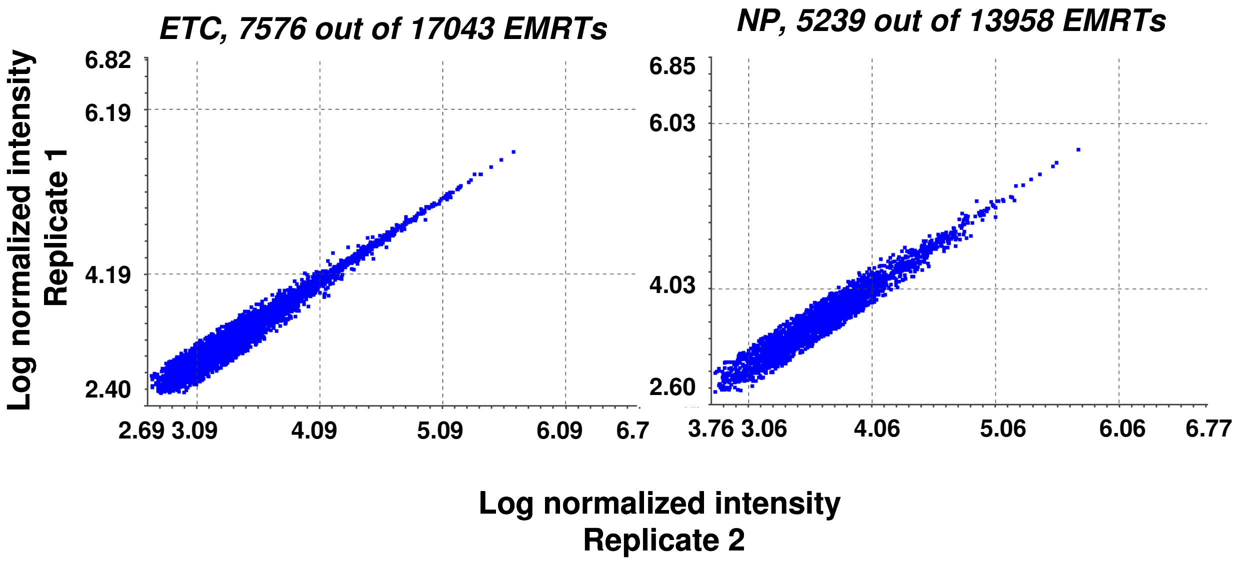

Figure A 4: Representative peptide intensity plots for the LC-MS analysis of ETC and NP proteins. The reproducibility of two LC runs is demonstrated for both tissues by a comparison between the logarithmic signal intensities of exact mass retention time (EMRT*)* pairs.

Table A 1: List of proteins identified in barley leaf epidermis tissue using 2-D gel electrophoresis. Shown are the spot number, protein name, accession number, method used for identification, Mascot score, number of peptides, sequence coverage, theoretical molecular weight, theoretical isoelectric point and presumed protein function.

Spot number	Protein	Accession number	Method	Score*	Number of peptides	Sequence coverage in %	Theor. molecular mass	Theor. isoelectric point	Function
133	Not identified								Not identified
134	Not identified								Not identified
137	Cell division control protein 48 (*A. thaliana*)	35_14849	MALDI-TOF MS	154	17	22	97958	5.64	Cell cycle
142	Cell division control protein 48 (*A. thaliana*)	35_14849	MALDI-TOF MS	248	25	30	97958	5.64	Cell cycle
143	Aconitate hydratase cytoplasmic (*O. sativa*)	35_15479	LC-ESI-Q-TOF	10.84	5	16	106302	6.45	Metabolism
147	Putative aconitate hydratase (*O. sativa*)	35_15073	MALDI-TOF MS	103	11	12	125371	9.00	Metabolism
152	Os12g0514500 protein n 1 (*O. sativa*)	35_1935	LC-ESI-Q-TOF	10.84	8	10	91480	5.21	Protein destination
153	Heat-shock protein precursor (*S. cereale*)	35_15596	MALDI-TOF MS	86	9	12	76334	8.67	Disease/Defence
156	Putative methyl-binding domain protein MBD115 (*Z. mays*)	35_38487	MALDI-TOF MS	90	7	36	23890	7.86	Unclassified
166	Not identified								Not identified
169	Stromal 70 kDa heat shock-related protein (*O. sativa*)	35_15224	MALDI-TOF MS	92	9	18	67590	9.15	Disease/Defence
170	Stromal 70 kDa heat shock-related protein (*O. sativa*)	35_15224	LC-ESI-Q-TOF	10.84	11	6	67590	9.15	Disease/Defence
	OSJNBb0034I13 6 protein (*O. sativa*)	35_5234	LC-ESI-Q-TOF	10.84	5	9	67723	5.18	Unclassified
171	Putative reductase (*O. sativa*)	35_15568	MALDI-TOF MS	63	9	18	95662	8.49	Transport
173	Not identified								Not identified
177	Transketolase (*Z. mays*)	35_14496	MALDI-TOF MS	75	8	14	67111	6.55	Metabolism
182	Stromal 70 kDa heat shock-related protein (*O. sativa*)	35_15224	MALDI-TOF MS	105	11	20	67590	9.15	Disease/Defence
185	Luminal-binding protein 3 precursor (*Z. mays*)	35_14470	MALDI-TOF MS	187	22	31	90239	7.63	Unclassified
186	Luminal-binding protein 3 precursor (*Z. mays*)	35_14470	MALDI-TOF MS	1207	21	29	90239	7.63	Unclassified
187	Heat shock cognate 70 kDa protein 2 (*S. lycopersicum*)	35_453	MALDI-TOF MS	76	8	13	83278	5.61	Disease/Defence
188	Luminal-binding protein 3 precursor (*Z. mays*)	35_14470	MALDI-TOF MS	103	17	26	90239	7.63	Unclassified
189	Phenylalanine ammonia-lyase (*O. sativa*)	35_14243	MALDI-TOF MS	69	8	11	92013	8.66	Secondary metabolism
190	Heat shock cognate 70 kDa protein 2 (*S. lycopersicum*)	35_453	MALDI-TOF MS	100	14	24	83278	5.61	Disease/Defence

194	Putative diphosphonucleotide phosphatase (*O. sativa*)	35_14519	MALDI-TOF MS	79	10	17	80490	8.71	Unclassified
196	Putative subtilisin-like proteinase (*O. sativa*)	35_2125	MALDI-TOF MS	91	9	18	73085	5.87	Protein destination
198	Putative stress induced protein sti1 (*O. sativa*)	35_15495	LC-ESI-Q-TOF	10.84	5	8	64914	6.03	Unclassified
199	Heat shock 70 kDa protein (*O. sativa*)	35_1230	MALDI-TOF MS	136	13	20	85409	8.99	Disease/Defence
200	Beta-D-glucan exohydrolase, isoenzyme ExoII (*H. vulgare*)	35_15245	MALDI-TOF MS	78	8	10	83580	9.19	Metabolism
201	Beta-D-glucan exohydrolase, isoenzyme ExoII (*H. vulgare*)	35_15245	MALDI-TOF MS	62	7	9	83580	9.19	Metabolism
202	Heat shock 70 kDa protein (*P. sativum*)	35_16829	MALDI-TOF MS	96	12	20	83514	7.69	Disease/Defence
203	Putative stress induced protein sti1 (*O. sativa*)	35_15495	MALDI-TOF MS	133	15	26	82173	8.02	Unclassified
204	Vacuolar ATP synthase (*H. vulgare*)	35_15178	MALDI-TOF MS	224	21	29	87728	6.29	Transport
206	Vacuolar ATP synthase (*H. vulgare*)	35_15178	MALDI-TOF MS	332	37	42	87728	6.29	Transport
207	Vacuolar ATP synthase (*H. vulgare*)	35_15178	LC-ESI-Q-TOF	10.84	18	23	87728	6.29	Transport
213	Beta-D-glucan exohydrolase, isoenzyme ExoII (*H. vulgare*)	35_15245	LC-ESI-Q-TOF	10.84	5	9	83580	9.19	Metabolism
214	Putative diphosphonucleotide phosphatase (*O. sativa*)	35_14519	MALDI-TOF MS	130	12	15	80490	8.70	Unclassified
215	Putative diphosphonucleotide phosphatase (*O. sativa*)	35_14519	MALDI-TOF MS	130	12	15	80490	8.70	Unclassified
218	Not identified								Not identified
222	Putative diphosphonucleotide phosphatase (*O. sativa*)	35_14519	MALDI-TOF MS	176	16	24	80490	8.71	Unclassified
225	Alpha-L- arabinofuranosidase/beta-D- xylosidase isoenzyme (*H. vulgare*)	35_1801	LC-ESI-Q-TOF	10.84	4	6	81995	5.59	Metabolism
292	Alpha-L- arabinofuranosidase/beta-D- xylosidase isoenzyme (*H. vulgare*)	35_180	MALDI-TOF MS	129	16	19	105500	8.71	Metabolism
228	Os05g0556100 protein (*O. sativa*)	35_16017	MALDI-TOF MS	83	8	10	88324	9.21	Unclassified
229	Beta-D-glucan-exohydrolase isoenzyme ExoI (*H. vulgare*)	35_1758	LC-ESI-Q-TOF	10.84	7	12	67906	6.24	Metabolism
230	Putative WD40 repeat protein (*O. sativa*)	35_17334	LC-ESI-Q-TOF	10.84	4	7	66283	6.48	Unclassified
231	Protein disulfide-isomerase precursor (*T. aestivum*)	35_14571	MALDI-TOF MS	225	19	30	69183	6.23	Disease/Defence
233	Beta-D-xylosidase (*H. vulgare*)	35_2345	LC-ESI-Q-TOF	10.84	2	2	83529	6.36	Metabolism
235	Putative WD40 repeat protein (*O. sativa*)	35_17334	MALDI-TOF MS	76	9	13	82133	8.34	Unclassified
239	Not identified								Not identified
240	Hypothetical protein (*O. sativa*)	35_17203	MALDI-TOF MS	79	8	12	76012	4.94	Unclassified

241	putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (*O. sativa*)	35_15021	MALDI-TOF MS	80	10	20	73116	8.09	Metabolism
242	Protein disulfide-isomerase precursor (*T. aestivum*)	35_14571	MALDI-TOF MS	238	20	31	69183	6.23	Disease/Defence
243	putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (*O. sativa*)	35_15021	MALDI-TOF MS	151	14	27	73116	8.09	Metabolism
245	Protein disulfide-isomerase precursor (*T. aestivum*)	35_14571	MALDI-TOF MS	230	21	31	69183	6.23	Disease/Defence
246	Not identified								Not identified
248	putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (*O. sativa*)	35_15021	MALDI-TOF MS	117	13	30	73116	8.09	Metabolism
330	H0212B02.14 protein (*O. sativa*)	35_16267	MALDI-TOF MS	154	15	20	74278	9.00	Metabolism
251	NADP malic enzyme (*O. sativa*)	35_960	MALDI-TOF MS	70	7	9	80858	8.25	Metabolism
254	Not identified								Not identified
255	Not identified								Not identified
258	Putative nucleic acid binding protein (*O. sativa*)	35_16721	MALDI-TOF MS	69	10	18	64354	6.01	Unclassified
259	RuBisCO large subunit-binding protein subunit alpha (*T. aestivum*)	35_15221	MALDI-TOF MS	144	11	20	74375	8.60	Energy metabolism
260	Chaperonin CPN60-1 (*Z. mays*)	35_20633	MALDI-TOF MS	73	12	31	42195	8.92	Disease/Defence
261	Not identified								Not identified
262	RuBisCO large subunit-binding protein subunit beta (*A. thaliana*)	35_360	MALDI-TOF MS	137	17	26	81879	7.86	Disease/Defence
263	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	35_15245	LC-ESI-Q-TOF	10.84	2	3	67422	7.96	Metabolism
264	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (*R. communis*)	35_15071	LC-ESI-Q-TOF	10.84	4	6	79430	8.81	Energy metabolism
265	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (*R. communis*)	35_15071	MALDI-TOF MS	88	10	14	79430	8.81	Energy metabolism
266	RuBisCO large subunit-binding protein subunit beta (*A. thaliana*)	35_360	MALDI-TOF MS	178	22	35	81879	7.86	Disease/Defence
267	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (*R. communis*)	35_15071	MALDI-TOF MS	177	16	23	79430	8.81	Energy metabolism
268	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (*R. communis*)	35_15071	MALDI-TOF MS	114	16	22	79430	8.81	Energy metabolism
269	Not identified								Not identified
271	Not identified								Not identified

274	RuBisCO large subunit-binding protein subunit alpha (*T. aestivum*)	35_15221	MALDI-TOF MS	206	20	37	74375	8.60	Protein destination
277	RuBisCO large subunit-binding protein subunit alpha (*T. aestivum*)	35_15221	MALDI-TOF MS	73	9	16	74375	8.60	Protein destination
279	Putative t-complex protein 1 theta chain (*O. sativa*)	35_1953	MALDI-TOF MS	143	15	28	75535	7.64	Protein destination
282	Not identified								Not identified
284	Not identified								Not identified
286	Pore-forming toxin-like protein Hfr-2 (*T. aestivum*)	35_2720	MALDI-TOF MS	141	20	41	67600	6.59	Unclassified
	Os11g0142500 protein (*O. sativa*)	35_2720	MALDI-TOF MS	110	18	35	79512	8.05	Unclassified
288	Nucleosome assembly protein 1 (*O. sativa*)	35_1627	MALDI-TOF MS	98	10	23	58676	4.56	DNA binding
290	ATP synthase subunit alpha (*O. sativa*)	35_47498	LC-ESI-Q-TOF	10.84	6	12			Transport
	Dihydrolipoamide dehydrogenase precursor (*S. tuberosum*)	35_1714	LC-ESI-Q-TOF	10.84	6	12	68360	8.86	Disease/Defence
293	Pore-forming toxin-like protein Hfr-2 (*T. aestivum*)	35_14520	MALDI-TOF MS	128	15	24	67600	6.59	Unclassified
294	Dihydrolipoamide dehydrogenase precursor (*S. tuberosum*)	35_1714	LC-ESI-Q-TOF	10.84	6	11	68360	8.86	Disease/Defence
295	Dihydrolipoamide dehydrogenase precursor (*S. tuberosum*)	35_1714	MALDI-TOF MS	146	14	34	68360	8.86	Disease/Defence
296	Os11g0142500 protein (*O. sativa*)	35_2720	MALDI-TOF MS	95	18	35	79512	8.05	Unclassifed
297	Beta-amylase (*T. aestivum*)	35_14442	MALDI-TOF MS	102	9	17	71272	7.79	Metabolism
299	Mitochondrial processing peptidase beta subunit (*O. sativa*)	35_15129	MALDI-TOF MS				58752	5.49	Protein destination
303	ATP synthase subunit beta, mitochondrial precursor (*Z. mays*)	35_14757	MALDI-TOF MS	107	15	30	79700	9.15	Transport
304	Tubulin beta-2/beta-3 chain (*A. thaliana*)	35_14334	MALDI-TOF MS	82	12	17	66306	5.42	Cell wall
306	Mitochondrial processing peptidase beta subunit (*O. sativa*)	35_15129	MALDI-TOF MS	166	17	23	78075	8.53	Protein destination
307	Putative alanine aminotransferase (*Z. mays*)	35_18222	MALDI-TOF MS	73	11	18	78658	8.41	Metabolism
308	Phospho-2-dehydro-3-deoxyheptonate aldolase 2 (*O. sativa*)	35_15607	MALDI-TOF MS	161	15	23	78603	9.19	Metabolism
311	Nucleosome assembly protein 1-like protein 2 (*O. sativa*)	35_49655	MALDI-TOF MS	69	5	35	16583	5.08	DNA binding
	Hypothetical protein B1121A12.15 (*O. sativa*)	35_20268	MALDI-TOF MS	70	7	33	20216	9.55	Unclassified
312	Tubulin beta-2/beta-3 chain (*A. thaliana*)	35_14333	MALDI-TOF MS	102	14	25	63449	5.25	Cell wall

314	ATP synthase subunit beta, mitochondrial precursor (*Z. mays*)	35_14758	MALDI-TOF MS	232	26	42	77870	8.89	Transport
318	ATP synthase subunit beta, mitochondrial precursor (*Z. mays*)	35_14758	MALDI-TOF MS	186	16	29	77870	8.89	Transport
320	UTP--glucose-1-phosphate uridylyltransferase (*H. vulgare*)	35_751	MALDI-TOF MS	134	17	32	70748	8.29	Metabolism
	ATP synthase subunit beta, mitochondrial precursor (*Z. mays*)	35_14758	MALDI-TOF MS	82	13	24	77870	8.89	Transport
324	Enolase 2 (*Z. mays*)	35_14444	MALDI-TOF MS	133	16	38	66629	8.83	Energy metabolism
326	Phospho-2-dehydro-3-deoxyheptonate aldolase 2 (*O. sativa*)	35_15607	MALDI-TOF MS	75	9	14	78603	9.19	Metabolism
327	Leucine aminopeptidase 2, chloroplast precursor (*O. sativa*)	35_15893	MALDI-TOF MS	117	14	34	66018	6.89	Protein destination
328	Not identified								Not identified
330	26S protease regulatory subunit 6A homolog (*A. thaliana*)	35_15440	MALDI-TOF MS	131	13	25	64906	6.20	Protein destination
331	Enolase 2 (*Z. mays*)	35_14451	MALDI-TOF MS,	207	23	51	63649	8.57	Energy metabolism
332	Not identified								Not identified
334	Enolase 2 (*Z. mays*)	35_14444	MALDI-TOF MS	131	10	23	66629	8.83	Metabolism
335	ATP synthase subunit beta, mitochondrial precursor (*Z. mays*)	35_14758	MALDI-TOF MS	157	21	36	77870	8.89	Transport
	UTP--glucose-1-phosphate uridylyltransferase (*H. vulgare*)	35_751	MALDI-TOF MS	109	16	29	70748	8.29	Metabolism
338	Putative glycine hydroxymethyltransferase (*O. sativa*)	35_14714	MALDI-TOF MS	154	15	27	70161	8.69	Metabolism
	Serine hydroxymethyltransferase (*O. sativa*)	35_14717	MALDI-TOF MS	81	10	25	54408	9.21	Metabolism
340	Catalase isozyme 1 (*H. vulgare*)	35_844	MALDI-TOF MS	71	7	12	72792	9.39	Disease/Defence
341	Not identified								Not identified
347	Tubulin beta-2/beta-3 chain (*A. thaliana*)	35_14334	MALDI-TOF MS	92	8	13	66306	5.42	Cell wall
348	Serine hydroxymethyltransferase (*O. sativa*)	35_605	MALDI-TOF MS	84	10	18	64956	8.72	Metabolism
350	NADP-dependent isocitrate dehydrogenase (*O. sativa*)	35_20462	MALDI-TOF MS	72	10	30	41764	10	Metabolism
351	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	MALDI-TOF MS	172	26	32	65671	8.23	Energy metabolism
354	Tubulin alpha-2 chain (*Z. mays*)	35_14073	MALDI-TOF MS	182	17	33	61460	5.56	Cell wall
356	Calreticulin-like protein (*T. aestivum*)	35_14693	MALDI-TOF MS	126	13	27	60032	4.79	Protein destination

357	Mitochondrial processing peptidase alpha-chain (*D. glomerata*)	35_1200	MALDI-TOF MS	83	9	21	57814	8.48	Protein destination
358	26S protease regulatory subunit 6A homolog (*A. thaliana*)	35_15440	MALDI-TOF MS	197	19	38	64906	6.20	Protein destination
360	Not identified								Not identified
361	Not identified								Not identified
363	UTP--glucose-1-phosphate uridylyltransferase (*H. vulgare*)	35_751	MALDI-TOF MS	223	19	37	70748	8.29	Metabolism
364	Os05g0524300 protein (*O. sativa*)	35_16793	MALDI-TOF MS	90	10	18	69109	9.00	Protein destination
366	Tubulin alpha-2 chain (*Z. mays*)	35_14073	MALDI-TOF MS	156	20	40	61460	5.56	Cell wall
	Not identified								Not identified
371	Alanine aminotransferase (*O. sativa*)	35_14602	MALDI-TOF MS	245	25	47	66960	8.60	Metabolism
372	Mitochondrial processing peptidase alpha-chain (*D. glomerata*)	35_1200	MALDI-TOF MS	83	8	16	57814	8.48	Protein destination
377	Not identified								Not identified
378	Not identified								Not identified
384	Putative fumarylacetoacetate hydrolase (*O. sativa*)	35_16553	MALDI-TOF MS	66	7	17	57828	5.74	Metabolism
386	Cytosolic 6-phosphogluconate dehydrogenase (*O. sativa*)	35_802	MALDI-TOF MS	207	18	34	70177	8.77	Disease/Defence
387	AAA ATPase (*M. truncatula*)	35_15941	MALDI-TOF MS	88	8	16	67288	8.92	Unclassified
388	SGT1 (*H. vulgare*)	35_1570	LC-ESI-Q-TOF	10.84	4	9	40997	4.96	Unclassified
390	Putative RAD23 protein (*O. sativa*)	35_15614	MALDI-TOF MS	102	10	24	54087	5.58	Unclassified
391	Os06g0288300 protein (*O. sativa*)	35_21909	MALDI-TOF MS	74	7	28	36167	6.23	Metabolism
392	Fumarate hydratase 1 (*O. sativa*)	35_16117	MALDI-TOF MS	89	9	10	71332	9.58	Metabolism
393	Hypothetical protein At2g31400 (*A. thaliana*)	35_18266	MALDI-TOF MS	71	7	17	101624	8.72	Unclassified
394	Putative aminoacylase (*O. sativa*)	35_1864	MALDI-TOF MS	174	14	29	63992	8.74	Metabolism
397	Not identified								Not identified
399	Beta-D-glucan exohydrolase-like protein (*A. thaliana*)	35_7528	MALDI-TOF MS	65	6	39	25156	10.64	Metabolism
401	26S protease regulatory subunit 7 (*A. thaliana*)	35_14987	MALDI-TOF MS	114	13	26	59333	8.58	Protein destination
402	Not identified								Not identified
404	Not identified								Not identified
405	Thiol protease (*T. aestivum*)	35_15079	MALDI-TOF MS	101	8	18	50528	8.51	Protein destination
406	H0718E12.4 protein (*O. sativa*)	35_1969	MALDI-TOF MS	91	10	21	61914	9.45	Energy metabolism
409	Ribulose bisphosphate carboxylase/oxygenase activase A (*H. vulgare*)	35_13897	MALDI-TOF MS	90	9	24	42994	8.87	Energy metabolism

414	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	MALDI-TOF MS	75	8	19	56813	9.21	Unclassified
416a	Not identified								Not identified
416b	Not identified								Not identified
416c	Not identified								Not identified
418	Translational elongation factor Tu (*O. sativa*)	35_976	MALDI-TOF MS	146	16	33	61303	8.86	Protein biosynthesis
420	Hypothetical protein OSJNBa0053E05.13 (*O. sativa*)	35_15299	MALDI-TOF MS	86	9	18	57144	9.44	Unclassified
421	S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_368	MALDI-TOF MS	98	10	24	60567	7.29	Metabolism
423	S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_366	MALDI-TOF MS	79	8	19	62324	8.08	Metabolism
428	Putative thiolase (*O. sativa*)	35_2313	MALDI-TOF MS	115	10	24	61467	9.41	Metabolism
429	S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_366	MALDI-TOF MS	102	8	19	62324	8.08	Metabolism
431	S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_366	MALDI-TOF MS	94	10	25	62324	8.08	Metabolism
432	S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_368	MALDI-TOF MS	160	17	37	60567	7.29	Metabolism
434	Actin-75 (*S. tuberosum*)	35_14167	MALDI-TOF MS	77	8	50	20339	4.85	Cell wall
435	Not identifiefied								Not identified
436	Putative heterogeneous nuclearribonucleo-protein A2 (*O. sativa*)	35_12281	MALDI-TOF MS	74	7	39	28641	5.60	Unclassified
438	30S ribosomal protein S1 (*O. sativa*)	35_477	MALDI-TOF MS	107	10	16	61881	6.35	Protein biosynthesis
439	Actin-5C (*D. melanogaster*)	35_14174	MALDI-TOF MS	116	11	27	58328	6.96	Cell wall
440	Not identifiefied								Not identifiefied
441	Putative pectinacetylesterase (*O. sativa*)	35_3926	MALDI-TOF MS	104	11	33	36755	6.59	Unclassified
442	Delta-COP (*Z. mays*)	35_1297	MALDI-TOF MS	73	8	14	72877	8.71	Transport
444	Actin-5C (*D. melanogaster*)	35_14174	MALDI-TOF MS	156	16	40	58328	6.96	Cell wall
445a	S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_366	MALDI-TOF MS	62	10	23	62324	8.08	Metabolism
445b	GDP-mannose 3,5-epimerase (*A. thaliana*)	35_192	MALDI-TOF MS	93	12	26	53928	6.97	Metabolism
446	Not identified								Not identified
447	Actin-75 (*S. tuberosum*)	35_14167	MALDI-TOF MS	69	6	36	20339	4.85	Cell wall
449	F27F5.8 (*A. thaliana*)	35_1345	MALDI-TOF MS	106	12	18	58868	6.41	Protein destination
451	Not identified								Not identified
452	Glutamine synthetase leaf isozyme, chloroplast precursor (*H. vulgare*)	35_834	MALDI-TOF MS	117	12	23	74251	9.21	Metabolism
454	3-ketoacyl CoA thiolase 2, peroxisomal precursor (*A. thaliana*)	35_15093	LC-ESI-Q-TOF	10.84	4	8	48579	8.62	Metabolism

458	3-ketoacyl CoA thiolase 2, peroxisomal precursor (*A. thaliana*)	35_15093	MALDI-TOF MS	123	11	22	63726	9.62	Metabolism
459	Alcohol dehydrogenase class 3 (*Z. mays*)	35_14629	LC-ESI-Q-TOF	10.84	4	8	63726	9.62	Metabolism
463	Putative 12-oxophytodienoate reductase (*O. sativa*)	35_3732	MALDI-TOF MS	162	12	31	56549	9.20	Metabolism
465	UDP-D-glucuronate decarboxylase (*H. vulgare*)	35_14654	MALDI-TOF MS	167	19	37	56349	9.48	Metabolism
466	12-oxo-phytodienoic acid reductase (*Z. mays*)	35_14747	MALDI-TOF MS	104	15	31	52558	8.09	Metabolism
468	Pyruvate dehydrogenase E1 beta subunit (*Z. mays*)	35_1108	LC-ESI-Q-TOF	10.84	4	9	39963	5.46	Disease/Defence
	Putative 3 isopropylmalate dehydrogenase (*O. sativa*)	35_16060	LC-ESI-Q-TOF	10.84	5	10	43371	5.86	Metabolism
469	Ribulose bisphosphate carboxylase/oxygenase activase A (*H. vulgare*)	35_13900	MALDI-TOF MS	83	8	15	66003	9.17	Energy metabolism
472	Os09g0252100 protein (*O. sativa*)	35_15494	MALDI-TOF MS	125	12	32	55355	8.25	Metabolism
477	Magnesium chelatase 40-kDa subunit (*H. vulgare*)	35_1697	MALDI-TOF MS	97	8	23	54066	6.80	Metabolism
478	H0215F08.10 protein (*O. sativa*)	35_429	MALDI-TOF MS	84	8	16	59363	9.07	Metabolism
479	Succinyl-CoA ligase [GDP-forming] beta-chain (*O. sativa*)	35_15472	MALDI-TOF MS	79	9	20	58533	8.51	Energy metabolism
481	Ribulose bisphosphate carboxylase/oxygenase activase A (*H. vulgare*)	35_13900	MALDI-TOF MS	79	11	27	66003	9.17	Energy metabolism
482	Translational elongation factor Tu (*O. sativa*)	35_975	MALDI-TOF MS	70	9	21	56436	6.63	Protein biosynthesis
485	Phosphoribulokinase (*T. aestivum*)	35_14461	MALDI-TOF MS	96	8	14	60828	8.89	Energy metabolism
488	O-methyltransferase (*S. cereale*)	35_15363	LC-ESI-Q-TOF	10.84	5	11	38845	6.70	Metabolism
491	Os01g0321700 protein (*O. sativa*)	35_7205	MALDI-TOF MS	69	8	13	63719	9.64	Transport
492	Glutamine synthetase cytosolic isozyme 1-1 (*O. sativa*)	35_531	MALDI-TOF MS	93	9	15	62203	9.46	Metabolism
494	Putative family II lipase EXL4 (*O. sativa*)	35_15387	MALDI-TOF MS	106	9	17	56775	8.86	Metabolism
496	Alpha-1,4-glucan-protein synthase [UDP-forming] (*Z. mays*)	35_272	MALDI-TOF MS	126	13	30	56825	8.35	Cell wall
498	Putative chloroplast nucleoid DNA-binding protein cnd41 (*O. sativa*)	35_16984	MALDI-TOF MS	82	8	20	69663	5.46	Protein destination
501	Adenosine kinase (*Z. mays*)	35_14937	MALDI-TOF MS	144	15	39	56357	9.12	Metabolism
502	Glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_286	MALDI-TOF MS	79	9	23	51874	9.09	Energy metabolism
504	UDP-D-glucuronate decarboxylase (*H. vulgare*)	35_14654	MALDI-TOF MS	89	10	17	56349	9.48	Metabolism

506	Putative glycolate oxidase (*O. sativa*)	35_14657	MALDI-TOF MS	87	9	17	56233	9.77	Metabolism
508	Phosphoglycerate kinase (*T. aestivum*)	35_38455	MALDI-TOF MS	98	12	27	25215	8.61	Energy metabolism
511	UDP-D-glucuronate decarboxylase (*H. vulgare*)	35_14654	MALDI-TOF MS	113	14	26	56349	9.48	Metabolism
513	Ribulose bisphosphate carboxylase/oxygenase activase B, chloroplast precursor (*H. vulgare*)	35_13901	MALDI-TOF MS	148	19	28	76492	9.04	Energy metabolism
514	Putative phosphoserine aminotransferase (*O. sativa*)	35_16572	MALDI-TOF MS	126	20	44	55899	9.16	Metabolism
517	Phosphoglycerate kinase, cytosolic (*T. aestivum*)	35_384	MALDI-TOF MS	128	12	27	57505	9.29	Energy metabolism
520	Glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_286	MALDI-TOF MS	60	8	20	51874	9.09	Energy metabolism
523	Fructose-bisphosphate aldolase (*O. sativa*)	35_14099	MALDI-TOF MS	78	8	21	53061	8.67	Energy metabolism
526	Aspartate aminotransferase (*O. sativa*)	35_14619	MALDI-TOF MS	108	17	27	68727	9.51	Metabolism
	Fructose-bisphosphate aldolase cytoplasmic isozyme (*O. sativa*)	35_14100	MALDI-TOF MS	74	12	29	56646	8.96	Energy metabolism
529	Adenosine kinase (*Z. mays*)	35_14937	MALDI-TOF MS	82	9	27	56357	9.12	Metabolism
530	Fructose-bisphosphate aldolase cytoplasmic isozyme (*O. sativa*)	35_14100	MALDI-TOF MS	127	12	28	56646	8.96	Energy metabolism
532	Putative disulfide-isomerase (*O. sativa*)	35_15052	MALDI-TOF MS	81	7	18	56416	9.37	Disease/Defence
533	H0716A07.7 protein (*O. sativa*)	35_15753	MALDI-TOF MS	162	15	25	63950	9.02	Energy metabolism
534	PM2 protein (*H. vulgare*)	35_275	MALDI-TOF MS	54	8	20	48696	8.21	Metabolism
538	Malate dehydrogenase (*O. sativa*)	35_14420	MALDI-TOF MS	151	15	40	51476	9.21	Energy metabolism
544	Succinyl-CoA ligase alpha 2 subunit (*S. lycopersicum*)	35_1287	MALDI-TOF MS	74	10	28	51897	9.32	Energy metabolism
545	Putative isocitrate dehydrogenase (*O. sativa*)	35_1485	MALDI-TOF MS	77	10	19	66910	9.30	Energy metabolism
547	Fructose-bisphosphate aldolase (*O. sativa*)	35_14099	MALDI-TOF MS	209	18	53	53061	8.67	Energy metabolism
549a	Putative ribosomal protein S5 (*O. sativa*)	35_15537	MALDI-TOF MS	65	7	14	52630	8.76	Protein synthesis
549b	Putative ribosomal protein S5 (*O. sativa*)	35_15537	MALDI-TOF MS	74	7	15	52630	8.76	Protein synthesis
553	Not identified								Not identified
555	Not identified								Not identified
556	Glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_49	MALDI-TOF MS	98	11	27	50986	8.89	Energy metabolism
557	Putative auxin-induced protein (*O. sativa*)	35_15773	MALDI-TOF MS	102	11	26	51123	9.50	Disease/Defence
561	Fructokinase-2 (*O. sativa*)	35_15398	MALDI-TOF MS	82	8	30	22670	5.31	Metabolism
562	Fructose-bisphosphate aldolase (*O. sativa*)	35_13817	MALDI-TOF MS	75	9	20	58730	9.24	Energy metabolism
566	Glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_49	MALDI-TOF MS	174	17	43	50986	8.89	Energy metabolism
568	Fructokinase-1 (*Z. mays*)	35_472	MALDI-TOF MS	107	13	34	54038	9.01	Metabolism

569	C2 domain-containing protein *(H. vulgare*)	35_16633	MALDI-TOF MS	104	8	23	45180	8.72	Unclassified
575	Peroxidase 10 (*T. monococcum*)	35_13856	MALDI-TOF MS	115	14	37	48032	8.52	Disease/Defence
	Malate dehydrogenase (*O. sativa*)	35_165	MALDI-TOF MS	76	11	34	57137	9.21	Energy metabolism
578	RNA binding protein (*O. sativa*)	35_14947	MALDI-TOF MS	146	11	23	58192	9.71	Metabolism
579	Hypothetical protein P0436E04.19 (*O. sativa*)	35_1354	MALDI-TOF MS	123	10	28	51182	6.40	Unclassified
581	Malate dehydrogenase (*O. sativa*)	35_169	MALDI-TOF MS	97	11	33	48055	9.57	Energy metabolism
582	Not identified								Not identified
583	Hypothetical protein P0436E04.19 (*O. sativa*)	35_1354	MALDI-TOF MS	127	13	35	51182	6.40	Unclassified
584	Not identified								Not identified
585	Hypothetical protein P0436E04.19 (*O. sativa*)	35_1354	MALDI-TOF MS	109	9	25	51182	6.40	Unclassified
587	Putative C2 domain-containing protein (*O. sativa*)	35_3249	MALDI-TOF MS	95	8	30	36871	10.07	Unclassified
589	Putative plastidic cysteine synthase 1 (*O. sativa*)	35_2213	MALDI-TOF MS	105	9	23	57206	9.38	Metabolism
590	Not identified								Not identified
591	Hypothetical protein P0436E04.19 (*O. sativa*)	35_1354	MALDI-TOF MS	102	10	28	51182	6.40	Unclassified
	Malate dehydrogenase (*O. sativa*)	35_169	MALDI-TOF MS	76	7	23	48055	9.57	Energy metabolism
592	Not identified								Not identified
	Putative chloroplast ribosomal protein L1 (*O. sativa*)	35_725	MALDI-TOF MS	72	10	23	55884	8.99	Translation
771	Osr40g2 protein *(O. sativa*)	35_403	MALDI-TOF MS	125	15	44	44276	6.56	Unclassified
	Putative annexin P35 (*O. sativa*)	35_15136	MALDI-TOF MS	82	12	26	48134	9.00	Unclassified
595	Peroxidase 10 (*T. monococcum*)	35_13856	MALDI-TOF MS	141	12	27	48032	8.52	Disease/Defence
596	Peroxidase precursor (*T. aestivum*)	35_13826	MALDI-TOF MS	85	8	25	48991	9.21	Disease/Defence
597	Putative annexin P35 (*O. sativa*)	35_15136	MALDI-TOF MS	117	15	33	48134	9.00	Unclassified
599	Not identified								Not identified
602	Class III peroxidase 137 precursor (*O. sativa*)	35_22397	MALDI-TOF MS	77	7	47	20160	4.43	Disease/Defence
603	Putative PrMC3 (*O. sativa*)	35_16547	MALDI-TOF MS	125	12	46	43401	6.97	Metabolism
605	Osr40c1 protein (*O. sativa*)	35_277	MALDI-TOF MS	170	17	40	52524	9.07	Unclassified
607	Lactoylglutathione lyase (*O. sativa*)	35_131	MALDI-TOF MS	126	17	30	55893	8.73	Secondary Metabolism
608	UCW116 (*H. vulgare*)	35_717	MALDI-TOF MS	74	8	19	59575	9.32	Metabolism
611	50S ribosomal protein L4 (*O. sativa*)	35_2677	MALDI-TOF MS	83	8	14	43485	8.74	Translation
612	OSIGBa0076I14.3 protein (*O. sativa*)	35_16347	MALDI-TOF MS	116	14	28	45737	8.28	Disease/Defence
616	Not identified								Not identified
617	Glucan endo-1,3-beta-glucosidase GI (*H. vulgare*)	35_406	MALDI-TOF MS	86	8	25	51850	9.84	Disease/Defence
618	Not identified								Not identified

622	Radc1 (*O. sativa*)	35_1089	MALDI-TOF MS	84	7	16	59411	9.28	Protein destination
624	Carbonic anhydrase (*H. vulgare*)	35_194	MALDI-TOF MS	69	8	15	78516	9.20	Metabolism
625	Putative annexin (*O. sativa*)	35_15137	MALDI-TOF MS	214	18	39	54823	9.45	Unclassified
628	Not identified								Not identified
631	Os11g0210100 protein (*O. sativa*)	35_13832	MALDI-TOF MS	80	10	24	56384	9.38	Disease/Defence
632	Not identified								Not identified
633	Vacuolar ATP synthase subunit E (*T.aestivum*)	35_14632	MALDI-TOF MS	143	15	43	42657	9.23	Transport
634	Not identified								Not identified
635	Hypothetical protein OSJNBa0003O19.2 (*O. sativa*)	35_4843	MALDI-TOF MS	78	9	26	40211	6.29	Unclassified
636	Putative cytochrome c oxidase subunit (*T.aestivum*)	35_15404	MALDI-TOF MS	69	7	22	38914	6.32	Energy metabolism
640	Radc1 (*O. sativa*)	35_1089	MALDI-TOF MS	71	7	16	59411	9.28	Protein destination
642	Salt-stress root protein RS1 (*O. sativa*)	35_14981	MALDI-TOF MS	83	9	25	44423	9.16	Disease/Defence
644	Not identified								Not identified
645	Oxygen-evolving enhancer protein 1 (*T.aestivum*)	35_404	MALDI-TOF MS	128	12	36	46666	8.62	Energy metabolism
648	Vacuolar ATP synthase subunit E (*T.aestivum*)	35_14632	MALDI-TOF MS	101	13	32	42657	9.23	Transport
650	Glucose and ribitol dehydrogenase homolog (*O. sativa*)	35_794	MALDI-TOF MS	117	11	25	48698	9.55	Disease/Defence
651	Not identified								Not identified
652	Glucose and ribitol dehydrogenase homolog (*O. sativa*)	35_794	MALDI-TOF MS	73	7	17	48698	9.55	Disease/Defence
655	Os02g0768600 protein (*O. sativa*)	35_15866	MALDI-TOF MS	97	8	18	44313	9.25	Metabolism
658	Peroxidase 6 (*T. monococcum*)	35_1037	MALDI-TOF MS	66	9	29	53690	9.54	Disease/Defence
659	Not identified								Not identified
662	Voltage dependent anion channel (*T. aestivum*)	35_1085	LC-ESI-Q-TOF	10.84	4	10	29316	9.33	Transport
664	Not identified								Not identified
667	Glyceraldehyde 3 phosphate dehydrogenase (*Z. mays*)	35_155	MALDI-TOF MS, LC-ESI-Q-TOF	10.84	3	10	36523	6.46	Energy metabolism
670	Glucan endo-1,3-beta-glucosidase GI (*H. vulgare*)	35_406	MALDI-TOF MS	67	8	27	51850	9.84	Disease/Defence
673	Proteasome subunit alpha type 7 (*O. sativa*)	35_15114	MALDI-TOF MS	83	8	27	37875	9.37	Protein destination
674	Putative elongation factor 1 beta (*H. vulgare*)	35_47232	MALDI-TOF MS	59	5	27	20068	9.79	Protein
675	Not identified								Not identified
676	Not identified								Not identified
678	Adenylate kinase B (*O. sativa*)	35_15202	MALDI-TOF MS				26675	7.65	Metabolism

684	Not identified								Not identified
685	Not identified								Not identified
695	Peroxisome type ascorbate peroxidase (*H. vulgare*)	35_903	MALDI-TOF MS	66	7	15	47640	9.56	Disease/Defence
696	Putative caffeoyl-CoA O-methyltransferase 1 (*O. sativa*)	35_14101	MALDI-TOF MS	86	8	24	42362	7.66	Secondary metabolism
697	Putative cytochrome b5 reductase (*O. sativa*)	35_16725	MALDI-TOF MS	93	8	20	52886	9.58	Disease/Defence
698	Porin-like protein (*O. sativa*)	35_13822	MALDI-TOF MS	153	12	33	48986	9.29	Transport
706	IN2-1 protein (*O. sativa*)	35_1086	MALDI-TOF MS	92	9	36	37982	8.78	Disease/Defence
709	Not identified		MALDI-TOF MS,						Not identified
711	IN2-1 protein (*O. sativa*)	35_1087	MALDI-TOF MS	87	9	27	51843	9.35	Disease/Defence
717	Not identified								Not identified
719	Chitinase (*O. sativa*)	35_2523	MALDI-TOF MS				32203	8.43	Disease/Defence
721	Ascorbate peroxidase (*H. vulgare*)	35_14510	MALDI-TOF MS	51	6	20	44252	8.97	Disease/Defence
722	Not identified								Not identified
723	Ascorbate peroxidase (*H. vulgare*)	35_14510	MALDI-TOF MS	56	22		44252	8.97	Disease/Defence
725	Ascorbate peroxidase (*H. vulgare*)	35_14510	MALDI-TOF MS	108	13	38	44252	8.97	Disease/Defence
726	Ascorbate peroxidase (*H. vulgare*)	35_14510	MALDI-TOF MS	64	7	23	44252	8.97	Disease/Defence
727	Not identified								Not identified
729	Not identified								Not identified
732	Mitochondrial ATP synthase (*T. aestivum*)	35_15350	MALDI-TOF MS	138	13	33	45549	9.52	Unclassified
734	Chalcone isomerase (*O. sativa*)	35_2839	MALDI-TOF MS	114	10	38	33347	8.65	Secondary metabolism
735	Chalcone isomerase (*O. sativa*)	35_2839	MALDI-TOF MS	82	7	35	33347	8.65	Secondary metabolism
738	L-ascorbate peroxidase 1 (*O. sativa*)	35_14509	MALDI-TOF MS	58	6	25	39071	9.09	Disease/Defence
740	L-ascorbate peroxidase 1 (*O. sativa*)	35_14509	MALDI-TOF MS	130	10	38	39071	9.09	Disease/Defence
742	Putative chaperonin 21 (*O. sativa*)	35_1799	MALDI-TOF MS	106	8	30	37386	8.96	Protein destination
745	Glutathione-S-transferase 19E50 (*T. aestivum*)	35_14472	MALDI-TOF MS	62	8	19	42142	8.89	Metabolism
746	Proteasome subunit alpha type 6 (*O. sativa*)	35_15462	MALDI-TOF MS	95	9	26	44612	9.55	Protein destination
748	Hypothetical protein NCU09469.1 (*N. crassa*)	35_46174	MALDI-TOF MS	80	6	35	20340	9.20	Unclassified
752	Triosephosphate isomerise (*T. aestivum*)	35_14505	LC-ESI-Q-TOF	10.84	6	18	26737	5.39	Energy metabolism
753	Putative triosephosphate isomerase (*O. sativa*)	35_15548	MALDI-TOF MS	112	10	25	53908	9.36	Energy metabolism
754	Not identified								Not identified
756	Not identified								Not identified
759	B0616E02-H0507E05 5 protein (*O. sativa*)	35_16860	LC-ESI-Q-TOF	10.83	4	20	28769	5.73	Unclassified
768	1-Cys-peroxiredoxine (*T. aestivum*)	35_15249	MALDI-TOF MS	64	7	27	34196	9.50	Disease/Defence

770	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	MALDI-TOF MS	81	6	25	39367	9.00	Protein destination
773	Oxygen-evolving enhancer protein 2 (*T. aestivum*)	35_14635	MALDI-TOF MS	133	11	31	40660	9.55	Energy metabolism
774	Proteasome subunit beta type 1 (*O. sativa*)	35_1748	MALDI-TOF MS	82	6	17	37897	9.35	Protein destination
779	Triosephosphate isomerase (*H. vulgare*)	35_14505	MALDI-TOF MS	88	10	27	44724	9.46	Energy metabolism
780	Not identified								Not identified
781	Dehydroascorbate reductase (*T. aestivum*)	35_860	MALDI-TOF MS	150	13	48	39941	9.46	Disease/Defence
783	Glutathione transferase (*T. aestivum*)	35_14832	MALDI-TOF MS	76	7	17	45246	9.59	Metabolism
792	Putative thioredoxin peroxidase (*O. sativa*)	35_837	LC-ESI-Q-TOF	10.84	3	8	28097	5.67	Disease/Defence
794	Superoxide dismutase [Mn] (*O. sativa*)	35_1190	MALDI-TOF MS	100	8	22	43541	9.42	Disease/Defence
795	Glutathione transferase F5 (*T. aestivum*)	35_14091	MALDI-TOF MS	79	8	38	32734	9.11	Metabolism
797	Hypothetical protein p23k-1 (*H. vulgare*)	35_14316	MALDI-TOF MS	90	7	29	34966	9.02	Unclassified
798	Hypothetical protein p23k-1 (*H. vulgare*)	35_14315	MALDI-TOF MS	106	9	34	34191	8.70	Unclassified
803	Not identified								Not identified
805	Not identified								Not identified
808	Cold shock domain protein 3 (*T. aestivum*)	35_14737	MALDI-TOF MS	92	8	52	35532	9.40	DNA binding
814	Putative ATP synthase delta chain (*O. sativa*)	35_1022	LC-ESI-Q-TOF	10.69	2	9	21213	5.72	Transport
815	Cold shock domain protein 3 (*T. aestivum*)	35_14737	MALDI-TOF MS	123	9	54	35532	9.40	DNA binding
822	Not identified								Not identified
826	Not identified								Not identified
827	Not identified								Not identified
838	Cold acclimation protein WCOR615 (*T. aestivum*)	35_1538	MALDI-TOF MS				17785	4.92	Unclassified
842	Not identified								Not identified
843	Cold shock domain protein 2 (*T. aestivum*)	35_14738	MALDI-TOF MS	90	8	49	34773	9.29	DNA binding
847	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	MALDI-TOF MS	95	8	27	34405	8.84	Protein biosynthesis
851	Salt tolerant protein (*T. aestivum*)	35_786	MALDI-TOF MS	74	6	24	30064	8.74	Disease/Defence
853	Glutathione peroxidase-like protein (*T. aestivum*)	35_726	MALDI-TOF MS	66	5	15	31785	9.55	Disease/Defence
858	Not identified								Not identified
859	Expressed protein (*O. sativa*)	35_17236	MALDI-TOF MS	95	7	29	34523	9.48	Unclassified
862	Not identified								Not identified
874	50S ribosomal protein (*S. cereale*)	35_3451	MALDI-TOF MS	71	6	33	29566	9.06	Translation
884	Not identified								Not identified
885	Cyclophilin A-3 (*T. aestivum*)	35_14255	MALDI-TOF MS	71	8	25	35832	9.98	Protein destination
891	Not identified								Not identified

892	S-adenosylmethionine:2-demethylmenaquinone methyltransferase- like (*O. sativa*)	35_16832	MALDI-TOF MS	67	7	27	32866	8.76	Metabolism
896	Putative actin depolymerizing factor (*O. sativa*)	35_14854	MALDI-TOF MS	78	7	29	35415	9.72	Cell wall
897	Peroxiredoxin (*O. sativa*)	35_35528	MALDI-TOF MS	79	5	30	21117	5.07	Disease/Defence
899	Not identified								Not identified
901	High light protein (*H. vulgare*)	35_3541	MALDI-TOF MS	98	7	32	29860	5.03	Unclassified
903	S-adenosylmethionine:2-demethylmenaquinone methyltransferase- like (*O. sativa*)	35_16832	LC-ESI-Q-TOF	10.84	3	11	18065	5.35	Metabolism
904	Alanyl-tRNA synthetase (*A. thaliana*)	35_19085	MALDI-TOF MS	70	7	16	61518	9.71	Transcription
908	Not identified								Not identified
913	Glycine rich protein, RNA binding protein (*H. vulgare*)	35_13932	MALDI-TOF MS	87	6	47	21410	8.70	Unclassified
914	Not identified								Not identified
916	Os09g0514600 protein (*O. sativa*)	35_2113	LC-ESI-Q-TOF	10.84	3	10	17146	6.90	Unclassified
922	Not identified								Not identified
924	Glycine rich protein, RNA binding protein (*H. vulgare*)	35_13932	MALDI-TOF MS	73	6	28	21410	8.70	Unclassified
925	Oxygen-evolving complex (*T. aestivum*)	35_14958	MALDI-TOF MS	67	5	25	31568	10.00	Energy metabolism
931	Not identified								Not identified
932	Glycine rich protein, RNA binding protein (*H. vulgare*)	35_13963	MALDI-TOF MS	78	7	32	35975	9.32	Unclassified
934	Not identified								Not identified
936	Not identified								Not identified
940	Ribulose bisphosphate carboxylase small chain (*H. vulgare*)	35_28146	MALDI-TOF MS	128	12	41	24318	9.15	Energy metabolism
941	Ribulose bisphosphate carboxylase small chain (*H. vulgare*)	35_28146	MALDI-TOF MS	102	9	37	24318	9.15	Energy metabolism
944	Nucleoside diphosphate kinase (*L. perenne*)	35_610	MALDI-TOF MS	101	9	26	29611	9.06	Metabolism
953	Not identified								Not identified
954	10 kDa chaperonin (*O. sativa*)	35_14278	MALDI-TOF MS	74	8	22	36043	9.73	Protein destination
992	Not identified								Not identified
994	Not identified								Not identified
1023	Not identified								Not identified

Table A 2: List of proteins identified in barley leaf epidermis tissue using nanoLC-based separation coupled to ESI-Q-TOF MS/MS detection. Shown are the protein name, accession number, , PLGS score, number of peptides, sequence coverage, theoretical molecular weight, theoretical isoelectric point and presumed protein function.

Protein	Accession number	Score 1/2/3	Number of peptides 1/2/3	Sequence coverage in % 1/2/3	Theor. molecular mass in Da	Theor. isoelectric point	Function
Cell division control protein 48 (*A. thaliana*)	35_14849	772/1121/1098	12/17/18	21/30/34	93131	5.1	Cell cycle
Tubulin alpha 1 chain (*A. thaliana*)	35_14081	409/447/560	5/5/7	12/14/22	55696	5.1	Cell wall
Actin 5C (*D. melanogaster*)	35_14172	1351/1212/1471	10/11/13	35/43/45	41829	5.0	Cell wall
Actin 5C (*D. melanogaster*)	35_14174	1420/1216/1601	10/12/13	32/42/46	45614	5.4	Cell wall
Actin 5C (*D. melanogaster*)	35_14175	841/1028/1116	9/7/10	35/30/42	41918	5.2	Cell wall
Tubulin beta 2 chain (*Z. mays*)	35_14329	615/585/1081	11/9/12	42/29/37	53012	4.8	Cell wall
Tubulin beta 5 chain (*G. hirsutum*)	35_14331	1047/868/1110	14/10/16	43/29/41	52753	4.8	Cell wall
Tubulin beta 2 beta 3 chain (*A. thaliana*)	35_14334	872/964/900	11/11/11	30/34/30	52393	4.6	Cell wall
Tubulin beta 1 chain (*T. aestivum*)	35_14335	629/679/1308	11/9/14	35/24/41	53136	4.8	Cell wall
Tubulin beta 1 chain (*T. aestivum*)	35_14338	752/773/1387	14/10/16	52/28/48	53474	4.8	Cell wall
Villin 2 (*A. thaliana*)	35_14846	267/159/259	5/3/5	14/8/14	74214	5.3	Cell wall
Putative actin depolymerizing factor (*O. sativa*)	35_14854	192/185/165	2/3/4	10/18/30	21552	6.7	Cell wall
Alpha-1,4-glucan-protein synthase [UDP-forming] (*Z. mays*)	35_272	548/574/726	7/11/11	28/35/41	45926	5.5	Cell wall
Profilin 2 (*T. aestivum*)	35_28972	400/509/514	2/2/2	17/17/17	20636	10.2	Cell wall
Peroxidase 6 (*T. monococcum*)	35_1037	363/330/645	9/4/6	48/28/30	34895	8,1	Disease/Defence
USP family protein (*T. aestivum*)	35_1067	217/276/221	4/4/4	37/37/31	21810	6.5	Disease/Defence
IN2 1 protein (*O. sativa*)	35_1086	221/164/209	4/2/2	23/11/17	29394	5.8	Disease/Defence
Heat shock 70 kDa protein (*O. sativa*)	35_1230	340/300/227	9/10/7	17/19/15	74450	5.7	Disease/Defence
Heat shock cognate 70 kDa (*S. lycopersicum*)	35_137	436/676/767	10/6/7	34/20/25	46756	4.8	Disease/Defence
Peroxidase 10 (*T. monococcum*)	35_13856	869/570/893	7/6/10	24/25/37	39753	6.5	Disease/Defence
Heat shock protein 81 2 (*A. thaliana*)	35_14120	1257/1023/1105	20/12/15	32/18/25	85577	4.9	Disease/Defence
Heat shock protein 90 (*T. aestivum*)	35_14129	1013/929/1089	12/11/14	25/21/30	83504	4.8	Disease/Defence
L-ascorbate peroxidase 1 (*O. sativa*)	35_14509	482/644/277	8/9/9	43/39/41	30756	6.4	Disease/Defence
Superoxide dismutase Cu Zn 2 (O. sativa)	35_14923	230/171/178	1/1/2	11/11/18	20797	6.7	Disease/Defence
Putative heat shock protein (O. sativa)	35_14978	249/286/351	11/12/11	19/16/15	93424	4.8	Disease/Defence
Putative disulfide isomerase (O. sativa)	35_15052	293/313/319	6/8/7	33/21/29	42041	6.1	Disease/Defence
Stromal 70 kDa heat shock related protein (*O. sativa*)	35_15224	258/222/127	3/4/3	10/12/7	47200	8.7	Disease/Defence
Chaperonin CPN60 1 (*Z. mays*)	35_16286	555/388/350	8/5/9	21/16/11	66684	6.7	Disease/Defence
Chitinase (*H. vulgare*)	35_18202	199/210/209	4/3/5	19/16/28	37124	7.7	Disease/Defence
Heat shock protein 70 (*C. sativa*)	35_1834	257/235/180	5/5/5	12/10/13	77068	5.0	Disease/Defence

Chaperonin CPN60-1 (*Z. mays*)	35_20633	235/116/187	4/4/2	21/13/6	41875	8.8	Disease/Defence
Class III peroxidase 137 precursor (*O. sativa*)	35_22397	232/331/315	2/2/3	20/20/29	20159	4.2	Disease/Defence
Similar to late embryogenesis abundant proteins (*A. thaliana*)	35_31693	201/109/160	4/2/3	22/21/22	16798	4.8	Disease/Defence
Chaperonin CPN60 1 (*Z. mays*)	35_3277	224/193/176	4/3/5	14/13/21	36247	4.8	Disease/Defence
Beta-ketoacyl reductase (*Z. mays*)	35_3443	549/429/534	9/6/7	39/28/33	37328	10.1	Disease/Defence
Beta-ketoacyl reductase (*Z. mays*)	35_3451	374/328/286	4/3/7	36/31/35	20583	5.4	Disease/Defence
Peroxiredoxin (*O. sativa*)	35_35528	336/150/354	7/4/4	46/33/33	20003	5.0	Disease/Defence
Heat shock cognate 70 kDa protein 2 (*S. lycopersicum*)	35_432	1507/1624/1764	14/12/14	25/26/27	72264	5.0	Disease/Defence
Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	1731/1937/2234	14/16/18	30/35/42	72202	5.0	Disease/Defence
UDP-glucose 6-dehydrogenase (*G. max*)	35_51	521/549/701	8/9/12	27/28/37	52989	5.8	Disease/Defence
1-aminocyclopropane-1-carboxylate oxidase (*P. edulis*)	35_575	242/155/249	5/1/5	25/4/22	38670	6.0	Disease/Defence
Protein disulfide isomerase (*Z. mays*)	35_675	328/181/300	8/3/5	29/8/14	49452	5.0	Disease/Defence
Putative vacuolar defense protein (*T. aestivum*)	35_771	238/182/240	3/2/3	19/12/19	19543	7.1	Disease/Defence
Salt tolerant protein (*T. aestivum*)	35_788	273/227/356	5/4/3	30/23/24	22541	9.2	Disease/Defence
Putative thioredoxin peroxidase (*O. sativa*)	35_837	335/289/251	7/5/4	41/30/21	30714	7.8	Disease/Defence
CI2C (*H. vulgare*)	35_906	249/270/218	2/2/2	43/43/43	8578	5.1	Disease/Defence
Os01g0835900 protein (*O. sativa*)	35_13882	523/417/428	6/5/6	48/39/39	13258	12.1	DNA binding
14 3 3 like protein GF14 A (*O. sativa*)	35_14379	252/298/301	4/5/6	15/24/44	31242	4.9	DNA binding
14 3 3 like protein A (*H. vulgare*)	35_14382	1049/1240/1235	9/10/10	50/55/50	29717	4.6	DNA binding
14 3 3 like protein GF14 D (*O. sativa*)	35_14383	259/344/2/2	6/5/6	29/27/35	32953	4.8	DNA binding
14 3 3 like protein B (*H. vulgare*)	35_14384	682/787/729	7/11/7	37/51/32	30369	4.5	DNA binding
14 3 3 like protein GF14 B (*O. sativa*)	35_14385	594/672/750	11/7/8	47/33/45	30252	4.5	DNA binding
Phosphoenolpyruvate carboxylase 2 (*Z. mays*)	35_1118	355/305/310	6/6/9	9/8/15	113773	5.6	Energy metabolism
Putative legumin (*O. sativa*)	35_1242	410/370/413	9/7/11	26/23/42	39445	5.6	Energy metabolism
Ribulose bisphosphate carboxylase large chain precursor (*O. sativa*)	35_136	1552/1432/1534	20/15/18	48/35/36	53965	6.3	Energy Metabolism
Fructose bisphosphate aldolase chloroplast precursor (*O. sativa*)	35_13817	631/395/535	7/7/8	35/28/38	42859	6.4	Energy metabolism
Ribulose bisphosphate carboxylase oxygenase activase A (*H. vulgare*)	35_13900	689/757/678	7/10/8	31/37/30	47905	7.8	Energy metabolism
Ribulose bisphosphate carboxylase oxygenase activase B (*H. vulgare*)	35_13901	834/470/369	12/6/8	37/21/29	49408	8.4	Energy metabolism
Fructose bisphosphate aldolase (*O. sativa*)	35_14090	334/537/312	3/4/4	19/22/26	21464	10.6	Energy metabolism
Fructose bisphosphate aldolase (*O. sativa*)	35_14100	641/926/799	14/10/8	44/37/31	41335	8.1	Energy metabolism
Malate dehydrogenase (*O. sativa*)	35_14420	917/686/694	11/8/9	49/31/37	37174	5.7	Energy metabolism
Enolase 2 (*Z. mays*)	35_14444	891/745/863	10/11/10	39/43/40	51437	5.6	Energy metabolism

Enolase 2 (*Z. mays*)	35_14451	843/698/808	10/11/10	40/44/40	50919	5.6	Energy metabolism
Triosephosphate isomerase (*H. vulgare*)	35_14505	1120/1030/947	8/9/8	38/45/40	30534	7.7	Energy metabolism
Putative cytochrome b5 (*O. sativa*)	35_14940	130/167/127	4/4/4	33/35/32	18570	6.7	Energy metabolism
Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (*R. communis*)	35_15071	343/408/466	7/8/11	25/20/30	64658	6.8	Energy metabolism
Pyruvate kinase family protein (*O. sativa*)	35_15127	301/167/264	10/2/5	28/9/22	58054	6.5	Energy metabolism
Succinyl-CoA ligase [GDP-forming] subunit beta (*O. sativa*)	35_15472	327/218/223	9/3/7	29/16/24	46161	6.6	Energy metabolism
Putative plastidic aldolase (*O. sativa*)	35_15473	314/244/189	6/6/6	20/19/28	45219	8.1	Energy metabolism
Triosephosphate isomerase (*O. sativa*)	35_15548	332/282/321	7/7/9	41/30/39	32564	7.2	Energy metabolism
NAD malate dehydrogenase (*O. sativa*)	35_15552	453/336/273	5/4/3	18/12/12	47020	8.6	Energy metabolism
Putative stress related like protein interactor (*O. sativa*)	35_1563	227/225/153	7/5/4	17/10/8	53654	9.6	Energy metabolism
Malate dehydrogenase (*O. sativa*)	35_165	596/665/689	9/6/9	43/35/46	39809	8.4	Energy metabolism
Malate dehydrogenase (*O. sativa*)	35_169	422/445/502	8/9/10	54/57/61	38587	9.5	Energy metabolism
Os06g0326400 protein (*O. sativa*)	35_1867	365/420/557	8/11/12	27/24/38	70370	7.4	Energy metabolism
Fructose-bisphosphate aldolase cytoplasmic isozyme (*O. sativa*)	35_37662	433/499/321	3/5/2	24/25/17	26537	9.8	Energy metabolism
Phosphoglycerate kinase (*Z. mays*)	35_384	991/837/1168	14/12/12	43/40/48	46643	7.6	Energy metabolism
Fructose-bisphosphate aldolase cytoplasmic isozyme (*O. sativa*)	35_38591	299/288/403	3/3/3	36/36/36	18505	5.6	Energy metabolism
Oxygen-evolving enhancer protein 1 (*T. aestivum*)	35_404	689/676/536	12/8/8	51/47/46	35743	6.0	Energy metabolism
Chlorophyll a-b binding protein (*O. sativa*)	35_412	240/165/178	4/3/2	23/19/18	31303	5.2	Energy metabolism
Glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_49	998/857/1120	12/9/11	50/36/43	40464	6.7	Energy metabolism
Os01g0869800 protein (*O. sativa*)	35_546	170/190/199	4/3/3	20/16/16	28461	9.4	Energy metabolism
Putative cytochrome P450 (*O. sativa*)	35_7903	583/601/585	10/8/7	36/30/27	37773	7.3	Energy metabolism
Putative cytochrome P450 (*O. sativa*)	35_826	221/296/177	5/3/4	18/9/15	63898	6.4	Energy metabolism
Methylenetetrahydrofolate reductase 1 (*Z. mays*)	35_1049	274/234/401	8/8/12	20/26/28	67311	5,3	Metabolism
Putative tetrafunctional protein of glyoxysomal fatty acid beta-oxidation (*O. sativa*)	35_1259	218/202/278	6/6/8	13/15/19	83245	9.3	Metabolism
O-methyltransferase (*O. sativa*)	35_1280	570/347/552	7/5/6	31/19/20	41459	5.9	Metabolism
O-methyltransferase (*O. sativa*)	35_1282	501/449/556	6/5/8	26/24/39	41838	6.2	Metabolism
Phospholipase D alpha 1 (*Z. mays*)	35_14127	279/216/263	6/8/6	14/14/15	93267	5.2	Metabolism
Lipoxygenase 2 (*H. vulgare*)	35_14193	832/1121/1303	16/15/21	25/25/39	98091	6.5	Metabolism
Lipoxygenase 1 (*H. vulgare*)	35_14194	324/219/293	9/4/8	16/9/15	97394	5.8	Metabolism
Methionine synthase 2 (*H. vulgare*)	35_14375	608/599/824	10/9/17	21/18/29	87776	6.0	Metabolism
Methionine synthase 2 (*H. vulgare*)	35_14376	946/1443/1550	20/16/18	34/31/34	87079	6.2	Metabolism
Putative transaldolase (*O. sativa*)	35_14408	406/490/462	12/101/10	39/25/34	49333	7.1	Metabolism

Beta amylase (*T. aestivum*)	35_14442	677/578/730	11/9/12	34/33/39	57417	5.2	Metabolism
Transketolase (*Z. mays*)	35_14494	380/362/272	8/9/11	25/25/32	57871	5.8	Metabolism
O-methyltransferase (*O. sativa*)	35_14495	659/165/488	13/6/8	52/24/34	42516	5.6	Metabolism
Transketolase (*Z. mays*)	35_14496	459/431/410	7/6/8	26/24/33	49086	5.8	Metabolism
Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	674/858/737	11/10/14	32/25/44	55144	5.7	Metabolism
UDP-D-glucuronate decarboxylase (*H. vulgare*)	35_14654	518/516/459	11/8/9	47/35/43	40167	7.4	Metabolism
Adenosine kinase (*Z. mays*)	35_14937	1149/960/976	14/13/11	64/60/51	37704	5.2	Metabolism
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (*O. sativa*)	35_15021	310/327/371	12/12/12	35/30/31	62968	5.7	Metabolism
Phosphoglucomutase (*B. inermis*)	35_15040	741/701/698	16/11/11	34/29/31	70941	6.6	Metabolism
Adenylate kinase B (*O. sativa*)	35_15202	293/222/155	5/6/1	22/27/5	32071	7.3	Metabolism
O-methyltransferase (*S. cereale*)	35_15363	548/679/754	5/5/5	23/19/19	40074	5.8	Metabolism
Os05g0132100 protein (*O. sativa*)	35_16083	327/372/412	10/12/13	20/24/22	77956	7.2	Metabolism
ATP citrate lyase (*A. thaliana*)	35_16115	619/815/804	13/12/14	31/30/33	65987	6.9	Metabolism
Phosphoglycerate kinase (*T. aestivum*)	35_19	825/750/712	14/16/16	45/45/49	47108	6.7	Metabolism
GDP-mannose 3,5-epimerase (*A. thaliana*)	35_192	193/170/215	5/2/5	14/7/19	45152	5.9	Metabolism
Putative proline rich protein APG (*O. sativa*)	35_19452	296/406/422	4/5/6	24/18/34	43422	5.6	Metabolism
NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_1962	351/231/273	8/5/4	23/14/21	55604	6.6	Metabolism
N-methyltransferase (*H. vulgare*)	35_21542	475/492/465	2/3/2	17/26/17	24376	5.7	Metabolism
Os02g0653400 protein (*O. sativa*)	35_24186	178/187/274	4/2/3	37/20/31	15993	5.9	Metabolism
S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_366	558/752/517	4/5/7	15/26/31	44034	5.8	Metabolism
S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_368	631/779/666	6/6/5	24/26/21	44483	5.4	Metabolism
Vacuolar invertase1 (*T. monococcum*)	35_369	322/261/274	6/6/7	19/21/19	51105	4.4	Metabolism
Os03g0129300 protein (*O. sativa*)	35_435	448/478/484	9/8/11	25/21/27	48450	6.2	Metabolism
Carbonic anhydrase (*H. vulgare*)	35_47883	524/484/773	6/6/7	30/30/30	38768	8.7	Metabolism
S-adenosylmethionine synthetase 1 (*H. vulgare*)	35_519	432/440/260	5/6/3	30/34/21	29519	9.2	Metabolism
Glutamine synthetase cytosolic isozyme 1-1 (*O. sativa*)	35_531	199/322/593	5/7/10	18/24/35	46686	6.8	Metabolism
NADP-specific isocitrate dehydrogenase (*O. sativa*)	35_545	342/455/449	8/11/15	24/29/37	48941	6.0	Metabolism
Putative fatty acyl coA reductase (*O. sativa*)	35_5786	150/183/232	4/3/3	22/23/18	26557	8.2	Metabolism
Serine hydroxymethyltransferase (*O. sativa*)	35_605	325/193/240	7/6/5	25/15/14	53342	6.9	Metabolism
Nucleoside diphosphate kinase (*L. perenne*)	35_610	307/321/458	6/4/5	38/32/40	17194	9.1	Metabolism
Ketol-acid reductoisomerase (*O. sativa*)	35_730	216/156/155	5/3/4	17/6/11	65784	6.3	Metabolism
UTP--glucose-1-phosphate uridylyltransferase (*H. vulgare*)	35_751	642/816/821	12/12/15	36/37/43	53929	5.1	Metabolism
Dehydroascorbate reductase (*T. aestivum*)	35_860	256/547/528	7/8/5	38/39/27	29164	8.2	Metabolism
Acetyl-CoA carboxylase (*T. aestivum*)	35_8822	245/243/260	8/9/8	23/24/21	54277	5.5	Metabolism
NADP malic enzyme *(O. sativa*)	35_960	223/235/265	5/8/4	17/20/14	68581	6.8	Metabolism

Putative 3-oxoacyl-[acyl-carrier-protein] synthase I (*O. sativa*)	35_977	235/228/257	3/6/5	11/21/21	45557	5.9	Metabolism
Lactoylglutathione lyase (*O. sativa*)	35_118	538/417/491	8/7/9	32/30/38	37195	6.3	Secondary metabolism
Putative caffeoyl-CoA O-methyltransferase (*O. sativa*)	35_14101	187/115/166	2/2/2	15/15/15	30567	4.9	Secondary metabolism
Phenylalanine ammonia-lyase (*O. sativa*)	35_14228	525/570/556	11/10/9	28/18/22	77239	5.8	Secondary metabolism
Phenylalanine ammonia-lyase (*T. aestivum*)	35_14236	583/506/460	7/10/8	13/17/15	83594	5.9	Secondary metabolism
Phenylalanine ammonia-lyase (*T. aestivum*)	35_14239	459/530/425	6/9/6	15/19/13	64439	6.2	Secondary metabolism
Chalcone synthase WHP1 (*Z. mays*)	35_15644	613/577/574	7/4/4	32/18/26	44873	5.9	Secondary metabolism
Chalcone-flavanone isomerase family protein (*O. sativa*)	35_2198	645/406/545	9/7/9	63/42/66	25948	4.6	Secondary metabolism
Elongation factor 1 alpha (*A. thaliana*)	35_13745	641/577/424	5/4/4	20/11/20	49441	9.5	Protein biosynthesis
Putative elongation factor 1 beta (*H. vulgare*)	35_14285	208/216/178	5/5/5	34/38/26	24730	4.3	Protein biosynthesis
60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	260/229/168	3/4/3	15/24/17	30163	11.5	Protein biosynthesis
40S ribosomal protein S6 1 (*A. thaliana*)	35_14418	312/272/335	3/4/5	18/16/18	32519	11.5	Protein biosynthesis
40S ribosomal protein S4 (*Z. mays*)	35_14431	197/334/207	7/6/4	24/25/17	30442	10.5	Protein biosynthesis
Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	193/296/214	3/4/3	20/23/21	17464	5.5	Protein biosynthesis
Putative 40S ribosomal protein contains C terminal domain (*O. sativa*)	35_14622	177/299/172	4/3/1	24/12/11	29996	9.7	Protein biosynthesis
60S acidic ribosomal protein P0 (*O. sativa*)	35_14696	540/463/539	6/5/6	30/27/30	35914	5.5	Protein biosynthesis
40S ribosomal protein S19 (*O. sativa*)	35_14825	179/220/197	3/6/5	33/36/26	18532	10.8	Protein biosynthesis
40S ribosomal protein S12 (*H. vulgare*)	35_14828	226/181/212	3/3/3	25/25/25	19987	5.4	Protein biosynthesis
Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	648/717/584	8/10/7	27/28/22	46087	11.1	Protein biosynthesis
40S ribosomal protein S13 (*Z. mays*)	35_15055	249/170/214	3/4/3	12/26/20	21402	10.9	Protein biosynthesis
Elongation factor 2 (*B. vulgaris*)	35_373	537/501/508	9/7/7	13/10/11	94353	6.0	Protein biosynthesis
40S ribosomal protein (*O. sativa*)	35_465	265/192/202	3/6/3	16/26/16	33197	4.7	Protein biosynthesis
40S ribosomal protein S5 (*O. sativa*)	35_556	486/388/404	5/3/4	30/24/34	17106	10.7	Protein biosynthesis
Elongation factor 1-gamma 3 (*O. sativa*)	35_593	344/335/417	6/10/9	19/31/27	51016	7.7	Protein biosynthesis
40S ribosomal protein S3a (*O. sativa*)	35_685	295/287/250	6/6/5	29/33/32	32896	10.4	Protein biosynthesis
40S ribosomal protein S3a (*O. sativa*)	35_686	246/261/187	5/3/4	26/14/23	34519	10.2	Protein biosynthesis
40S ribosomal protein S14 2 (*A. thaliana*)	35_859	168/252/251	3/2/3	20/21/32	19748	11.5	Protein biosynthesis
Translational elongation factor Tu (*O. sativa*)	35_976	299/349/329	7/9/8	31/28/28	54127	6.1	Protein biosynthesis
Mitochondrial processing peptidase alpha chain (*D. glomerata*)	35_1199	167/108/108	4/3/3	24/19/24	24197	9.7	Protein destination
Mitochondrial processing peptidase *(D. glomerata*)	35_1200	264/158/213	6/7/7	15/22/30	54504	7.3	Protein destination
Endoplasmin homolog precursor (*H. vulgare*)	35_14098	789/696/661	11/11/9	18/19/15	95312	4.7	Protein destination
Putative 20 kDa chaperonin (*O. sativa*)	35_1423	332/269/146	5/5/4	30/35/36	25996	8.4	Protein destination
OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	434/342/387	11/7/7	25/18/18	64067	4.6	Protein destination
Luminal binding protein 3 (*Z. mays*)	35_14470	1497/1445/1437	19/17/16	36/33/32	77498	5.5	Protein destination

Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	993/917/673	20/13/13	39/32/35	57460	4.9	Protein destination
Calreticulin like protein (*T. aestivum*)	35_14693	733/792/667	13/13/11	36/43/38	51112	4.3	Protein destination
Triticain alpha (*T. aestivum*)	35_15015	346/315/426	3/5/5	9/16/15	52076	4.8	Protein destination
Thiol protease *(T. aestivum*)	35_15079	223/244/444	6/8/12	26/28/34	42781	6.6	Protein destination
RuBisCO large subunit-binding protein subunit alpha (*T. aestivum*)	35_15221	707/549/367	16/13/14	38/29/30	65335	5.3	Protein destination
Aspartic proteinase (*T. aestivum*)	35_15366	240/238/283	8/4/7	26/10/21	54492	5.8	Protein destination
Protease inhibitor/seed storage/LTP family protein (*O. sativa*)	35_1573	172/228/127	3/3/2	17/17/12	20351	8.6	Protein destination
Leucine aminopeptidase 2 (*O. sativa*)	35_15893	199/160/216	7/6/7	22/19/25	50388	5.6	Protein destination
Cyclophilin like protein (*T. aestivum*)	35_1696	245/98/84	4/3/3	24/16/17	28131	9.9	Protein destination
Os09g0381400 protein (*O. sativa*)	35_23175	280/239/469	5/3/3	32/23/28	33410	5.4	Protein destination
RuBisCO large subunit-binding protein subunit beta (*A. thaliana*)	35_360	1119/897/713	15/11/10	34/24/27	68128	5.8	Protein destination
Proteasome subunit alpha type-1 (*O. sativa*)	35_966	139/96/120	5/2/5	19/15/24	36162	5.5	Protein destination
ATP synthase subunit beta (*H. vulgare*)	35_10965	346/365/438	6/8/8	39/46/54	26370	9.5	Transport
ADP ATP carrier protein 1, mitochondrial precursor (*Z. mays*)	35_14437	271/503/531	5/6/8	15/15/21	46971	10.1	Transport
Vacuolar ATP synthase subunit E (*T. aestivum*)	35_14632	334/300/385	3/6/4	12/22/15	31709	8.2	Transport
GTP binding nuclear protein Ran 1 (*A. thaliana*)	35_14667	290/197/202	6/5/5	34/23/23	28481	7.9	Transport
ATP synthase subunit beta mitochondrial precursor (*Z. mays*)	35_14757	1225/1191/1211	13/10/11	40/25/29	59813	6.0	Transport
ATP synthase subunit beta mitochondrial precursor (*Z. mays*)	35_14758	1379/1349/1344	11/10/15	32/27/38	60013	5.9	Transport
Vacuolar ATP synthase catalytic subunit A (*H. vulgare*)	35_15178	1419/1266/1472	22/16/21	47/35/49	73799	5.0	Transport
B0403H10-OSIGBa0105A11.13 protein (*O. sativa*)	35_15204	548/145/500	1/3/4	12/43/32	15481	9.1	Transport
Outer mitochondrial membrane protein porin (*T. aestivum*)	35_15208	222/210/249	4/3/6	32/15/37	32130	8.8	Transport
Hypothetical protein (*O. sativa*)	35_15295	273/226/182	6/4/3	38/23/17	24517	5.5	Transport
Importin alpha 1b subunit (*O. sativa*)	35_15530	332/191/350	5/5/9	15/13/39	54986	7.0	Transport
ETC complex I subunit conserved region family protein (*O. sativa*)	35_15703	183/203/112	4/3/3	26/25/20	20736	4.4	Transport
Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	124/147/243	5/3/5	15/27/22	35656	6.4	Transport
Lipid transfer protein (*T. aestivum*)	35_16845	347/292/302	5/6/6	40/37/37	24191	9.9	Transport
Putative vacuolar ATP synthase subunit C (*O. sativa*)	35_1739	435/258/419	7/6/10	29/20/35	46906	7.4	Transport
Phospholipid transfer protein precursor (*H. vulgare*)	35_335	179/200/157	3/2/5	28/22/34	12348	8.7	Transport
ATP synthase subunit alpha (*T. aestivum*)	35_36498	244/314/434	4/4/6	44/32/48	14397	4.7	Transport
Non-specific lipid-transfer protein Cw18 *(H. vulgare*)	35_47	202/185/212	4/3/4	46/36/45	11528	9.2	Transport

60S acidic ribosomal protein P2B (*Z. mays*)	35_1145	427/445/518	3/4/4	48/54/48	12106	4.2	Translation
OSJNBa0038P21 4 (*O. sativa*)	35_14504	176/272/245	7/6/4	39/32/20	26663	10.9	Translation
P0648C09 9 protein (*O. sativa*)	35_10566	172/280/219	2/2/4	11/11/15	28183	4,1	Unclassified
Pore forming toxin like protein Hfr 2 (*T. aestivum*)	35_11261	173/198/187	3/4/4	18/32/32	27906	4.9	Unclassified
Os05g0399100 protein (*O. sativa*)	35_1225	237/157/308	4/3/3	46/27/37	21629	4.8	Unclassified
OSJNBb0039L24 13 (*O. sativa*)	35_1276	126/152/101	6/5/5	31/24/31	27394	5.4	Unclassified
Hypothetical protein P0436E04 19 (*O. sativa*)	35_1354	287/183/221	3/3/3	13/12/13	38232	5.7	Unclassified
AT4g05320 (*A. thaliana*)	35_13719	538/393/358	4/3/2	28/23/18	19215	6.5	Unclassified
Thaumatin like protein TLP5 (*H. vulgare*)	35_14148	571/681/664	8/7/9	67/51/60	26389	6.9	Unclassified
ATP citrate synthase (*O. sativa*)	35_1428	230/257/374	7/5/8	20/17/29	47368	5.4	Unclassified
Hypothetical protein p23k 1 (*H. vulgare*)	35_14320	194/358/342	3/4/5	17/24/34	24758	6.6	Unclassified
Putative diphosphonucleotide phosphatase (*O. sativa*)	35_14519	393/188/275	10/6/9	22/15/19	71478	6.6	Unclassified
Pore forming toxin like protein Hfr 2 (*T. aestivum*)	35_14520	845/634/700	11/9/10	35/29/29	57559	5.6	Unclassified
Translationally controlled tumor protein homolog (*T. aestivum*)	35_14522	469/347/308	3/3/3	19/19/19	22587	4.6	Unclassified
Salt stress root protein RS1 (*O. sativa*)	35_14980	382/406/341	3/4/3	24/18/22	20675	10.6	Unclassified
Cp31AHv protein (*H. vulgare*)	35_14983	273/134/175	5/2/4	26/9/16	35377	4.,7	Unclassified
Cp31AHv protein (*H. vulgare*)	35_14986	169/174/168	2/6/3	16/31/12	33409	4.7	Unclassified
Putative annexin P35 (*O. sativa*)	35_15136	321/295/287	12/9/8	39/31/43	38910	6.3	Unclassified
Putative annexin (*O. sativa*)	35_15137	382/421/453	11/12/12	43/38/41	40387	8.8	Unclassified
Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515	135/233/182	3/3/2	26/27/17	16184	4.6	Unclassified
Mitochondrial ATP synthase (*T. aestivum*)	35_15350	327/418/374	5/6/6	25/33/37	28062	9.2	Unclassified
Putative stress induced protein sti1 (*O. sativa*)	35_15495	641/457/390	15/12/9	31/24/23	68201	6.3	Unclassified
Expressed protein (*O. sativa*)	35_16282	333/333/356	6/3/4	40/23/34	26219	5.9	Unclassified
Putative stress induced protein sti1 (*O. sativa*)	35_17705	310/199/202	9/6/5	25/16/14	52561	7.2	Unclassified
RNase S-like protein (*H. vulgare*)	35_1948	808/611/471	5/3/4	18/14/18	30335	8.5	Unclassified
Os06g0288300 protein (*O. sativa*)	35_21909	474/238/508	11/10/9	59/52/49	31147	4.9	Unclassified
Ribosomal protein L10E (*M. truncatula*)	35_264	228/227/231	2/3/2	17/19/9	27654	11.6	Translation
Osr40g2 protein (*O. sativa*)	35_268	194/305/403	3/4/4	12/19/18	30280	11.1	Unclassified
Hypothetical protein OJ1200 C08 123 (*O. sativa*)	35_2718	216/161/194	6/3/4	26/19/25	29069	5.2	Unclassified
Osr40c1 protein (*O. sativa*)	35_277	520/397/450	9/8/9	36/31/32	40646	6.6	Unclassified
Putative ML domain protein (*O. sativa*)	35_2792	173/104/129	1/1/2	8/8/8	18573	7.6	Unclassified
ATP citrate synthase *(O. sativa*)	35_3165	147/165/172	2/5/4	6/16/11	49790	6.2	Unclassified
P0432B10 23 protein (*O. sativa*)	35_3373	221/95/327	2/3/2	20/31/20	21539	7.8	Unclassified
P0648C09 9 protein (*O. sativa*)	35_49779	151/105/119	3/3/3	41/41/41	16292	7.2	Unclassified
Putative acid phosphatase (*H. vulgare*)	35_553	326/267/239	5/3/2	21/12/8	31764	9.3	Unclassified

Guanine nucleotide-binding protein subunit beta-like protein (*O. sativa*)	35_590	165/268/263	5/8/6	26/39/33	36993	6.5	Unclassified
RNA binding protein Rp120 (*O. sativa*)	35_617	500/404/462	12/7/13	15/9/19	114040	8.1	Unclassified

Table A 3: Complete list of exact mass retention time (EMRT) clusters detected in the protein profiling of barley grain development. Shown are the group, number of experiment (Exp. #), class, protein name, accession number, PLGS score, peptide sequence, database used for identification, presumed protein function and EMRT ID.

Group	Exp. #	Class	Protein	Accession	PLGS score	Sequence	Database	Function	EMRT ID
I	1	2	Glutaredoxin (*T. aestivum*)	35 1143	248.42	HIGGCDDTLALNK	Harvest Hv	Disease/Defence	1608
I	1	2	Glutaredoxin (*T. aestivum*)	35_1143	187.51	AIELDTESDGPEMQSALAEWTGQR	Harvest Hv	Disease/Defence	5033
I	1	2	Glutaredoxin (*T. aestivum*)	35_1143	187.51	LVALLTEAGAISGSTSK	Harvest Hv	Disease/Defence	7698
I	1	2	Glutaredoxin (*T. aestivum*)	35_1143	187.51	KLFTQLGASFK	Harvest Hv	Disease/Defence	9134
I	1	5	Glutaredoxin (*T. aestivum*)	35_1143	248.42	EIVASAPVVVFSK	Harvest Hv	Disease/Defence	499
I	2	2	Glutaredoxin (*T. aestivum*)	35_1143	132.27	HIGGCDDTLALNK	Harvest Hv	Disease/Defence	2371
I	2	4	Glutaredoxin (*T. aestivum*)	35_1143	278.7	EIVASAPVVVFSK	Harvest Hv	Disease/Defence	45
I	2	4	Glutaredoxin (*T. aestivum*)	35_1143	278.7	AIELDTESDGPEMQSALAEWTGQR	Harvest Hv	Disease/Defence	2842
I	2	8	Glutaredoxin (*T. aestivum*)	35_1143	206.6	TVPNVFINGK	Harvest Hv	Disease/Defence	556
I	2	8	Glutaredoxin (*T. aestivum*)	35_1143	206.6	SYCPFCVQVK	Harvest Hv	Disease/Defence	2793
I	2	8	Glutaredoxin (*T. aestivum*)	35_1143	206.6	AKEIVASAPVVVFSK	Harvest Hv	Disease/Defence	4847
I	2	8	Glutaredoxin (*T. aestivum*)	35_1143	206.6	KLFTQLGASFK	Harvest Hv	Disease/Defence	9161
I	2	8	Glutaredoxin (*T. aestivum*)	35_1143	206.6	LVALLTEAGAISGSTSK	Harvest Hv	Disease/Defence	16818
I	1	2	OsS5a (*O. sativa*)	35_120	67.46	VLVTPTSDLGK	Harvest Hv	Unclassified	354
I	1	2	OsS5a (*O. sativa*)	35_120	67.46	FQAQADAVNLICGAK	Harvest Hv	Unclassified	891
I	2	6	OsS5a (*O. sativa*)	35_120	138.43	VLVTPTSDLGK	Harvest Hv	Unclassified	27148
I	2	8	OsS5a (*O. sativa*)	35_120	145.32	SSALTEAPSQLDESDSK	Harvest Hv	Unclassified	1792
I	2	8	OsS5a (*O. sativa*)	35_120	145.32	IIVFIGSPVK	Harvest Hv	Unclassified	4850
I	2	8	OsS5a (*O. sativa*)	35_120	145.32	FQAQADAVNLICGAK	Harvest Hv	Unclassified	5107
I	2	8	OsS5a (*O. sativa*)	35_120	145.32	SFVTSILNSLPGVDPNDPSVK	Harvest Hv	Unclassified	10361
I	1	2	Putative enoyl ACP reductase (*O. sativa*)	35_1359	131.27	VLAFEAGR	Harvest Hv	Metabolism	3839
I	1	2	Putative enoyl ACP reductase (*O. sativa*)	35_1359	131.27	TIPGYGGGMSSAK	Harvest Hv	Metabolism	6793
I	2	6	Putative enoyl ACP reductase (*O. sativa*)	35_1359	179.63	ALSTRTGFASCVK	Harvest Hv	Metabolism	12565
I	2	6	Putative enoyl ACP reductase (*O. sativa*)	35_1359	179.63	TIPGYGGGMSSAK	Harvest Hv	Metabolism	27258
I	1	2	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	136.3	AVSGEGSSSGLPIDLR	Harvest Hv	Metabolism	850
I	1	2	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	159.52	YAGSSNWTVK	Harvest Hv	Metabolism	9040
I	2	6	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	193.16	IPGYGGGMSSAK	Harvest Hv	Metabolism	3723
I	2	6	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	193.16	SGYLAAISASSYSFVSLLK	Harvest Hv	Metabolism	14431
I	2	6	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	193.16	INLALGAGSFASCPR	Harvest Hv	Metabolism	16052
I	2	6	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	193.16	AVSGEGSSSGLPIDLR	Harvest Hv	Metabolism	16979
I	2	8	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	390.45	TIPGYGGGMSSAK	Harvest Hv	Metabolism	544

I	2	8	Enoyl ACP reductase precursor (*O. sativa*)	35_1360	390.45	AVSGEGSSSGLPIDLR	Harvest Hv	Metabolism	1687
I	1	2	OSJNBb0006N15 8 protein (*O. sativa*)	35_13701	93.29	VLTVISQK	Harvest Hv	Protein synthesis	1238
I	1	2	OSJNBb0006N15 8 protein (*O. sativa*)	35_13701	90.44	LTVISQK	Harvest Hv	Protein synthesis	1376
I	1	2	OSJNBb0006N15 8 protein (*O. sativa*)	35_13701	93.29	TELQGQLK	Harvest Hv	Protein synthesis	4561
I	2	2	OSJNBb0006N15 8 protein (*O. sativa*)	35_13701	114.8	LLPLDLRPK	Harvest Hv	Protein synthesis	945
I	2	2	OSJNBb0006N15 8 protein (*O. sativa*)	35_13701	114.8	TELQGQLK	Harvest Hv	Protein synthesis	1462
I	2	2	OSJNBb0006N15 8 protein (*O. sativa*)	35_13701	114.8	PLDLRPK	Harvest Hv	Protein synthesis	1471
I	1	2	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	149.55	YTSLKPLGDR	Harvest Hv	Protein destination	5725
I	1	2	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	121.35	LSAAEEK	Harvest Hv	Protein destination	9326
I	1	5	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	149.55	TIGGILLPSSAQSKPQGGEIVAVGGGR	Harvest Hv	Protein destination	8392
I	2	4	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	140.69	TIGGILLPSSAQSKPQGGEIVAVGGGR	Harvest Hv	Protein destination	3532
I	2	8	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	156.39	YAGTEVEYNNSK	Harvest Hv	Protein destination	2305
I	2	8	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	156.39	LSQTSAVRVCSSR	Harvest Hv	Protein destination	2508
I	2	8	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	156.39	TEAGLILTETTK	Harvest Hv	Protein destination	2618
I	2	8	Putative 20 kDa chaperonin (*O. sativa*)	35_1423	156.39	YTSLKPLGDR	Harvest Hv	Protein destination	6633
I	1	2	Putative chaperonin 21 (*O. sativa*)	35_1424	126.97	QPLSVSPGSTVLYSK	Harvest Hv	Protein destination	663
I	1	2	Putative chaperonin 21 (*O. sativa*)	35_1424	126.97	TEAGLILTETTK	Harvest Hv	Protein destination	2078
I	1	2	Putative chaperonin 21 (*O. sativa*)	35_1424	103.99	KVEVSIPTGSQVVYSK	Harvest Hv	Protein destination	6893
I	1	5	Putative chaperonin 21 (*O. sativa*)	35_1424	126.97	GTDGTNYIVLR	Harvest Hv	Protein destination	1953
I	2	2	Putative chaperonin 21 (*O. sativa*)	35_1424	116.62	EDDIIGILESDDVK	Harvest Hv	Protein destination	1267
I	2	2	Putative chaperonin 21 (*O. sativa*)	35_1424	116.62	GTDGTNYIVLR	Harvest Hv	Protein destination	3776
I	2	2	Putative chaperonin 21 (*O. sativa*)	35_1424	116.62	KVEVSIPTGSQVVYSK	Harvest Hv	Protein destination	7352
I	2	7	Putative chaperonin 21 (*O. sativa*)	35_1424	103.78	GTDGTNYIVLR	Harvest Hv	Protein destination	1891
I	2	8	Putative chaperonin 21 (*O. sativa*)	35_1424	180.96	EKPSIGTVVAVGPGSLDEEGNR	Harvest Hv	Protein destination	6245
I	1	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	248.26	AEEAAAGASEGLSEFQK	Harvest Hv	Protein destination	10070
I	1	5	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	338.67	VATSVLEKTWKPK	Harvest Hv	Protein destination	7264
I	2	6	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	217.48	AEEAAAGASEGLSEFQK	Harvest Hv	Protein destination	14564
I	2	6	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	217.48	ANFLSADDFEPALIPSK	Harvest Hv	Protein destination	17691
I	2	6	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	217.48	SDGHEDYGLLVSEPAR	Harvest Hv	Protein destination	22906
I	2	8	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	248.9	ILVDGVEK	Harvest Hv	Protein destination	3713
I	2	8	OSJNBb0012E08 10 protein (*O. sativa*)	35_14270	248.9	SPPSVPYDK	Harvest Hv	Protein destination	7211
I	1	2	40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411	405.03	LVTPLTLQR	Harvest Hv	Protein synthesis	140
I	1	4	40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411	405.03	ISQEVVGDLLGEEFK	Harvest Hv	Protein synthesis	51
I	1	4	40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411	405.03	LNIANPTTGCQK	Harvest Hv	Protein synthesis	833
I	2	8	40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411	129.39	LVTPLTLQR	Harvest Hv	Protein synthesis	821
I	2	8	40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411	129.39	LNIANPTTGCQK	Harvest Hv	Protein synthesis	1195
I	2	8	40S ribosomal protein S6 1 (*Magnoliophyta*)	35_14411	129.39	KGENDLPGLTDTEKPR	Harvest Hv	Protein synthesis	8060

I	1	2	40S ribosomal protein S4 (*Z. mays*)	35_14431	95.31	LNAPSHWMLDK	Harvest Hv	Protein synthesis	5174
I	1	2	40S ribosomal protein S4 (*Z. mays*)	35_14431	95.31	RLNAPSHWMLDK	Harvest Hv	Protein synthesis	12967
I	1	2	40S ribosomal protein S4 (*Z. mays*)	35_14431	95.31	LGNVFTIGK	Harvest Hv	Protein synthesis	14543
I	1	2	40S ribosomal protein S4 (*Z. mays*)	35_14431	95.31	GNVFTIGK	Harvest Hv	Protein synthesis	53144
I	1	5	40S ribosomal protein S4 (*Z. mays*)	35_14431	236.25	GTKPWVSLPK	Harvest Hv	Protein synthesis	2840
I	2	6	40S ribosomal protein S4 (*Z. mays*)	35_14431	220.52	SVQFGQK	Harvest Hv	Protein synthesis	8256
I	2	6	40S ribosomal protein S4 (*Z. mays*)	35_14431	220.52	ECLPLILILR	Harvest Hv	Protein synthesis	10723
I	2	6	40S ribosomal protein S4 (*Z. mays*)	35_14431	220.52	GIPYLNTYDGR	Harvest Hv	Protein synthesis	25620
I	2	6	40S ribosomal protein S4 (*Z. mays*)	35_14431	220.52	GTFETIHVEDAQGHQFATR	Harvest Hv	Protein synthesis	30556
I	2	6	40S ribosomal protein S4 (*Z. mays*)	35_14431	220.52	EVQSILMQR	Harvest Hv	Protein synthesis	33844
I	2	8	40S ribosomal protein S4 (*Z. mays*)	35_14431	178.73	EVQSILMQR	Harvest Hv	Protein synthesis	765
I	2	8	40S ribosomal protein S4 (*Z. mays*)	35_14431	178.73	LTIIEEQR	Harvest Hv	Protein synthesis	3364
I	2	8	40S ribosomal protein S4 (*Z. mays*)	35_14431	178.73	TYPAGFMDIISIPK	Harvest Hv	Protein synthesis	3736
I	2	8	40S ribosomal protein S4 (*Z. mays*)	35_14431	178.73	GIPYLNTYDGR	Harvest Hv	Protein synthesis	7589
I	2	8	40S ribosomal protein S4 (*Z. mays*)	35_14431	178.73	GTFETIHVEDAQGHQFATR	Harvest Hv	Protein synthesis	16871
I	1	2	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	212.96	GVNPDEAVAFGAAVQGSILSGEGGDETK	Harvest Hv	Unclassified	7485
I	1	2	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	115.51	EALEWLDENQTAEK	Harvest Hv	Unclassified	10691
I	1	4	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	443.15	ITPSWVGFTDGER	Harvest Hv	Unclassified	660
I	1	5	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	443.15	IINEPTAAAIAYGLDKR	Harvest Hv	Unclassified	2928
I	1	5	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	212.96	LKEVEAVCNPIVSAVYQR	Harvest Hv	Unclassified	7207
I	2	2	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	655.38	ITPSWVGFTDGER	Harvest Hv	Unclassified	834
I	2	2	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	655.38	VFSPEEVSAMILGK	Harvest Hv	Unclassified	1246
I	2	6	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	431.5	NQLETYVYNMK	Harvest Hv	Unclassified	10857
I	2	6	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	431.5	GTPQIEVTFEVDANGILNVK	Harvest Hv	Unclassified	15741
I	2	6	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	431.5	EAEEFAEEDKK	Harvest Hv	Unclassified	20313
I	2	6	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	431.5	VFSPEEVSAMILGK	Harvest Hv	Unclassified	29349
I	2	6	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	431.5	NQAAVNPER	Harvest Hv	Unclassified	31976
I	2	6	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	431.5	EGKPYIQVK	Harvest Hv	Unclassified	32317
I	2	8	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	615.47	IMDYFIK	Harvest Hv	Unclassified	827
I	2	8	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	615.47	FDLSGIPAAPR	Harvest Hv	Unclassified	14174
I	2	8	Luminal binding protein 3 precursor (*Magnoliophyta*)	35_14470	615.47	ITPSWVGFTDGER	Harvest Hv	Unclassified	21628
I	1	2	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	173.88	DLILSVMSAMGEEQICAVK	Harvest Hv	Protein synthesis	1640
I	1	3	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	173.88	LPTDDVLLGQIK	Harvest Hv	Protein synthesis	441
I	1	3	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	149.30	KLEDIVPSSHNCDVPHVDR	Harvest Hv	Protein synthesis	8766
I	1	5	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	173.88	DDLKLPTDDVLLGQIK	Harvest Hv	Protein synthesis	896
I	1	5	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	173.88	TFPQQAGAIR	Harvest Hv	Protein synthesis	5398
I	2	4	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	182.71	DLILSVMSAMGEEQICAVK	Harvest Hv	Protein synthesis	15291

I	2	4	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	182.71	KLEDIVPSSHNCDVPHVDR	Harvest Hv	Protein synthesis	27652
I	2	6	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	167.58	TFPQQAGAIR	Harvest Hv	Protein synthesis	13882
I	2	6	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	167.58	LEDIVPSSHNCDVPHVDR	Harvest Hv	Protein synthesis	32571
I	2	6	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	167.58	CHFVAIDIFNGK	Harvest Hv	Protein synthesis	32827
I	2	7	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	161.39	TFPQQAGAIR	Harvest Hv	Protein synthesis	219
I	2	7	Eukaryotic translation initiation factor 5A1 (*T. aestivum*)	35_14477	161.39	DDLKLPTDDVLLGQIK	Harvest Hv	Protein synthesis	1318
I	1	5	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	248.1	HQLITATVADGK	Harvest Hv	Energy metabolism	1517
I	1	5	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	248.1	TDSEGGFESDAVATANVLESSAPVVDGK	Harvest Hv	Energy metabolism	2385
I	2	2	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	94.27	QYYSITVLTR	Harvest Hv	Energy metabolism	10896
I	2	4	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	212.41	TITDYGSPEEFLSQVGFLLGQQSYGGK	Harvest Hv	Energy metabolism	2839
I	2	4	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	212.41	TDSEGGFESDAVATANVLESSAPVVDGK	Harvest Hv	Energy metabolism	3559
I	2	4	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	212.41	NTDFVAYSGEGFK	Harvest Hv	Energy metabolism	12500
I	2	8	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	236.92	KNTDFVAYSGEGFK	Harvest Hv	Energy metabolism	5491
I	2	8	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	236.92	EFPGQVLR	Harvest Hv	Energy metabolism	9120
I	2	8	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	236.92	HQLITATVADGK	Harvest Hv	Energy metabolism	12214
I	2	8	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	236.92	KTITDYGSPEEFLSQVGFLLGQQSYGGK	Harvest Hv	Energy metabolism	20777
I	2	8	Oxygen evolving enhancer protein 2 (*T. aestivum*)	35_14635	236.92	TADGDEGGKHQLITATVADGK	Harvest Hv	Energy metabolism	50092
I	1	2	Ribosomal protein L11 (*T. aestivum*)	35_14636	131.96	IACYVTIR	Harvest Hv	Protein synthesis	81
I	1	2	Ribosomal protein L11 (*T. aestivum*)	35_14636	106.26	NFSDTGCFGFGIQEHIDLGMK	Harvest Hv	Protein synthesis	7977
I	1	2	Ribosomal protein L11 (*T. aestivum*)	35_14636	106.26	LVLNISVGESGDR	Harvest Hv	Protein synthesis	8835
I	2	6	Ribosomal protein L11 (*T. aestivum*)	35_14636	158.37	AMQLLESGLK	Harvest Hv	Protein synthesis	8560
I	2	6	Ribosomal protein L11 (*T. aestivum*)	35_14636	158.37	IACYVTIR	Harvest Hv	Protein synthesis	22682
I	2	6	Ribosomal protein L11 (*T. aestivum*)	35_14636	158.37	YEGVILNKSHAS	Harvest Hv	Protein synthesis	23567
I	2	6	Ribosomal protein L11 (*T. aestivum*)	35_14636	158.37	VLEQLSGQSPVFSK	Harvest Hv	Protein synthesis	30033
I	2	8	Ribosomal protein L11 (*T. aestivum*)	35_14636	133.41	VLEQLSGQSPVFSK	Harvest Hv	Protein synthesis	817
I	2	8	Ribosomal protein L11 (*T. aestivum*)	35_14636	133.41	IACYVTIR	Harvest Hv	Protein synthesis	1016
I	1	1	Calreticulin like protein (*T. aestivum*)	35_14693	76.45	PDPEDVKPEGYDDIPK	Harvest Hv	Protein destination	43601
I	1	5	Calreticulin like protein (*T. aestivum*)	35_14693	308.23	TFAEETWAK	Harvest Hv	Protein destination	597
I	1	5	Calreticulin like protein (*T. aestivum*)	35_14693	172.44	KPEDWDDEEDGEWTAPTIPNPEYK	Harvest Hv	Protein destination	3983
I	1	5	Calreticulin like protein (*T. aestivum*)	35_14693	172.44	FGGDTPYSIMFGPDICGYSTK	Harvest Hv	Protein destination	4157
I	1	5	Calreticulin like protein (*T. aestivum*)	35_14693	76.45	KPEDWDDKEYIPDPEDVKPEGYDDIPK	Harvest Hv	Protein destination	16099
I	2	4	Calreticulin like protein (*T. aestivum*)	35_14693	544	AGEDDDDLDDEDADDEDKDDK	Harvest Hv	Protein destination	972
I	2	4	Calreticulin like protein (*T. aestivum*)	35_14693	544	TLVLQFTVK	Harvest Hv	Protein destination	15486
I	2	4	Calreticulin like protein (*T. aestivum*)	35_14693	544	KPEDWDDKEYIPDPEDVKPEGYDDIPK	Harvest Hv	Protein destination	49792
I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	AAFDEAEKK	Harvest Hv	Protein destination	5376
I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	APMIANPDFQDDPYIYAFDSLK	Harvest Hv	Protein destination	6622
I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	IKNPNYQGK	Harvest Hv	Protein destination	7158

I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	LDCGGGYVK	Harvest Hv	Protein destination	18659
I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	LLGGDVDQK	Harvest Hv	Protein destination	21886
I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	KDENMAGEWNHTSGK	Harvest Hv	Protein destination	29144
I	2	6	Calreticulin like protein (*T. aestivum*)	35_14693	246.84	FGGDTPYSIMFGPDICGYSTK	Harvest Hv	Protein destination	30209
I	2	7	Calreticulin like protein (*T. aestivum*)	35_14693	1092.37	APMIANPDFQDDPYIYAFDSLK	Harvest Hv	Protein destination	686
I	2	7	Calreticulin like protein (*T. aestivum*)	35_14693	1092.37	SGTLFDNILITDDAALAK	Harvest Hv	Protein destination	892
I	2	7	Calreticulin like protein (*T. aestivum*)	35_14693	1092.37	TFAEETWAK	Harvest Hv	Protein destination	1282
I	2	8	Calreticulin like protein (*T. aestivum*)	35_14693	480.43	APPPPPEMAIR	Harvest Hv	Protein destination	3682
I	2	8	Calreticulin like protein (*T. aestivum*)	35_14693	480.43	TFAEETWAK	Harvest Hv	Protein destination	16530
I	2	8	Calreticulin like protein (*T. aestivum*)	35_14693	480.43	LLSLDWCVRAPPPPPEMAIR	Harvest Hv	Protein destination	20260
I	2	8	Calreticulin like protein (*T. aestivum*)	35_14693	480.43	KFGGDTPYSIMFGPDICGYSTK	Harvest Hv	Protein destination	27849
I	2	8	Calreticulin like protein (*T. aestivum*)	35_14693	480.43	DVPCETDQLSHVYTLIIRPDATYSILIDNEEK	Harvest Hv	Protein destination	28175
I	2	8	Calreticulin like protein (*T. aestivum*)	35_14693	480.43	AGEDDDDLDDEDADDEDKDDK	Harvest Hv	Protein destination	28439
I	1	2	Ribosomal protein L10A (*T. aestivum*)	35_14911	116.08	EAITQVVADAK	Harvest Hv	Protein synthesis	883
I	1	2	Ribosomal protein L10A (*T. aestivum*)	35_14911	116.08	VCMLGDAQHVGEAEK	Harvest Hv	Protein synthesis	2174
I	2	2	Ribosomal protein L10A (*T. aestivum*)	35_14911	162.81	EAITQVVADAK	Harvest Hv	Protein synthesis	399
I	2	6	Ribosomal protein L10A (*T. aestivum*)	35_14911	215.73	EAITQVVADAK	Harvest Hv	Protein synthesis	11997
I	2	6	Ribosomal protein L10A (*T. aestivum*)	35_14911	215.73	KVLCMGVAVGNLSMEEK	Harvest Hv	Protein synthesis	24045
I	2	6	Ribosomal protein L10A (*T. aestivum*)	35_14911	215.73	VCMLGDAQHVGEAEK	Harvest Hv	Protein synthesis	31656
I	2	6	Ribosomal protein L10A (*T. aestivum*)	35_14911	215.73	VLCMGVAVGNLSMEEK	Harvest Hv	Protein synthesis	35850
I	1	2	Putative cytochrome b5 (*O. sativa*)	35_14940	139.4	DATDDFEDVGHSTTAR	Harvest Hv	Unclassified	4440
I	1	2	Putative cytochrome b5 (*O. sativa*)	35_14940	139.4	VFTLEEVAK	Harvest Hv	Unclassified	5757
I	1	2	Putative cytochrome b5 (*O. sativa*)	35_14940	139.4	FLDDHPGGDDVLLSSTAK	Harvest Hv	Unclassified	9030
I	2	2	Putative cytochrome b5 (*O. sativa*)	35_14940	210.12	VFTLEEVAK	Harvest Hv	Unclassified	1550
I	2	8	Putative cytochrome b5 (*O. sativa*)	35_14940	122.66	DDCWLVIAGK	Harvest Hv	Unclassified	3968
I	2	8	Putative cytochrome b5 (*O. sativa*)	35_14940	122.66	VFTLEEVAK	Harvest Hv	Unclassified	7272
I	1	2	Oxygen evolving complex (*T. aestivum*)	35_14958	176.81	ESAQDILNLKPLIDK	Harvest Hv	Energy metabolism	4250
I	1	2	Oxygen evolving complex (*T. aestivum*)	35_14958	176.81	ESAQDILNLKPLIDK	Harvest Hv	Energy metabolism	9068
I	1	2	Oxygen evolving complex (*T. aestivum*)	35_14958	141.53	ESAQDILNLKPLIDKK	Harvest Hv	Energy metabolism	9964
I	1	5	Oxygen evolving complex (*T. aestivum*)	35_14958	176.81	FYLQPLPPAQAAVR	Harvest Hv	Energy metabolism	2622
I	1	5	Oxygen evolving complex (*T. aestivum*)	35_14958	176.81	VGPPPPLSGGLPGTDNSDEAR	Harvest Hv	Energy metabolism	4152
I	2	4	Oxygen evolving complex (*T. aestivum*)	35_14958	149.18	TVLGDVLAK	Harvest Hv	Energy metabolism	325
I	2	4	Oxygen evolving complex (*T. aestivum*)	35_14958	149.18	FYLQPLPPAQAAVR	Harvest Hv	Energy metabolism	1332
I	2	4	Oxygen evolving complex (*T. aestivum*)	35_14958	149.18	ESAQDILNLKPLIDK	Harvest Hv	Energy metabolism	3197
I	1	2	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	845.24	ESVGIRPGK	Harvest Hv	Protein synthesis	5285
I	1	3	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	845.24	IEGVPEFPLVVSDSAEGIEK	Harvest Hv	Protein synthesis	71
I	1	3	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	845.24	VLEQLGAFADAEK	Harvest Hv	Protein synthesis	824

I	1	5	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	269.24	LNLLDLAPGGHLGR	Harvest Hv	Protein synthesis	7122
I	1	5	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	269.24	WLGVSQ	Harvest Hv	Protein synthesis	12430
I	2	4	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	113.13	ALEGDMATDAAGVPMPHVMTAPIRPDVITFVHR	Harvest Hv	Protein synthesis	49925
I	2	7	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	709.46	IEGVPEFPLVVSDSAEGIEK	Harvest Hv	Protein synthesis	29
I	2	7	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	709.46	VLEQLGAFADAEK	Harvest Hv	Protein synthesis	1837
I	2	8	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	241.19	MTNADLGR	Harvest Hv	Protein synthesis	2819
I	2	8	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	241.19	MAVLAEAAR	Harvest Hv	Protein synthesis	15577
I	2	8	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	241.19	LSAEEASK	Harvest Hv	Protein synthesis	16455
I	1	2	60S ribosomal protein L13 (*A. thaliana*)	35_15048	68.71	TWFNQPAR	Harvest Hv	Protein synthesis	2469
I	1	2	60S ribosomal protein L13 (*A. thaliana*)	35_15048	68.71	AFKAYGK	Harvest Hv	Protein synthesis	2706
I	1	2	60S ribosomal protein L13 (*A. thaliana*)	35_15048	68.71	AGDSTPEELATATQVQGDYMPITR	Harvest Hv	Protein synthesis	3781
I	1	2	60S ribosomal protein L13 (*A. thaliana*)	35_15048	68.71	GFTLEELK	Harvest Hv	Protein synthesis	24948
I	2	6	60S ribosomal protein L13 (*A. thaliana*)	35_15048	125.6	SLEGMQSNIQR	Harvest Hv	Protein synthesis	16182
I	2	6	60S ribosomal protein L13 (*A. thaliana*)	35_15048	125.6	AGDSTPEELATATQVQGDYMPITRGEK	Harvest Hv	Protein synthesis	30696
I	1	2	Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515	87.65	LVAEAAR	Harvest Hv	Unclassified	650
I	1	2	Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515	87.65	VAAASADILDSAAK	Harvest Hv	Unclassified	9548
I	2	8	Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515	238.88	TDAPAAADAPKPDAPK	Harvest Hv	Unclassified	2414
I	2	8	Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515	238.88	SSDGFGLDDVMK	Harvest Hv	Unclassified	8389
I	2	8	Hypothetical protein OSJNBb0008A05 1 (*O. sativa*)	35_1515	238.88	LEDKPVGQYLEK	Harvest Hv	Unclassified	14132
I	1	2	Nuclear transport factor 2 (*O. sativa*)	35_15374	106.86	LGSLPFQQCQHK	Harvest Hv	Transport	1293
I	1	2	Nuclear transport factor 2 (*O. sativa*)	35_15374	106.86	PFQQCQHK	Harvest Hv	Transport	3526
I	1	2	Nuclear transport factor 2 (*O. sativa*)	35_15374	106.86	FSQMFHLLPAGGSFYVQNDMFR	Harvest Hv	Transport	4471
I	1	2	Nuclear transport factor 2 (*O. sativa*)	35_15374	106.86	LGSLPFQQCQHK	Harvest Hv	Transport	7708
I	1	2	Nuclear transport factor 2 (*O. sativa*)	35_15374	106.86	AALVGLYQDGSMLTFEGEK	Harvest Hv	Transport	10113
I	1	2	Nuclear transport factor 2 (*O. sativa*)	35_15374	106.86	AFVQHYYQTFDSNR	Harvest Hv	Transport	13878
I	2	8	Nuclear transport factor 2 (*O. sativa*)	35_15374	115.19	LGSLPFQQCQHK	Harvest Hv	Transport	915
I	2	8	Nuclear transport factor 2 (*O. sativa*)	35_15374	115.19	FGGPAAIAGK	Harvest Hv	Transport	2663
I	2	8	Nuclear transport factor 2 (*O. sativa*)	35_15374	115.19	AFVQHYYQTFDSNR	Harvest Hv	Transport	17532
I	1	2	Putative stress related like protein interactor (*O. sativa*)	35_1563	106.11	IATLQSEITSLQK	Harvest Hv	Unclassified	2359
I	1	2	Putative stress related like protein interactor (*O. sativa*)	35_1563	106.11	ISALESDIADR	Harvest Hv	Unclassified	3606
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	TGSVAAEEQAGK	Harvest Hv	Unclassified	10014
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	TGSVAAEEQAGKAIAR	Harvest Hv	Unclassified	14972
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	EISDPYFQEAK	Harvest Hv	Unclassified	15663
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	EIEAQSSQR	Harvest Hv	Unclassified	16653
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	FKEISDPYFQEAK	Harvest Hv	Unclassified	24928
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	QAQATISDYLHQHEITK	Harvest Hv	Unclassified	28979

I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	NEGFWVTGGGDMGISR	Harvest Hv	Unclassified	31321
I	2	6	Putative stress related like protein interactor (*O. sativa*)	35_1563	245.12	ISKPYIDQVAEVTKPHVEK	Harvest Hv	Unclassified	32020
I	2	8	Putative stress related like protein interactor (*O. sativa*)	35_1563	251.7	EISDPYFQEAK	Harvest Hv	Unclassified	276
I	2	8	Putative stress related like protein interactor (*O. sativa*)	35_1563	251.7	VAEEELMR	Harvest Hv	Unclassified	1166
I	2	8	Putative stress related like protein interactor (*O. sativa*)	35_1563	251.7	IATLQSEITSLQK	Harvest Hv	Unclassified	1580
I	2	8	Putative stress related like protein interactor (*O. sativa*)	35_1563	251.7	LQLEASTK	Harvest Hv	Unclassified	2179
I	2	8	Putative stress related like protein interactor (*O. sativa*)	35_1563	251.7	TPVDNSLR	Harvest Hv	Unclassified	2659
I	1	2	Ankyrin domain protein (*N. tabacum*)	35_15734	99.46	IKDDPSLKPILDEIER	Harvest Hv	Unclassified	9999
I	1	2	Ankyrin domain protein (*N. tabacum*)	35_15734	99.46	NTPLHYAAGYGR	Harvest Hv	Unclassified	47583
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	SAQGTGEQGVPSLDPQAYLETMTK	Harvest Hv	Unclassified	201
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	YWNDPEILQK	Harvest Hv	Unclassified	1281
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	EMAEQIASDPVFNQMAEQLQK	Harvest Hv	Unclassified	1495
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	VMQNPQFMSMAER	Harvest Hv	Unclassified	2327
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	ALDGGANKDEEDVEGR	Harvest Hv	Unclassified	3462
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	SEGLAAGAGLPSPFDFSNMSSLLNDPSIR	Harvest Hv	Unclassified	4410
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	LGNSLMQDPAMSSMLENLTSPAHK	Harvest Hv	Unclassified	10995
I	2	8	Ankyrin domain protein (*N. tabacum*)	35_15734	708.92	HGAAVMLQNLDGK	Harvest Hv	Unclassified	22017
I	1	2	Eukaryotic initiation factor (*T. aestivum*)	35_15745	89.54	ELVANPQLTPR	Harvest Hv	Protein synthesis	442
I	1	2	Eukaryotic initiation factor (*T. aestivum*)	35_15745	89.54	IPSSINKPSPINPR	Harvest Hv	Protein synthesis	3890
I	1	2	Eukaryotic initiation factor (*T. aestivum*)	35_15745	89.54	FMVRDLIDLR	Harvest Hv	Protein synthesis	6128
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	AKTISEIHTEAEK	Harvest Hv	Protein synthesis	3721
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	ELLGSDK	Harvest Hv	Protein synthesis	3945
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	NAPGGPLSPGGFSVNRPGTGGMMPGMPGSRK	Harvest Hv	Protein synthesis	11106
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	NGRNAPGGPLSPGGFSVNRPGTGGMMPGMPGSR	Harvest Hv	Protein synthesis	30148
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	NAPGGPLSPGGFSVNRPGTGGMMPGMPGSR	Harvest Hv	Protein synthesis	30281
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	ELVANPQLTPR	Harvest Hv	Protein synthesis	30475
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	KACPDEEHVEAICQFFNTIGK	Harvest Hv	Protein synthesis	30730
I	2	6	Eukaryotic initiation factor (*T. aestivum*)	35_15745	161.76	VLLNNCQEAFEGADSLR	Harvest Hv	Protein synthesis	36468
I	1	2	Putative p23 co chaperone (*O. sativa*)	35_15864	312.28	SIFCILEK	Harvest Hv	Unclassified	2906
I	1	4	Putative p23 co chaperone (*O. sativa*)	35_15864	312.28	VYITVQLPDAK	Harvest Hv	Unclassified	66
I	1	4	Putative p23 co chaperone (*O. sativa*)	35_15864	312.28	ADAAQISQEVEGK	Harvest Hv	Unclassified	323
I	2	4	Putative p23 co chaperone (*O. sativa*)	35_15864	215.94	VNLEPDGVFSFFATAGTDGNSYESK	Harvest Hv	Unclassified	3741
I	2	7	Putative p23 co chaperone (*O. sativa*)	35_15864	368.23	SIFCILEK	Harvest Hv	Unclassified	967
I	2	7	Putative p23 co chaperone (*O. sativa*)	35_15864	368.23	ADAAQISQEVEGK	Harvest Hv	Unclassified	3095

I	2	7	Putative p23 co chaperone (*O. sativa*)	35_15864	368.23	VYITVQLPDAK	Harvest Hv	Unclassified	3149
I	1	2	Putative plastid protein (*O. sativa*)	35_15958	120.42	WVLPDSYLDVR	Harvest Hv	Unclassified	3603
I	1	2	Putative plastid protein (*O. sativa*)	35_15958	120.42	TLAQVVGSEDEAR	Harvest Hv	Unclassified	5274
I	2	8	Putative plastid protein (*O. sativa*)	35_15958	91.99	WVLPDSYLDVR	Harvest Hv	Unclassified	3786
I	2	8	Putative plastid protein (*O. sativa*)	35_15958	91.99	TLAQVVGSEDEAR	Harvest Hv	Unclassified	7115
I	1	2	Putative nucleic acid binding protein (*O. sativa*)	35_16721	123.26	LVVPGAQAINLIGK	Harvest Hv	Unclassified	1991
I	1	2	Putative nucleic acid binding protein (*O. sativa*)	35_16721	123.26	DEYVLPMKR	Harvest Hv	Unclassified	4667
I	1	2	Putative nucleic acid binding protein (*O. sativa*)	35_16721	123.26	VLEGPVGATER	Harvest Hv	Unclassified	5556
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	EDPGLELPPAMDALIR	Harvest Hv	Unclassified	184
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	LVVPGAQAINLIGK	Harvest Hv	Unclassified	278
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	VLEGPVGATER	Harvest Hv	Unclassified	1293
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	AIQEGTGATIR	Harvest Hv	Unclassified	5474
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	MVVPVLK	Harvest Hv	Unclassified	6278
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	SSYAGLDPLYR	Harvest Hv	Unclassified	6314
I	2	8	Putative nucleic acid binding protein (*O. sativa*)	35_16721	185.4	GTSSQVQSAQQLIQDSLAAHR	Harvest Hv	Unclassified	14615
I	1	2	Putative Hsp70 binding protein (*O. sativa*)	35_16911	115.47	AAEVVSTVVQNNPK	Harvest Hv	Unclassified	2461
I	1	2	Putative Hsp70 binding protein (*O. sativa*)	35_16911	115.47	SVAEEIGLPNQLIHLASSEDSGVR	Harvest Hv	Unclassified	2858
I	1	2	Putative Hsp70 binding protein (*O. sativa*)	35_16911	115.47	WSLAHGADGTNPPR	Harvest Hv	Unclassified	6422
I	1	2	Putative Hsp70 binding protein (*O. sativa*)	35_16911	148.88	SVAEEIGLPNQLIHLASSEDSGVR	Harvest Hv	Unclassified	10343
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	AAEVVSTVVQNNPK	Harvest Hv	Unclassified	128
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	GLVVLPGEDEPQQPPPDVAGK	Harvest Hv	Unclassified	1778
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	ECYGEPSSLR	Harvest Hv	Unclassified	2062
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	IEGISTMDADDLQAAR	Harvest Hv	Unclassified	2517
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	EAALGGLLELAR	Harvest Hv	Unclassified	4164
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	WSLAHGADGTNPPR	Harvest Hv	Unclassified	6902
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	MFEPPLR	Harvest Hv	Unclassified	7936
I	2	8	Putative Hsp70 binding protein (*O. sativa*)	35_16911	247.13	SVAEEIGLPNQLIHLASSEDSGVR	Harvest Hv	Unclassified	8131
I	1	2	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	172.19	QLLQNPSLPK	Harvest Hv	Protein destination	1620
I	1	2	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	172.19	ATYNQCIER	Harvest Hv	Protein destination	3072
I	1	2	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	106.52	NLHAVDPSSPLFK	Harvest Hv	Protein destination	8023
I	2	8	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	671.96	QLLQNPSLPK	Harvest Hv	Protein destination	1795
I	2	8	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	671.96	ATYNQCIER	Harvest Hv	Protein destination	2497
I	2	8	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	671.96	GQPMLDLCTK	Harvest Hv	Protein destination	2710
I	2	8	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	671.96	DCTDAVAAIDDCTR	Harvest Hv	Protein destination	6563
I	2	8	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	671.96	NLHAVDPSSPLFK	Harvest Hv	Protein destination	7238
I	2	8	Hypothetical protein P0473D02 34 (*O. sativa*)	35_17703	671.96	NNAIGQALYSCNFSTFFK	Harvest Hv	Protein destination	14013
I	1	1	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	161.54	NVLHAMYCILNK	Harvest Hv	Transport	47871

I	1	2	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	161.54	AIEHFTYDTAK	Harvest Hv	Transport	2997
I	1	2	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	161.54	ARPADDVAHQLAAAGDAGVQQAQK	Harvest Hv	Transport	10158
I	1	2	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	162.95	KYLTPEAGEPAK	Harvest Hv	Transport	19471
I	2	6	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	505.66	AAHVSVLSSFLEMAAAMAATTMVTKNNGGSLAMDK	Harvest Hv	Transport	16677
I	2	6	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	505.66	ARPADDVAHQLAAAGDAGVQQAQKAK	Harvest Hv	Transport	28844
I	2	6	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	505.66	AAHVSVLSSFLEMAAAMAATTMVTKNNGGSLAMDK	Harvest Hv	Transport	30063
I	2	6	Plastidial ADP glucose transporter (*H. vulgare*)	35_17753	505.66	ASGKEEVGNVPTLLIGSAAGAIASTATFPLE	Harvest Hv	Transport	30103
I	1	2	Ubiquitin family protein (*O. sativa*)	35_1872	99.54	ALVAESCDVPAPQQR	Harvest Hv	Unclassified	1348
I	1	2	Ubiquitin family protein (*O. sativa*)	35_1872	99.54	NPDLAHVLNDPSILR	Harvest Hv	Unclassified	6412
I	2	8	Ubiquitin family protein (*O. sativa*)	35_1872	429.44	NMMESNTQMR	Harvest Hv	Unclassified	1839
I	2	8	Ubiquitin family protein (*O. sativa*)	35_1872	429.44	ADLGATVGEFK	Harvest Hv	Unclassified	2163
I	2	8	Ubiquitin family protein (*O. sativa*)	35_1872	429.44	YATQLAQLQEMGFFDPQENIR	Harvest Hv	Unclassified	7468
I	1	2	KH domain containing protein NOVA like (*O. sativa*)	35_2063	260.81	IIMVSGLFDEVVK	Harvest Hv	Unclassified	383
I	1	2	KH domain containing protein NOVA like (*O. sativa*)	35_2063	260.81	GGSTINDFQSQSGAR	Harvest Hv	Unclassified	496
I	1	2	KH domain containing protein NOVA like (*O. sativa*)	35_2063	260.81	LVTITGPLNSQMR	Harvest Hv	Unclassified	958
I	1	2	KH domain containing protein NOVA like (*O. sativa*)	35_2063	274.62	SPANNDAQESHTIGVADEHIGAVVGR	Harvest Hv	Unclassified	12667
I	2	8	KH domain containing protein NOVA like (*O. sativa*)	35_2063	116.23	LVVPNSSCGGIIGK	Harvest Hv	Unclassified	677
I	2	8	KH domain containing protein NOVA like (*O. sativa*)	35_2063	116.23	LVTITGPLNSQMR	Harvest Hv	Unclassified	1801
I	2	8	KH domain containing protein NOVA like (*O. sativa*)	35_2063	116.23	EKPTHLRFLVSNTAAGCIIGK	Harvest Hv	Unclassified	5919
I	2	8	KH domain containing protein NOVA like (*O. sativa*)	35_2063	116.23	SFIEDSHAGIK	Harvest Hv	Unclassified	11246
I	1	2	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	140.15	CYISLSEQVR	Harvest Hv	Cell wall	1027
I	1	2	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	140.15	YVFTIDDDCFVAK	Harvest Hv	Cell wall	1757
I	2	6	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	229.3	KYVFTIDDDCFVAK	Harvest Hv	Cell wall	15376
I	2	6	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	229.3	NLLSPSTPFFFNTLYD	Harvest Hv	Cell wall	23374
I	2	6	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	229.3	YVFTIDDDCFVAK	Harvest Hv	Cell wall	25079
I	2	6	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	229.3	EGAPTAVSHGLWLNIPDYDAPTQMVKPR	Harvest Hv	Cell wall	30327
I	2	6	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	229.3	QLIGPAMYFGLMGDGQPIGR	Harvest Hv	Cell wall	31696
I	2	8	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	131.61	YVDAVLTIPK	Harvest Hv	Cell wall	1964
I	2	8	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	131.61	YVFTIDDDCFVAK	Harvest Hv	Cell wall	3846
I	2	8	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	131.61	CYISLSEQVREK	Harvest Hv	Cell wall	4888
I	2	8	Alpha 1 4 glucan protein synthase UDP forming (*Z. mays*)	35_272	131.61	YVFTIDDDCFVAKDPSGK	Harvest Hv	Cell wall	6831
I	1	4	Histone H2A 2 1 (*T. aestivum*)	35_30953	423.33	HLLLAIR	Harvest Hv	DNA binding	4761
I	1	4	Histone H2A 2 1 (*T. aestivum*)	35_30953	254.01	LLSGVTIAHGGVIPNINPVLLPK	Harvest Hv	DNA binding	16362
I	1	10	Histone H2A 2 1 (*T. aestivum*)	35_30953	423.33	LLSGVTIAHGGVIPNINPVLLPK	Harvest Hv	DNA binding	7033
I	2	4	Histone H2A 2 1 (*T. aestivum*)	35_30953	267.46	LLSGVTIAHGGVIPNINPVLLPK	Harvest Hv	DNA binding	27625

I	2	4	Histone H2A 2 1 (*T. aestivum*)	35_30953	267.46	HLLLAIR	Harvest Hv	DNA binding	49947
I	2	5	Histone H2A 2 1 (*T. aestivum*)	35_30953	220.74	LLSGVTIAHGGVIPNINPVLLPK	Harvest Hv	DNA binding	10240
I	2	5	Histone H2A 2 1 (*T. aestivum*)	35_30953	220.74	HLLLAIR	Harvest Hv	DNA binding	14875
I	1	2	Os03g0129300 protein (*O. sativa*)	35_435	93.13	TGITADDVNAAFR	Harvest Hv	Energy metabolism	1350
I	1	2	Os03g0129300 protein (*O. sativa*)	35_435	93.13	GILDVCDEPLVSVDFR	Harvest Hv	Energy metabolism	2965
I	2	8	Os03g0129300 protein (*O. sativa*)	35_435	132.11	GILDVCDEPLVSVDFR	Harvest Hv	Energy metabolism	1939
I	2	8	Os03g0129300 protein (*O. sativa*)	35_435	132.11	WPGAGTGGSGDPLEDYCK	Harvest Hv	Energy metabolism	20305
I	2	8	Os03g0129300 protein (*O. sativa*)	35_435	132.11	ENSPLEVIVINDSGGVRNASHLLK	Harvest Hv	Energy metabolism	28448
I	1	2	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	142.14	GIGFVSNDVGLDADHCK	Harvest Hv	Metabolism	9228
I	1	2	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	170.85	VHTVLISTQHDETVTNDEIAADLK	Harvest Hv	Metabolism	10196
I	1	2	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	170.85	EHVIKPVIPEQYLDENTIFHLNPSGR	Harvest Hv	Metabolism	14416
I	2	6	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	175.9	KNATCPWLRPDGK	Harvest Hv	Metabolism	4109
I	2	6	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	175.9	LCDQISDAVLDACLAEDPDSK	Harvest Hv	Metabolism	5239
I	2	6	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	175.9	TQVTVEYHNDNGAMVPIR	Harvest Hv	Metabolism	21710
I	2	6	S adenosylmethionine synthetase 2 (*A. thaliana*)	35_443	175.9	RPEEIGAGDQGHMFGYATDETPEFMPLSH VLATK	Harvest Hv	Metabolism	31402
I	1	1	Luminal binding protein 3 (*Z. mays*)	35_47882	117.8	VFSPEEVSAMILGK	Harvest Hv	Unclassified	29756
I	1	1	Luminal binding protein 3 (*Z. mays*)	35_47882	117.8	LSQEEIDRMVK	Harvest Hv	Unclassified	39416
I	1	2	Luminal binding protein 3 (*Z. mays*)	35_47882	401.67	NEPTAAAIAYGLDKR	Harvest Hv	Unclassified	694
I	1	2	Luminal binding protein 3 (*Z. mays*)	35_47882	91.25	ALSNQHQVR	Harvest Hv	Unclassified	4964
I	1	2	Luminal binding protein 3 (*Z. mays*)	35_47882	91.25	GTPQIEVTFEVDANGILNVKAEDK	Harvest Hv	Unclassified	27661
I	1	2	Luminal binding protein 3 (*Z. mays*)	35_47882	91.25	ITPSWVGFTDGERLIGEAAK	Harvest Hv	Unclassified	47818
I	2	6	Luminal binding protein 3 (*Z. mays*)	35_47882	405.79	GVNPDEAVAFGAAVQGSILSGEGGDETK	Harvest Hv	Unclassified	11050
I	2	6	Luminal binding protein 3 (*Z. mays*)	35_47882	405.79	KLGTVIGIDLGTTYSCVGVYK	Harvest Hv	Unclassified	20209
I	2	6	Luminal binding protein 3 (*Z. mays*)	35_47882	405.79	GTPQIEVT	Harvest Hv	Unclassified	25818
I	1	2	Os02g0131700 (*O. sativa*)	35_698	81.27	SVYVGNVPQNVTEADLENEFKK	Harvest Hv	Unclassified	852
I	1	2	Os02g0131700 (*O. sativa*)	35_698	81.27	FGQLIPDGVAIR	Harvest Hv	Unclassified	2117
I	2	6	Os02g0131700 (*O. sativa*)	35_698	124.91	FGQLIPDGVAIR	Harvest Hv	Unclassified	6039
I	2	6	Os02g0131700 (*O. sativa*)	35_698	124.91	GYFVLNDYFHFVDQEQVQPAQVR	Harvest Hv	Unclassified	19473
I	2	6	Os02g0131700 (*O. sativa*)	35_698	124.91	FIQMFFLAPQEK	Harvest Hv	Unclassified	20425
I	2	6	Os02g0131700 (*O. sativa*)	35_698	124.91	QIYVEERKPNSGIR	Harvest Hv	Unclassified	26736
I	1	2	Salt tolerant protein (*T. aestivum*)	35_788	301.25	LVQRPCVPCK	Harvest Hv	Disease/Defence	738
I	1	5	Salt tolerant protein (*T. aestivum*)	35_788	301.25	VTVQVTDK	Harvest Hv	Disease/Defence	867
I	1	5	Salt tolerant protein (*T. aestivum*)	35_788	286.03	LVSYSVVDGELVSFYK	Harvest Hv	Disease/Defence	7110
I	2	5	Salt tolerant protein (*T. aestivum*)	35_788	670.05	ESTELFPK	Harvest Hv	Disease/Defence	310
I	2	5	Salt tolerant protein (*T. aestivum*)	35_788	670.05	VTVQVTDK	Harvest Hv	Disease/Defence	1693
I	2	5	Salt tolerant protein (*T. aestivum*)	35_788	670.05	LVSYSVVDGELVSFYK	Harvest Hv	Disease/Defence	2892

I	2	6	Salt tolerant protein (*T. aestivum*)	35_788	210.76	LVSYSVVDGELVSFYK	Harvest Hv	Disease/Defence	7343
I	2	6	Salt tolerant protein (*T. aestivum*)	35_788	210.76	VTVQVTDK	Harvest Hv	Disease/Defence	19211
I	2	6	Salt tolerant protein (*T. aestivum*)	35_788	210.76	GSADGVGAVVNWTMDFAGCRGR	Harvest Hv	Disease/Defence	29762
I	2	6	Salt tolerant protein (*T. aestivum*)	35_788	210.76	ESTELFPK	Harvest Hv	Disease/Defence	30164
I	2	6	Salt tolerant protein (*T. aestivum*)	35_788	210.76	VEVADDEK	Harvest Hv	Disease/Defence	31157
I	2	8	Salt tolerant protein (*T. aestivum*)	35_788	118.83	HSPHFTDQVAGK	Harvest Hv	Disease/Defence	8738
I	1	4	Os05g0373700 protein (*O. sativa*)	35_836	237.29	APDLSSVISNPEASTAAQEDDEDCDETGVEPK	Harvest Hv	Unclassified	80
I	1	4	Os05g0373700 protein (*O. sativa*)	35_836	237.29	SPASDTYVIFGEAK	Harvest Hv	Unclassified	502
I	1	6	Os05g0373700 protein (*O. sativa*)	35_836	237.29	LAAQVQGDEPVVEDDDDEEEEDDDDEDDKDDDAEGVDASGR	Harvest Hv	Unclassified	4188
I	2	5	Os05g0373700 protein (*O. sativa*)	35_836	627.55	IEDLSSQLQSQAAEQFK	Harvest Hv	Unclassified	73
I	2	5	Os05g0373700 protein (*O. sativa*)	35_836	627.55	SADGDIVSAIMELTN	Harvest Hv	Unclassified	453
I	2	7	Os05g0373700 protein (*O. sativa*)	35_836	359.65	LAAQVQGDEPVVEDDDDEEEEDDDDEDDKDDDAEGVDASGR	Harvest Hv	Unclassified	535
I	2	7	Os05g0373700 protein (*O. sativa*)	35_836	359.65	DIELVMTQAGVPRPK	Harvest Hv	Unclassified	3123
I	1	2	Histone H2B 5 (*O. sativa*)	A2WKT4	60.65	KPTITSR	Uniref 90	DNA binding	6159
I	1	2	Histone H2B 5 (*O. sativa*)	A2WKT4	60.65	LAAEAAK	Uniref 90	DNA binding	8984
I	1	10	Histone H2B 5 (*O. sativa*)	A2WKT4	104.31	LVLPGELAK	Uniref 90	DNA binding	26
I	2	5	Histone H2B 5 (*O. sativa*)	A2WKT4	316.3	QVHPDIGISSK	Uniref 90	DNA binding	776
I	2	5	Histone H2B 5 (*O. sativa*)	A2WKT4	316.3	GLAAWSGQGGGGELAWSR	Uniref 90	DNA binding	3853
I	2	3	Histone H2B 5 (*O. sativa*)	A2WKT4	259.04	AMSIMNSFINDIFEK	Uniref 90	DNA binding	5071
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2X7R0	146.92	TVELKPDWA	Uniref 90	Unclassfied	1778
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2X7R0	146.92	DFETAIQHYTK	Uniref 90	Unclassfied	3518
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2X7R0	146.92	TVELKPDWAK	Uniref 90	Unclassfied	6109
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2X7R0	146.92	VYSNRAACYTK	Uniref 90	Unclassfied	10258
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2X7R0	146.92	AMELDDEDISYLTNR	Uniref 90	Unclassfied	24856
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2X7R0	353.1	NPSSLNMYLSDPR	Uniref 90	Unclassfied	4235
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2X7R0	353.1	EVEPEPEPEPMEVTDEEKER	Uniref 90	Unclassfied	9676
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2X7R0	353.1	LGAMPEGLK	Uniref 90	Unclassfied	15846
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2X7R0	353.1	CIELDPTFSK	Uniref 90	Unclassfied	22028
I	1	1	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.97	NPYFGTAR	Uniref 90	Protein synthesis	37357
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2XMW9	385.16	LINSDEVQSVVKPINK	Uniref 90	Protein synthesis	4701
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.97	LNLLDLAPGGHLGR	Uniref 90	Protein synthesis	25129
I	1	5	Putative uncharacterized protein (*O. sativa*)	A2XMW9	267.6	LNLLDLAPGGHLGR	Uniref 90	Protein synthesis	7122
I	2	4	Putative uncharacterized protein (*O. sativa*)	A2XMW9	105.93	LNLLDLAPGGHLGR	Uniref 90	Protein synthesis	12564
I	2	7	Putative uncharacterized protein (*O. sativa*)	A2XMW9	184.51	NLPGVDVANVER	Uniref 90	Protein synthesis	3086

I	2	7	Putative uncharacterized protein (*O. sativa*)	A2XMW9	184.51	LNLLDLAPGGHLGR	Uniref 90	Protein synthesis	12817
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	GPLIVYGTEGSK	Uniref 90	Protein synthesis	216
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	LAQRGQIPSDALPGR	Uniref 90	Protein synthesis	3257
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	QIGAYADAEK	Uniref 90	Protein synthesis	3672
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	RAGHQTSAESWGTGR	Uniref 90	Protein synthesis	4012
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	AGHQTSAESWGTGR	Uniref 90	Protein synthesis	6302
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	GQIPSDALPGRTNK	Uniref 90	Protein synthesis	17702
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	AGQGAFGNMCR	Uniref 90	Protein synthesis	28681
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XMW9	156.81	ITAVPGLHLFGESQLGSSNPIGR	Uniref 90	Protein synthesis	51551
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2XZH4	148.89	AVFPSIVGRPR	Uniref 90	Unclassified	3393
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2XZH4	148.89	AGFAGDDAPR	Uniref 90	Unclassified	5062
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XZH4	227.42	SYELPDGQVITIGAER	Uniref 90	Unclassified	23
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XZH4	227.42	AGFAGDDAPR	Uniref 90	Unclassified	3317
I	1	5	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	110.02	LTELK	Uniref 90	Protein destination	54
I	1	5	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	197.17	QAVVNPENTFFSVK	Uniref 90	Protein destination	472
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	AVITVPAYFNDSQR	Uniref 90	Protein destination	28
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	NQAESVIYQTEK	Uniref 90	Protein destination	68
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	LDCPAIGK	Uniref 90	Protein destination	1194
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	TTPSVVAYTK	Uniref 90	Protein destination	1414
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	ATTTFPTSTPFFAHHGR	Uniref 90	Protein destination	1523
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	NDEGIDLLK	Uniref 90	Protein destination	2074
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	QFAAEEISAQVLR	Uniref 90	Protein destination	4857
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	MELSSLTQTNISLPFITATADGPK	Uniref 90	Protein destination	11140
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2Y2Y4	257.09	VVGIDLGTTNSAVAAMEGGKPTIVTNAEGAR	Uniref 90	Protein destination	11979
I	1	2	Phosphoglycerate kinase (*O. sativa*)	A2Y650	200.13	AQGLSVGSSLVEEDK	Uniref 90	Energy metabolism	816
I	1	2	Phosphoglycerate kinase (*O. sativa*)	A2Y650	200.13	SVGDLTAADLEGK	Uniref 90	Energy metabolism	3262
I	1	2	Phosphoglycerate kinase (*O. sativa*)	A2Y650	200.13	IGVIESLLEK	Uniref 90	Energy metabolism	5738
I	1	2	Phosphoglycerate kinase (*O. sativa*)	A2Y650	200.13	SVGDLTAADLEGKR	Uniref 90	Energy metabolism	6724
I	1	2	Phosphoglycerate kinase (*O. sativa*)	A2Y650	200.13	RPFAAIVGGSK	Uniref 90	Energy metabolism	8925
I	2	4	Phosphoglycerate kinase (*O. sativa*)	A2Y650	127.66	FLKPSVAGFLLQK	Uniref 90	Energy metabolism	27786
I	2	8	Phosphoglycerate kinase (*O. sativa*)	A2Y650	150.05	ADLNVPLDDNQNITDDTR	Uniref 90	Energy metabolism	856
I	2	8	Phosphoglycerate kinase (*O. sativa*)	A2Y650	150.05	SVGDLTAADLEGKR	Uniref 90	Energy metabolism	5250
I	2	8	Phosphoglycerate kinase (*O. sativa*)	A2Y650	150.05	AEDVIGPDVEK	Uniref 90	Energy metabolism	7709
I	2	8	Phosphoglycerate kinase (*O. sativa*)	A2Y650	150.05	SVGDLTAADLEGK	Uniref 90	Energy metabolism	18495
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2YZ92	125.08	VNTISAGPLGSR	Uniref 90	Unclassified	417
I	1	4	Putative uncharacterized protein (*O. sativa*)	A2YZ92	125.08	MGASVTTGLQMAAARPCIPACQR	Uniref 90	Unclassified	595

I	2	6	Putative uncharacterized protein (*O. sativa*)	A2YZ92	223.86	MIEYSYVNAPLQK	Uniref 90	Unclassified	7324
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2YZ92	223.86	YAGSSNWTVK	Uniref 90	Unclassified	13409
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2YZ92	223.86	TASAGPFVSLNHK	Uniref 90	Unclassified	13959
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2YZ92	223.86	SLPFQHCFTGHVTDLQGVLAYEAGR	Uniref 90	Unclassified	26753
I	2	6	Putative uncharacterized protein (*O. sativa*)	A2YZ92	223.86	SLPFQHCFTGHVTDLQGVLAYEAGRK	Uniref 90	Unclassified	27506
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2YZ92	234.43	VNTISAGPLGSR	Uniref 90	Unclassified	660
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2YZ92	234.43	MIEYSYVNAPLQK	Uniref 90	Unclassified	939
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2YZ92	234.43	AIGFIEKMIEYSYVNAPLQK	Uniref 90	Unclassified	28404
I	1	1	Probable histone H2AXb (*O. sativa*)	A2ZL69	158.33	LLGAVTIAAGGVLPNIHQTLLPK	Uniref 90	DNA binding	30159
I	1	5	Probable histone H2AXb (*O. sativa*)	A2ZL69	101.82	HIQLAVR	Uniref 90	DNA binding	1212
I	1	10	Probable histone H2AXb (*O. sativa*)	A2ZL69	158.33	LLGAVTIAAGGVLPNIHQTLLPK	Uniref 90	DNA binding	44523
I	2	5	Probable histone H2AXb (*O. sativa*)	A2ZL69	190.21	HIQLAVR	Uniref 90	DNA binding	2976
I	2	8	Probable histone H2AXb (*O. sativa*)	A2ZL69	112.91	NDEELSR	Uniref 90	DNA binding	20598
I	2	8	Probable histone H2AXb (*O. sativa*)	A2ZL69	112.91	LLGAVTIAAGGVLPNIHQTLLPK	Uniref 90	DNA binding	49969
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	117.4	TTFSHLAWVQTDR	Uniref 90	Unclassified	2276
I	1	5	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	117.4	SFGVLIPDQGIALR	Uniref 90	Unclassified	471
I	2	6	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	133.43	SFGVLIPDQGIALR	Uniref 90	Unclassified	5017
I	2	6	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	133.43	HLLNLMLIHYSKYYGQSDTLK	Uniref 90	Unclassified	11482
I	2	6	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	133.43	EGVIQHSTINNLAIGR	Uniref 90	Unclassified	31749
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	159.61	SFGVLIPDQGIALR	Uniref 90	Unclassified	321
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	159.61	SMKPDPKGSK	Uniref 90	Unclassified	1104
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3A7Q0	159.61	LSDYIGK	Uniref 90	Unclassified	1142
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3ATH4	221.42	TIPDPDDKKPEDWDER	Uniref 90	Protein destination	2547
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3ATH4	221.42	YIRPQDAAWDAK	Uniref 90	Protein destination	2738
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3ATH4	221.42	PDPDDKKPEDWDER	Uniref 90	Protein destination	3688
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3ATH4	307.05	CEEAPGCGEWK	Uniref 90	Protein destination	3843
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3ATH4	307.05	WHAPLIDNPNYK	Uniref 90	Protein destination	7566
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3ATH4	307.05	CEEAPGCGEWKRPMK	Uniref 90	Protein destination	14533
I	1	5	Putative uncharacterized protein (*O. sativa*)	A3ATH4	307.05	LSHVYTAILKPDNEVR	Uniref 90	Protein destination	12572
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3ATH4	204.29	CEEAPGCGEWK	Uniref 90	Protein destination	228
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3ATH4	204.29	EKAEEAAAAAGDGLSEFQK	Uniref 90	Protein destination	2604
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3ATH4	204.29	TIPDPDDKKPEDWDER	Uniref 90	Protein destination	18871
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3ATH4	204.29	WHAPLIDNPNYK	Uniref 90	Protein destination	28433
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3ATH4	204.29	LSHVYTAILKPDNEVR	Uniref 90	Protein destination	50179
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3B7Q6	151.79	AAVEEGIVVGGGCTLLR	Uniref 90	Unclassified	1854
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3B7Q6	210.98	TNDLAGDGTTTSVVLAQGLIAEGVK	Uniref 90	Unclassified	2945
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3B7Q6	183.57	DLINVLEEAIR	Uniref 90	Unclassified	1315

I	2	8	Putative uncharacterized protein (*O. sativa*)	A3B7Q6	183.57	GYISPYFVTDSEK	Uniref 90	Unclassified	1539
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3B7Q6	183.57	EVELEDPVENIGAK	Uniref 90	Unclassified	3142
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3B7Q6	183.57	TNDLAGDGTTTSVVLAQGLIAEGVK	Uniref 90	Unclassified	6332
I	1	3	Histone H4 (*O. sativa*)	A3BZ47	651.31	DAVTYTEHAR	Uniref 90	DNA binding	70
I	1	4	Histone H4 (*O. sativa*)	A3BZ47	651.31	LAPRIVQTAK	Uniref 90	DNA binding	328
I	1	4	Histone H4 (*O. sativa*)	A3BZ47	132.51	IFLENVIR	Uniref 90	DNA binding	16355
I	1	10	Histone H4 (*O. sativa*)	A3BZ47	651.31	ISGLIYEETR	Uniref 90	DNA binding	9
I	1	10	Histone H4 (*O. sativa*)	A3BZ47	651.31	TVTAMDVVYALK	Uniref 90	DNA binding	385
I	1	10	Histone H4 (*O. sativa*)	A3BZ47	651.31	IFLENVIR	Uniref 90	DNA binding	2971
I	2	5	Histone H4 (*O. sativa*)	A3BZ47	150.61	DAVTYTEHAR	Uniref 90	DNA binding	2095
I	2	8	Histone H4 (*O. sativa*)	A3BZ47	202.88	MAGHIICMK	Uniref 90	DNA binding	4571
I	2	8	Histone H4 (*O. sativa*)	A3BZ47	202.88	DAVTYTEHAR	Uniref 90	DNA binding	6393
I	2	8	Histone H4 (*O. sativa*)	A3BZ47	202.88	IFLENVIR	Uniref 90	DNA binding	49748
I	2	3	Histone H4 (*O. sativa*)	A3BZ47	612.96	TVTAMDVVYALK	Uniref 90	DNA binding	162
I	2	3	Histone H4 (*O. sativa*)	A3BZ47	612.96	ISGLIYEETR	Uniref 90	DNA binding	175
I	2	3	Histone H4 (*O. sativa*)	A3BZ47	612.96	DNIQGITKPAIR	Uniref 90	DNA binding	185
I	2	3	Histone H4 (*O. sativa*)	A3BZ47	612.96	TLYGFGG	Uniref 90	DNA binding	237
I	2	3	Histone H4 (*O. sativa*)	A3BZ47	612.96	IFLENVIR	Uniref 90	DNA binding	701
I	1	2	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	MAASLQAAATLMPAKIGGR	Uniref 90	Energy metabolism	1149
I	1	2	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	146.96	LTFDEIQSK	Uniref 90	Energy metabolism	3118
I	1	2	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	146.96	AEGIQK	Uniref 90	Energy metabolism	4419
I	1	2	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	146.96	KFCLEPTSFTVK	Uniref 90	Energy metabolism	12645
I	1	2	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	146.96	LMTRLTYTLDEMEGPLEVGADGTLK	Uniref 90	Energy metabolism	25066
I	1	2	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	146.96	QLVATGKPESFSGPFLVPSYR	Uniref 90	Energy metabolism	25100
I	1	3	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	QLVATGKPESFSGPFLVPSYR	Uniref 90	Energy metabolism	3018
I	1	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	GGSTGYDNAVALPAGGR	Uniref 90	Energy metabolism	252
I	1	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	NASSSTGNITLSVTK	Uniref 90	Energy metabolism	544
I	1	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	FCLEPTSFTVK	Uniref 90	Energy metabolism	889
I	1	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	GTGTANQCPTIDGGVDSFPFK	Uniref 90	Energy metabolism	946
I	1	5	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	RLTFDEIQSK	Uniref 90	Energy metabolism	1843
I	1	5	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	631.14	DGIDYAAVTVQLPGGER	Uniref 90	Energy metabolism	2252
I	1	5	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	181.33	GGSTGYDNAVALPAGGRGDEEELAK	Uniref 90	Energy metabolism	2896
I	1	5	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	181.33	FCLEPTSFTVK	Uniref 90	Energy metabolism	24455
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	FCLEPTSFTVK	Uniref 90	Energy metabolism	96
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	NASSSTGNITLSVTK	Uniref 90	Energy metabolism	345
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	GGSTGYDNAVALPAGGR	Uniref 90	Energy metabolism	691
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	GSSFLDPK	Uniref 90	Energy metabolism	696

I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	GTGTANQCPTIDGGVDSFPFK	Uniref 90	Energy metabolism	886
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	DGIDYAAVTVQLPGGER	Uniref 90	Energy metabolism	2615
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	KFCLEPTSFTVK	Uniref 90	Energy metabolism	4863
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	RLTFDEIQSK	Uniref 90	Energy metabolism	6969
I	2	4	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	809.05	LTYTLDEMEGPLEVGADGTLK	Uniref 90	Energy metabolism	14971
I	2	7	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	286.62	VPFLFTVK	Uniref 90	Energy metabolism	858
I	2	7	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	286.62	QLVATGKPESFSGPFLVPSYR	Uniref 90	Energy metabolism	3994
I	2	8	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	236.19	GDEEELAKENVK	Uniref 90	Energy metabolism	4216
I	2	8	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	236.19	LTFDEIQSK	Uniref 90	Energy metabolism	5055
I	2	8	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	236.19	GGSTGYDNAVALPAGGRGDEEELAK	Uniref 90	Energy metabolism	10956
I	2	8	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	236.19	RLTFDEIQSK	Uniref 90	Energy metabolism	16314
I	2	8	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	236.19	QLVATGKPESFSGPFLVPSYR	Uniref 90	Energy metabolism	16326
I	2	8	Chloroplast oxygen evolving enhancer protein (*L. chinensis*)	A5JV93	236.19	KFCLEPTSFTVK	Uniref 90	Energy metabolism	28480
I	1	2	Actin (*P. salicina*)	A9UAM8	134.21	LAYVALDYEQELETAK	Uniref 90	Cell wall	6489
I	1	2	Actin (*P. salicina*)	A9UAM8	134.21	YSVWIGGSILASLSTFQQMWIA	Uniref 90	Cell wall	6722
I	1	2	Actin (*P. salicina*)	A9UAM8	134.21	YPIEHGIVSNWDDMEK	Uniref 90	Cell wall	12648
I	1	2	Actin (*P. salicina*)	A9UAM8	134.21	LAYVALDYEQELETA	Uniref 90	Cell wall	12937
I	1	5	Actin (*P. salicina*)	A9UAM8	134.21	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	Uniref 90	Cell wall	12506
I	2	8	Actin (*P. salicina*)	A9UAM8	178.49	CPEVLFQPSLIGMEAAGIHETTYNSIMK	Uniref 90	Cell wall	74
I	2	8	Actin (*P. salicina*)	A9UAM8	178.49	EITALAPSSMK	Uniref 90	Cell wall	1309
I	2	8	Actin (*P. salicina*)	A9UAM8	178.49	DAYVGDEAQSK	Uniref 90	Cell wall	2592
I	2	8	Actin (*P. salicina*)	A9UAM8	178.49	YPIEHGIVSNWDDMEK	Uniref 90	Cell wall	6221
I	1	2	Ascorbate peroxidase (*H. vulgare*)	O23983	114.6	FDNSYFTELLSGDK	Uniref 90	Disease/Defence	1398
I	1	2	Ascorbate peroxidase (*H. vulgare*)	O23983	114.6	QMGLSDQDIVALSGGHTLGR	Uniref 90	Disease/Defence	4519
I	1	2	Ascorbate peroxidase (*H. vulgare*)	O23983	114.6	KPAEQAHAANAGLDIAVR	Uniref 90	Disease/Defence	10083
I	2	4	Ascorbate peroxidase (*H. vulgare*)	O23983	354.1	FDNSYFTELLSGDKEGLLQLPSDK	Uniref 90	Disease/Defence	5845
I	2	4	Ascorbate peroxidase (*H. vulgare*)	O23983	354.1	TLLTDPVFRPLVEK	Uniref 90	Disease/Defence	6912
I	2	4	Ascorbate peroxidase (*H. vulgare*)	O23983	354.1	QMGLSDQDIVALSGGHTLGR	Uniref 90	Disease/Defence	10560
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	SYPVVSAEYLEAVEK	Uniref 90	Disease/Defence	103
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	NCSPLMLR	Uniref 90	Disease/Defence	401
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	SGFEGPWTR	Uniref 90	Disease/Defence	1022
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	FDNSYFTELLSGDK	Uniref 90	Disease/Defence	1770
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	LAWHSAGTFDVSSKTGGPFGTMK	Uniref 90	Disease/Defence	2337
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	EGLLQLPSDK	Uniref 90	Disease/Defence	3396
I	2	8	Ascorbate peroxidase (*H. vulgare*)	O23983	247.18	KPAEQAHAANAGLDIAVR	Uniref 90	Disease/Defence	28538
I	1	5	Ferredoxin, chloroplast precursor (*T. aestivum*)	P00228	90.98	SDIVIETHKEEELTA	Uniref 90	Transport	3962

I	1	5	Ferredoxin, chloroplast precursor (*T. aestivum*)	P00228	90.98	LVSGEIDQSDQSFLDDDQMEAGWVLTCHAYPK	Uniref 90	Transport	44795
I	2	4	Ferredoxin, chloroplast precursor (*T. aestivum*)	P00228	102.76	SDIVIETHKEEELTA	Uniref 90	Transport	5445
I	2	4	Ferredoxin, chloroplast precursor (*T. aestivum*)	P00228	102.76	LVSGEIDQSDQSFLDDDQMEAGWVLTCHAYPK	Uniref 90	Transport	27641
I	1	2	Calreticulin family protein (*O. sativa*)	Q10BR5	279.47	ELSAIDPGDPR	Uniref 90	Protein destination	1216
I	1	2	Calreticulin family protein (*O. sativa*)	Q10BR5	279.47	GIQTSEDYR	Uniref 90	Protein destination	3905
I	1	2	Calreticulin family protein (*O. sativa*)	Q10BR5	107.54	DVPVGNSVLVMYAK	Uniref 90	Protein destination	6938
I	1	4	Calreticulin family protein (*O. sativa*)	Q10BR5	279.47	FYAISAEYPEFSNK	Uniref 90	Protein destination	550
I	1	4	Calreticulin family protein (*O. sativa*)	Q10BR5	279.47	LAGVEPNGMSIACAISACASLKLLNQAK	Uniref 90	Protein destination	705
I	2	8	Calreticulin family protein (*O. sativa*)	Q10BR5	365.41	GMYSDVLALAVTMVEEGVLPDR	Uniref 90	Protein destination	9758
I	2	8	Calreticulin family protein (*O. sativa*)	Q10BR5	365.41	TLVLQFSVK	Uniref 90	Protein destination	18847
I	2	8	Calreticulin family protein (*O. sativa*)	Q10BR5	365.41	RDTATWNILIAGSVHNGYYDR	Uniref 90	Protein destination	21771
I	1	2	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENF0	159.05	GALVGGWGPIPDVK	Uniref 90	Protein destination	1184
I	1	2	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENF0	159.61	GEQQVVSGMNYR	Uniref 90	Protein destination	1371
I	1	2	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENF0	159.05	LFVDAADGSGR	Uniref 90	Protein destination	2029
I	1	2	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENF0	159.61	VDAADGSGR	Uniref 90	Protein destination	4470
I	2	8	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENE9	161.9	SENPAAANSLETDGLAR	Uniref 90	Protein destination	435
I	2	8	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENE9	161.9	ENALLEFVR	Uniref 90	Protein destination	3807
I	2	8	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENE9	161.9	HTGDATSFTISDLGAK	Uniref 90	Protein destination	6312
I	2	8	Cystatin Hv CPI8 (*H. vulgare*)	Q1ENE9	161.9	SNSLFPYELIEIVR	Uniref 90	Protein destination	8680
I	1	2	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	329.91	GNGTGGESIYGEK	Uniref 90	Protein destination	5310
I	1	3	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	329.91	VFFDMTVGGAPAGR	Uniref 90	Protein destination	1249
I	1	4	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	329.91	GNGTGGESIYGEK	Uniref 90	Protein destination	1161
I	2	8	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	203.85	GNGTGGESIYGEK	Uniref 90	Protein destination	3792
I	2	8	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	203.85	HDSPGILSMANAGPNTNGSQFFICTVPCSWLDGK	Uniref 90	Protein destination	8172
I	2	8	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	203.85	VFFDMTVGGAPAGR	Uniref 90	Protein destination	11330
I	1	2	Type 1 non specific lipid transfer protein precursor (*T. aestivum*)	Q2PCD1	154.37	GCCTGIQNLLAEANNSPDRR	Uniref 90	Transport	426
I	1	3	Type 1 non specific lipid transfer protein precursor (*T. aestivum*)	Q2PCD1	154.37	ISPSVDCNSIH	Uniref 90	Transport	840
I	1	4	Type 1 non specific lipid transfer protein precursor (*T. aestivum*)	Q2PCD1	154.37	PSVDCNSIH	Uniref 90	Transport	2317
I	2	7	Type 1 non specific lipid transfer protein precursor (*T. aestivum*)	Q2PCD1	195.64	ISPSVDCNSIH	Uniref 90	Transport	5110
I	2	3	Type 1 non specific lipid transfer protein precursor (*T. aestivum*)	Q2PCD1	184.35	ISPSVDCNSIH	Uniref 90	Transport	148
I	1	2	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	319.03	GFNLPLDLTCSSGDALR	Uniref 90	Unclassified	4534
I	1	3	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	244.43	GFNLPLDLTCSSGDALR	Uniref 90	Unclassified	1767
I	1	4	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	319.03	TGCSFDAAGSGLCR	Uniref 90	Unclassified	1288
I	1	4	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	324.71	AQVASSEGFYHYGITTDK	Uniref 90	Unclassified	3052

I	1	5	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	319.03	CATTDPPAPVTR	Uniref 90	Unclassified	1433
I	2	4	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	801.15	TGCSFDAAGSGLCR	Uniref 90	Unclassified	354
I	2	4	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	801.15	CATTDPPAPVTR	Uniref 90	Unclassified	1354
I	2	4	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	801.15	GFNLPLDLTCSSGDALR	Uniref 90	Unclassified	1783
I	2	4	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	801.15	AQVASSEGFYHYGITTDK	Uniref 90	Unclassified	1892
I	2	8	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	235.61	LQIVFCP	Uniref 90	Unclassified	5947
I	2	8	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	235.61	TADCGSGLR	Uniref 90	Unclassified	20247
I	2	8	Thaumatin like protein TLP3 (*H. vulgare*)	Q5MBN3	235.61	GFNLPLDLTCSSGDALR	Uniref 90	Unclassified	50419
I	1	2	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	147.32	LGIIEDATNR	Uniref 90	Disease/Defence	169
I	1	2	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	147.32	APHDLYESYYNSNK	Uniref 90	Disease/Defence	1695
I	1	2	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	147.32	ADGSFAISEDTWNEPLGR	Uniref 90	Disease/Defence	1850
I	1	2	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	147.32	KLQVNADDSTDELVDPPK	Uniref 90	Disease/Defence	2483
I	1	5	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	147.32	IMQSQTLSDASKQAYMR	Uniref 90	Disease/Defence	1258
I	2	8	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	214.19	ALLFVPPK	Uniref 90	Disease/Defence	2410
I	2	8	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	214.19	VLEINPR	Uniref 90	Disease/Defence	3052
I	2	8	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	214.19	LGIIEDATNR	Uniref 90	Disease/Defence	4441
I	2	8	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	214.19	LVYQTALMESGFNLPDPK	Uniref 90	Disease/Defence	5442
I	2	8	Heat shock protein 90 (*O. sativa*)	Q5Z9N8	214.19	QHVWESKADGSFAISEDTWNEPLGR	Uniref 90	Disease/Defence	50993
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	NTLQGLAAR	Uniref 90	DNA binding	2052
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	TYHMIDEDEPILEK	Uniref 90	DNA binding	4988
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	MYEPLYSK	Uniref 90	DNA binding	5106
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	AALEAK	Uniref 90	DNA binding	19384
I	2	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	164.32	MYEPLYSK	Uniref 90	DNA binding	709
I	2	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	164.32	TYHMIDEDEPILEK	Uniref 90	DNA binding	3738
I	1	6	QM (*T. aestivum*)	Q7X9L9	160.91	ENVSSEALEAAR	Uniref 90	Protein destination	91
I	1	6	QM (*T. aestivum*)	Q7X9L9	160.91	VAIGQVLLSVR	Uniref 90	Protein destination	979
I	2	8	QM (*T. aestivum*)	Q7X9L9	103.51	ENVSSEALEAAR	Uniref 90	Protein destination	442
I	2	8	QM (*T. aestivum*)	Q7X9L9	103.51	VAIGQVLLSVR	Uniref 90	Protein destination	5151
I	2	8	QM (*T. aestivum*)	Q7X9L9	103.51	MLSCAGADRLQTGMR	Uniref 90	Protein destination	9076
I	1	2	Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3	209.76	LSGDELLSDSFPYR	Uniref 90	Unclassified	4348
I	1	2	Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3	209.76	EGAADPTFLYFAHGLK	Uniref 90	Unclassified	7995
I	1	4	Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3	134.7	LSGDELLSDSFPYR	Uniref 90	Unclassified	577
I	1	5	Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3	134.7	VVDIVDTFR	Uniref 90	Unclassified	184
I	2	7	Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3	300.82	LSGDELLSDSFPYR	Uniref 90	Unclassified	93
I	2	7	Translationally controlled tumor protein homolog (*T. aestivum*)	Q9M5G3	300.82	VVDIVDTFR	Uniref 90	Unclassified	136
I	1	2	Heat shock 70 kDa protein (*O. sativa*)	35_1230	261.38	SSGGLSESEIEK	Harvest Hv	Disease/Defence	403
I	1	2	Heat shock 70 kDa protein (*O. sativa*)	35_1230	261.38	SQVFSTAADNQTQVGIR	Harvest Hv	Disease/Defence	3761

I	1	5	Heat shock 70 kDa protein (*O. sativa*)	35_1230	261.38	ELLLLDVTPLSLGIETLGGIFTR	Harvest Hv	Disease/Defence	4023
I	1	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	261.38	QAITNPQNTFFGTK	Harvest Hv	Disease/Defence	319
I	1	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	206.93	IINEPTAAALSYGTNNK	Harvest Hv	Disease/Defence	4898
I	2	2	Heat shock 70 kDa protein (*O. sativa*)	35_1230	124.97	SAMALRSTADR	Harvest Hv	Disease/Defence	2573
I	2	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	342.96	TTPSVVAFSQK	Harvest Hv	Disease/Defence	8779
I	2	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	342.96	ALIDIRNTADTTIYSIEK	Harvest Hv	Disease/Defence	19209
I	2	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	342.96	RSAMALR	Harvest Hv	Disease/Defence	24060
I	2	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	342.96	IINEPTAAALSYGTNNK	Harvest Hv	Disease/Defence	29277
I	2	6	Heat shock 70 kDa protein (*O. sativa*)	35_1230	342.96	NTADTTIYSIEK	Harvest Hv	Disease/Defence	29616
I	2	8	Heat shock 70 kDa protein (*O. sativa*)	35_1230	483.09	QAITNPQNTFFGTK	Harvest Hv	Disease/Defence	481
I	2	8	Heat shock 70 kDa protein (*O. sativa*)	35_1230	483.09	SSGGLSESEIEK	Harvest Hv	Disease/Defence	591
I	2	8	Heat shock 70 kDa protein (*O. sativa*)	35_1230	483.09	AEMASDDIEK	Harvest Hv	Disease/Defence	1877
I	2	8	Heat shock 70 kDa protein (*O. sativa*)	35_1230	483.09	TTPSVVAFSQK	Harvest Hv	Disease/Defence	2190
I	2	8	Heat shock 70 kDa protein (*O. sativa*)	35_1230	483.09	AKIELSSTAQTEINLPFITADAAGAK	Harvest Hv	Disease/Defence	5624
I	1	5	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	281.76	ELEALCNPIIAK	Harvest Hv	Disease/Defence	1175
I	1	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	166.58	VQQLLQDFFNGK	Harvest Hv	Disease/Defence	5574
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	222.46	ELEALCNPIIAK	Harvest Hv	Disease/Defence	555
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	222.46	VQQLLQDFFNGKELCK	Harvest Hv	Disease/Defence	3324
I	2	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	210.7	SINPDEAVAYGAAVQAAILTGEGNEK	Harvest Hv	Disease/Defence	24321
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	344.26	VQDLLLLDVTPLSQGLETAGGVMTILIPR	Harvest Hv	Disease/Defence	11250
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	344.26	ELEALCNPIIAK	Harvest Hv	Disease/Defence	13334
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_137	344.26	MKELEALCNPIIAK	Harvest Hv	Disease/Defence	18179
I	1	4	Os07g0173500 protein (*O. sativa*)	35_14252	374.98	FTQVVSNAVDMK	Harvest Hv	Unclassified	192
I	1	6	Os07g0173500 protein (*O. sativa*)	35_14252	374.98	AGELSSEEMDR	Harvest Hv	Unclassified	1593
I	2	2	Os07g0173500 protein (*O. sativa*)	35_14252	681.32	AGELSSEEMDR	Harvest Hv	Unclassified	245
I	2	2	Os07g0173500 protein (*O. sativa*)	35_14252	681.32	VLNTNVDGK	Harvest Hv	Unclassified	2352
I	2	8	Os07g0173500 protein (*O. sativa*)	35_14252	165.03	LMTVVANPR	Harvest Hv	Unclassified	11066
I	2	8	Os07g0173500 protein (*O. sativa*)	35_14252	165.03	FTQVVSNAVDMK	Harvest Hv	Unclassified	20651
I	1	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	309.34	SPPSVPYDK	Harvest Hv	Protein destination	2158
I	1	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	362	QKAEEAAAAESEDLSEFQK	Harvest Hv	Protein destination	10071
I	1	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	362	KPSATEADAAGSSGDKEDKEDEKDDTAAPR	Harvest Hv	Protein destination	13654
I	1	6	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	121.11	LQNGLECGGAYLK	Harvest Hv	Protein destination	939
I	2	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	228.1	ANFMSADDFEPALIPSK	Harvest Hv	Protein destination	1149
I	2	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	228.1	SDGHEDYGLLVSEPAR	Harvest Hv	Protein destination	4464
I	2	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	228.1	TIPDPDDKKPEDWDER	Harvest Hv	Protein destination	8003
I	2	2	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	228.1	LSHVYTAILKPDNEVR	Harvest Hv	Protein destination	15543

I	2	8	OSJNBb0012E08 10 protein (*O. sativa*)	35_14268	249.02	VAMSILEK	Harvest Hv	Protein destination	1141
I	1	6	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	150.94	ATLSVGNVLPLR	Harvest Hv	Protein synthesis	710
I	1	8	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	150.89	ATLSVGNVLPLR	Harvest Hv	Protein synthesis	48996
I	2	8	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	284.43	VTDVIHDPGR	Harvest Hv	Protein synthesis	2241
I	2	8	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	284.43	ATLSVGNVLPLR	Harvest Hv	Protein synthesis	2881
I	2	8	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	284.43	GVVTDVIHDPGR	Harvest Hv	Protein synthesis	3657
I	2	8	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	284.43	SVPEGGVICNVEHHVGDR	Harvest Hv	Protein synthesis	22570
I	2	8	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	284.43	PEGGVICNVEHHVGDR	Harvest Hv	Protein synthesis	28664
I	1	2	Putative transaldolase (*O. sativa*)	35_14408	140.08	LGIDWEEVGK	Harvest Hv	Energy metabolism	704
I	1	2	Putative transaldolase (*O. sativa*)	35_14408	140.08	TIDANVSEAEGIYSALEK	Harvest Hv	Energy metabolism	1128
I	1	2	Putative transaldolase (*O. sativa*)	35_14408	140.08	GVTSNPTIFQK	Harvest Hv	Energy metabolism	1280
I	1	2	Putative transaldolase (*O. sativa*)	35_14408	140.08	LANDTQGTVEAAK	Harvest Hv	Energy metabolism	3581
I	1	2	Putative transaldolase (*O. sativa*)	35_14408	85.32	LANDTQGTVEAAK	Harvest Hv	Energy metabolism	20499
I	1	6	Putative transaldolase (*O. sativa*)	35_14408	140.08	IPATAECVPSIK	Harvest Hv	Energy metabolism	709
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	GVTSNPTIFQK	Harvest Hv	Energy metabolism	204
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	IPATAECVPSIK	Harvest Hv	Energy metabolism	657
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	IANQLYLK	Harvest Hv	Energy metabolism	749
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	IGTPEALALR	Harvest Hv	Energy metabolism	1118
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	VTSVASFFVSR	Harvest Hv	Energy metabolism	1772
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	LANDTQGTVEAAK	Harvest Hv	Energy metabolism	2621
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	GSFDSLLTSLEEK	Harvest Hv	Energy metabolism	6389
I	2	8	Putative transaldolase (*O. sativa*)	35_14408	434.24	LGIDWEEVGK	Harvest Hv	Energy metabolism	8799
I	1	2	40S ribosomal protein S19 (*O. sativa*)	35_14825	150.89	NGSRPPHFCKSSGAVSR	Harvest Hv	Protein synthesis	977
I	1	2	40S ribosomal protein S19 (*O. sativa*)	35_14825	150.89	DLDQVAGTVPAEF	Harvest Hv	Protein synthesis	6934
I	1	2	40S ribosomal protein S19 (*O. sativa*)	35_14825	120.42	NGSRPPHFCKSSGAVSR	Harvest Hv	Protein synthesis	14537
I	1	5	40S ribosomal protein S19 (*O. sativa*)	35_14825	150.89	QGIGIGGFQK	Harvest Hv	Protein synthesis	1047
I	1	5	40S ribosomal protein S19 (*O. sativa*)	35_14825	145.55	NILQELQK	Harvest Hv	Protein synthesis	2321
I	1	8	40S ribosomal protein S19 (*O. sativa*)	35_14825	150.89	NGSRPPHFCKSSGAVSR	Harvest Hv	Protein synthesis	4732
I	2	5	40S ribosomal protein S19 (*O. sativa*)	35_14825	352.81	NILQELQK	Harvest Hv	Protein synthesis	271
I	2	7	40S ribosomal protein S19 (*O. sativa*)	35_14825	350.42	DLDQVAGTVPAEF	Harvest Hv	Protein synthesis	137
I	2	7	40S ribosomal protein S19 (*O. sativa*)	35_14825	350.42	QGIGIGGFQK	Harvest Hv	Protein synthesis	3051
I	2	8	40S ribosomal protein S19 (*O. sativa*)	35_14825	147.64	RDLDQVAGTVPAEF	Harvest Hv	Protein synthesis	2748
I	2	8	40S ribosomal protein S19 (*O. sativa*)	35_14825	147.64	DVNPHEFVK	Harvest Hv	Protein synthesis	20615
I	2	8	40S ribosomal protein S19 (*O. sativa*)	35_14825	147.64	NILQELQK	Harvest Hv	Protein synthesis	50032
I	1	5	Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299	72.99	SINEFLKPAEGER	Harvest Hv	Unclassified	1540
I	1	5	Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299	142.41	DGAAVVEEEKEEDNEMTLDEFEK	Harvest Hv	Unclassified	2343
I	1	5	Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299	72.99	SVSINEFLKPAEGER	Harvest Hv	Unclassified	8292

I	1	6	Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299	142.41	LPTKPPPPGQAANESR	Harvest Hv	Unclassified	4235
I	2	7	Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299	420.96	DGAAVVEEEKEEDNEMTLDEFEK	Harvest Hv	Unclassified	2005
I	2	7	Hypothetical protein OSJNBa0053E05 13 (*O. sativa*)	35_15299	420.96	LPTKPPPPGQAANESR	Harvest Hv	Unclassified	3172
I	1	2	BTF3b like transcription factor (*M. acuminata*)	35_15306	135.33	QVAAAGAIQPK	Harvest Hv	Transcription	2375
I	1	2	BTF3b like transcription factor (*M. acuminata*)	35_15306	139.95	VGVNTIPAIEEVNIFK	Harvest Hv	Transcription	2662
I	1	2	BTF3b like transcription factor (*M. acuminata*)	35_15306	139.95	MAGAVRTGGK	Harvest Hv	Transcription	10478
I	1	2	BTF3b like transcription factor (*M. acuminata*)	35_15306	139.95	LQDVLPSIINQLGPDNMEHLK	Harvest Hv	Transcription	25368
I	1	5	BTF3b like transcription factor (*M. acuminata*)	35_15306	135.33	EENDDDVPELVPGETFEEVAQETK	Harvest Hv	Transcription	1477
I	1	5	BTF3b like transcription factor (*M. acuminata*)	35_15306	78.1	VQASIAANTWVVSGTPQTK	Harvest Hv	Transcription	7287
I	2	2	BTF3b like transcription factor (*M. acuminata*)	35_15306	140.41	QVAAAGAIQPK	Harvest Hv	Transcription	1389
I	2	7	BTF3b like transcription factor (*M. acuminata*)	35_15306	146.97	EENDDDVPELVPGETFEEVAQETK	Harvest Hv	Transcription	2407
I	2	8	BTF3b like transcription factor (*M. acuminata*)	35_15306	340.38	EENDDDVPELVPGETFEEVAQETKA	Harvest Hv	Transcription	2747
I	2	8	BTF3b like transcription factor (*M. acuminata*)	35_15306	340.38	EENDDDVPELVPGETFEEVAQETK	Harvest Hv	Transcription	20773
I	2	8	BTF3b like transcription factor (*M. acuminata*)	35_15306	340.38	KLQDVLPSIINQLGPDNMEHLK	Harvest Hv	Transcription	50737
I	1	2	Cu Zn superoxide dismutase (*T. aestivum*)	35_15373	70.09	GGHELSLSTGNAGGR	Harvest Hv	Disease/Defence	4351
I	1	5	Cu Zn superoxide dismutase (*T. aestivum*)	35_15373	70.09	GTSQVEGVVTLTQDDDGPTTVNVR	Harvest Hv	Disease/Defence	5772
I	2	2	Cu Zn superoxide dismutase (*T. aestivum*)	35_15373	162.1	LACGVVGLTPL	Harvest Hv	Disease/Defence	114
I	2	2	Cu Zn superoxide dismutase (*T. aestivum*)	35_15373	162.1	GTSQVEGVVTLTQDDDGPTTVNVR	Harvest Hv	Disease/Defence	2472
I	2	2	Cu Zn superoxide dismutase (*T. aestivum*)	35_15373	162.1	HAGDLGNIVANAEGVAETTIVDSQIPLTGPNAVVGR	Harvest Hv	Disease/Defence	7016
I	2	8	Cu Zn superoxide dismutase (*T. aestivum*)	35_15373	299.51	HAGDLGNIVANAEGVAETTIVDSQIPLTGPNAVVGR	Harvest Hv	Disease/Defence	49996
I	1	2	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	143.1	EPEAEEAIPSTEESDEAPEETEEKPEIVIETAPADFR	Harvest Hv	Unclassified	3358
I	1	2	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	94.96	STTSTVAEVVPQK	Harvest Hv	Unclassified	4896
I	2	2	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	368.52	STTSTVAEVVPQK	Harvest Hv	Unclassified	637
I	2	2	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	368.52	DTETSPADETAAPVEEK	Harvest Hv	Unclassified	757
I	2	2	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	368.52	EVPVEKPAEEK	Harvest Hv	Unclassified	3429
I	2	2	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	368.52	STTSTVAEVVPQKDTETSPADETAAPVEEK	Harvest Hv	Unclassified	3667
I	2	4	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	102.19	SLCPSEWVER	Harvest Hv	Unclassified	293
I	2	4	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	102.19	EPEAEEAIPSTEESDEAPEETEEKPEIVIETAPADFR	Harvest Hv	Unclassified	1015
I	2	6	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	239.53	GDDAPECEK	Harvest Hv	Unclassified	49216
I	2	6	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	239.53	STTSTVAEVVPQK	Harvest Hv	Unclassified	51638
I	2	6	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	239.53	STTSTVAEVVPQKDTETSPADETAAPVEEK	Harvest Hv	Unclassified	51754

I	2	6	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	239.53	SLCPSEWVER	Harvest Hv	Unclassified	52140
I	2	6	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	239.53	VPTLAEEYSLPPK	Harvest Hv	Unclassified	52509
I	2	6	Putative cytochrome c oxidase subunit (*T. aestivum*)	35_15404	239.53	STTSTVAEVVPQKDTETSPADETAAPVEEK	Harvest Hv	Unclassified	55241
I	1	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	58.38	EEPEAEPLPPPVQLGEVDEEELR	Harvest Hv	Unclassified	415
I	1	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	58.38	MFYGPGGPYALFAGK	Harvest Hv	Unclassified	5539
I	1	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	58.38	KAFLGEEGTISTSPETATAEAETEK	Harvest Hv	Unclassified	53561
I	2	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	148.96	EEPEAEPLPPPVQLGEVDEEELR	Harvest Hv	Unclassified	281
I	2	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	148.96	GQIYDVTQSR	Harvest Hv	Unclassified	439
I	2	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	148.96	KAFLGEEGTISTSPETATAEAETEK	Harvest Hv	Unclassified	1426
I	2	2	Putative steroid membrane binding protein (*T. aestivum*)	35_15441	148.96	MFYGPGGPYALFAGK	Harvest Hv	Unclassified	10724
I	1	2	Putative plastidic aldolase (*O. sativa*)	35_15473	55.62	ANSLAQLGSYTGEGESDEAKK	Harvest Hv	Energy metabolism	2768
I	1	2	Putative plastidic aldolase (*O. sativa*)	35_15473	55.62	GLVPLPGSNNESWCQGLDGLASR	Harvest Hv	Energy metabolism	4533
I	1	6	Putative plastidic aldolase (*O. sativa*)	35_15473	55.62	TVVSIPCGPTALAVK	Harvest Hv	Energy metabolism	885
I	2	8	Putative plastidic aldolase (*O. sativa*)	35_15473	136.61	TVVSIPCGPTALAVK	Harvest Hv	Energy metabolism	1313
I	2	8	Putative plastidic aldolase (*O. sativa*)	35_15473	136.61	LASIGLDNTEVNR	Harvest Hv	Energy metabolism	2049
I	2	8	Putative plastidic aldolase (*O. sativa*)	35_15473	136.61	DQNIMPGIK	Harvest Hv	Energy metabolism	5522
I	1	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	117.87	AGEGEQGEELLAPSGWTK	Harvest Hv	DNA binding	1061
I	1	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	117.87	GTEVEMEDAEEAK	Harvest Hv	DNA binding	3727
I	1	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	117.87	AHPGGPALSEFVWATGNTPR	Harvest Hv	DNA binding	13275
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	AAESDVAPEEVEMPDPVSENK	Harvest Hv	DNA binding	194
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	GTEVEMEDAEEAK	Harvest Hv	DNA binding	360
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	AGEGEQGEELLAPSGWTK	Harvest Hv	DNA binding	595
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	KEEADSTINPATPPPAEVK	Harvest Hv	DNA binding	1233
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	DAPIADAPEKTDEDEGK	Harvest Hv	DNA binding	2076
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	FEVVFITPTGEQVK	Harvest Hv	DNA binding	3516
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	GKQEDAEDAEAESGDHADAEEAK	Harvest Hv	DNA binding	11101
I	2	2	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	589.81	AHPGGPALSEFVWATGNTPR	Harvest Hv	DNA binding	15109
I	2	4	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	135.96	AHPGGPALSEFVWATGNTPR	Harvest Hv	DNA binding	27667
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	719.83	ALTTYLK	Harvest Hv	DNA binding	22922
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	719.83	FEVVFITPTGEQVK	Harvest Hv	DNA binding	28841
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	719.83	NSNPEPPLQPSPPLADPHSSLAAAAR	Harvest Hv	DNA binding	30067
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	719.83	ATESPEDEKPAKR	Harvest Hv	DNA binding	30928
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	719.83	KEEADSTINP	Harvest Hv	DNA binding	31004
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	VTDLDLEMKEAENAQEEK	Harvest Hv	DNA binding	38613
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	KEADTVVQEDK	Harvest Hv	DNA binding	40600
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	EAENAQEEK	Harvest Hv	DNA binding	42654

I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	QPRAASMASGGDHEAAAAAAGEQTPLK	Harvest Hv	DNA binding	47724
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	EADTVAQEENKEAGTVVQEEK	Harvest Hv	DNA binding	52569
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	ATESPEDEKPAK	Harvest Hv	DNA binding	60000
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	KEEADSTINPATPPPAEVK	Harvest Hv	DNA binding	60837
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	AHPGGPALSEFVWATGNTPRR	Harvest Hv	DNA binding	62037
I	2	6	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	276.21	ATESPEDEKPAKR	Harvest Hv	DNA binding	64189
I	2	8	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	413.96	ALTTYLK	Harvest Hv	DNA binding	1716
I	2	8	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	413.96	ALTTYLK	Harvest Hv	DNA binding	2627
I	2	8	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	413.96	AESPEDPKPSR	Harvest Hv	DNA binding	8956
I	2	8	Methyl binding domain protein MBD109 (*Z. mays*)	35_15492	413.96	AHPGGPALSEFVWATGNTPR	Harvest Hv	DNA binding	50961
I	1	2	RAD23 protein (*O. sativa*)	35_15614	71.06	DEELAANYLLDHGHEFEEQQ	Harvest Hv	Disease/Defence	3053
I	1	5	RAD23 protein (*O. sativa*)	35_15614	186.82	APVSQSQPATPVAAATPPVPVASAAR	Harvest Hv	Disease/Defence	175
I	1	5	RAD23 protein (*O. sativa*)	35_15614	186.82	LIQENQAEFLR	Harvest Hv	Disease/Defence	512
I	1	6	RAD23 protein (*O. sativa*)	35_15614	186.82	AIDYLYSGIPESVEAPPVAR	Harvest Hv	Disease/Defence	1043
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	AIDYLYSGIPESVEAPPVAR	Harvest Hv	Disease/Defence	85
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	LIQENQAEFLR	Harvest Hv	Disease/Defence	536
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	APVSQSQPATPVAAATPPVPVASAAR	Harvest Hv	Disease/Defence	989
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	LVNETPESGAGGNILGALAAQMPQAVQVTPEER	Harvest Hv	Disease/Defence	1581
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	IIESAQGGQNVYPADQLMIIYQGK	Harvest Hv	Disease/Defence	2540
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	ILKDDTTLDANK	Harvest Hv	Disease/Defence	3315
I	2	2	RAD23 protein (*O. sativa*)	35_15614	608.7	DEELAANYLLDHGHEFEEQQ	Harvest Hv	Disease/Defence	5016
I	2	6	RAD23 protein (*O. sativa*)	35_15614	264.4	IIESAQGGQNVYPADQLMIIYQGK	Harvest Hv	Disease/Defence	14592
I	2	6	RAD23 protein (*O. sativa*)	35_15614	264.4	LIQENQAEFLR	Harvest Hv	Disease/Defence	18572
I	2	6	RAD23 protein (*O. sativa*)	35_15614	264.4	ILKDDTTLDANK	Harvest Hv	Disease/Defence	24719
I	2	6	RAD23 protein (*O. sativa*)	35_15614	264.4	APVSQSQPATPVAAATPPVPVASAAR	Harvest Hv	Disease/Defence	29445
I	1	1	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	62.16	AAPAAAAPEAAAPAPPAEPIAAA	Harvest Hv	Transport	29290
I	1	2	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	133.63	AISELIPQEIAHIEK	Harvest Hv	Transport	1129
I	1	2	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	133.63	AAPAAAAPEAAAPAPPAEPIAAA	Harvest Hv	Transport	2585
I	1	2	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	133.63	KPGIIVVQGPKPGK	Harvest Hv	Transport	10528
I	2	2	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	262.46	LFLSNQEK	Harvest Hv	Transport	619
I	2	2	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	262.46	QNALLLEEK	Harvest Hv	Transport	1861
I	2	2	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	262.46	AAPAAAAPEAAAPAPPAEPIAAA	Harvest Hv	Transport	3038
I	2	4	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	113.27	SQIILEAEEFKK	Harvest Hv	Transport	10649
I	2	8	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	202.51	SQIILEAEEFK	Harvest Hv	Transport	2112
I	2	8	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	202.51	KLNLETSK	Harvest Hv	Transport	4103
I	2	8	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	202.51	SQIILEAEEFKK	Harvest Hv	Transport	16093

I	2	8	Hypothetical protein B1206D04 26 (*O. sativa*)	35_15756	202.51	KPGIIVVQGPKPGK	Harvest Hv	Transport	28216
I	1	2	Putative cysteine proteinase (*O. sativa*)	35_16147	152.37	HGGVAAEDAYPYK	Harvest Hv	Protein destination	3750
I	1	2	Putative cysteine proteinase (*O. sativa*)	35_16147	223.42	HGGVAAE	Harvest Hv	Protein destination	7922
I	1	2	Putative cysteine proteinase (*O. sativa*)	35_16147	223.42	KPSAVVTIDGYEDVPANDETALKK	Harvest Hv	Protein destination	15136
I	1	6	Putative cysteine proteinase (*O. sativa*)	35_16147	152.37	CGTELDHGVAAVGYGTTVDGTK	Harvest Hv	Protein destination	1601
I	2	8	Putative cysteine proteinase (*O. sativa*)	35_16147	107.26	KPSAVVTIDGYEDVPANDETALK	Harvest Hv	Protein destination	309
I	2	8	Putative cysteine proteinase (*O. sativa*)	35_16147	107.26	CGTELDHGVAAVGYGTTVDGTK	Harvest Hv	Protein destination	4243
I	2	8	Putative cysteine proteinase (*O. sativa*)	35_16147	107.26	HGGVAAEDAYPYK	Harvest Hv	Protein destination	5876
I	2	8	Putative cysteine proteinase (*O. sativa*)	35_16147	107.26	DKEGLCGIAMEASYPVK	Harvest Hv	Protein destination	8708
I	1	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	273.26	GIQSQHDEIEAK	Harvest Hv	DNA binding	2956
I	1	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	209.09	TYHMVDEDDPILEK	Harvest Hv	DNA binding	6170
I	1	5	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	195.34	GIQSQHDEIEAK	Harvest Hv	DNA binding	193
I	1	5	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	273.26	TNEVLTEEIQER	Harvest Hv	DNA binding	419
I	1	5	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	209.09	MQSLAGLHADALESLSPNVR	Harvest Hv	DNA binding	12534
I	2	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	517.46	AIGTEIEWYPGK	Harvest Hv	DNA binding	287
I	2	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	517.46	LYEPLYAK	Harvest Hv	DNA binding	305
I	2	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	517.46	GIQSQHDEIEAK	Harvest Hv	DNA binding	2706
I	2	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	517.46	GIPDFWLTALK	Harvest Hv	DNA binding	3564
I	2	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	517.46	TYHMVDEDDPILEK	Harvest Hv	DNA binding	3735
I	2	2	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	517.46	TNEVLTEEIQER	Harvest Hv	DNA binding	7051
I	2	6	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	359.05	EPTTENAAEGGDSDAK	Harvest Hv	DNA binding	5413
I	2	6	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	359.05	AIGTEIEWYPGK	Harvest Hv	DNA binding	10370
I	2	6	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	359.05	LEFFFDTNPFFK	Harvest Hv	DNA binding	17441
I	2	6	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	359.05	TNEVLTEEIQER	Harvest Hv	DNA binding	18878
I	2	6	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	359.05	AGFTVTGGATMGGEK	Harvest Hv	DNA binding	24396
I	2	6	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	359.05	LYEPLYAK	Harvest Hv	DNA binding	28571
I	2	8	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	100.47	ENIDLSDLNISLPPAAAALSAEDR	Harvest Hv	DNA binding	447
I	2	8	Nucleosome assembly protein 1 like protein (*O. sativa*)	35_1627	100.47	AIGTEIEWYPGK	Harvest Hv	DNA binding	10986
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	92.78	GQAAAPSIEDQSQFPTLGGK	Harvest Hv	Unclassified	524
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	92.78	GGFGRGEPGR	Harvest Hv	Unclassified	1641
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	92.78	KANDEIFIK	Harvest Hv	Unclassified	3212
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	92.78	SLSINEFLKPAEGER	Harvest Hv	Unclassified	5921
I	2	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	153.55	GQAAAPSIEDQSQFPTLGGK	Harvest Hv	Unclassified	922
I	2	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	153.55	NSEFGDDSERPPR	Harvest Hv	Unclassified	1038
I	2	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	153.55	DGAAKEEEENEEDKEMTLEEYEK	Harvest Hv	Unclassified	5026
I	2	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	153.55	KANDEIFIK	Harvest Hv	Unclassified	11035
I	2	6	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	160.55	GQAAAPSIEDQSQFPTLGGK	Harvest Hv	Unclassified	28685

I	2	7	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	103.84	LPTKPAPPGQAAR	Harvest Hv	Unclassified	5471
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	207.79	DLQSLQPLSTK	Harvest Hv	Unclassified	2065
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	207.79	QGEQDDAPPTTEENKDQK	Harvest Hv	Unclassified	3862
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	207.79	ALANKPEAAPAGK	Harvest Hv	Unclassified	4649
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	207.79	ANKPEAAPAGK	Harvest Hv	Unclassified	5338
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	207.79	ANDEIFIK	Harvest Hv	Unclassified	6936
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_16328	207.79	KANDEIFIK	Harvest Hv	Unclassified	12907
I	1	2	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	59.87	DYLASLGAQLPAAAAGAK	Harvest Hv	Disease/Defence	2492
I	1	2	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	267.18	LEEAVEHLTK	Harvest Hv	Disease/Defence	4505
I	1	2	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	114.43	GQAMEAMSEGKLEEAVEHLTK	Harvest Hv	Disease/Defence	25878
I	1	5	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	267.18	AILLNPTSAIMYGTR	Harvest Hv	Disease/Defence	1455
I	1	5	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	170.57	AILLNPTSAIMYGTR	Harvest Hv	Disease/Defence	5706
I	2	2	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	152.22	GMANAMLGK	Harvest Hv	Disease/Defence	218
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	GQAMEAMSEGK	Harvest Hv	Disease/Defence	2865
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	MGDSSVEVTEENR	Harvest Hv	Disease/Defence	4184
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	DYLASLGAQLPAAAAGAK	Harvest Hv	Disease/Defence	5371
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	KDPSILADPALAFFRDYLASLGAQLPAAAAGAK	Harvest Hv	Disease/Defence	21684
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	SFVDACK	Harvest Hv	Disease/Defence	23332
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	RAEAQAAYDK	Harvest Hv	Disease/Defence	24155
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	TRGMANAMLGK	Harvest Hv	Disease/Defence	32063
I	2	6	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	219.3	DYLASLGAQLPAA	Harvest Hv	Disease/Defence	37599
I	2	8	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	173.11	MGDSSVEVTEENR	Harvest Hv	Disease/Defence	1807
I	2	8	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	173.11	LEEAVEHLTK	Harvest Hv	Disease/Defence	2349
I	2	8	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	173.11	MGDSSVEVTEENRDASQEAK	Harvest Hv	Disease/Defence	3911
I	2	8	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	173.11	DLHAASNIDYDDEINAVLK	Harvest Hv	Disease/Defence	22093
I	2	8	FAM10 family protein At4g22670 (*A. thaliana*)	35_1653	173.11	GQAMEAMSEGKLEEAVEHLTK	Harvest Hv	Disease/Defence	27952
I	1	2	Os09g0125100 protein (*O. sativa*)	35_16653	120.06	SAGYELPESLSFDDYAESLGK	Harvest Hv	Unclassified	516
I	1	2	Os09g0125100 protein (*O. sativa*)	35_16653	120.06	SPFAESLK	Harvest Hv	Unclassified	9344
I	2	2	Os09g0125100 protein (*O. sativa*)	35_16653	225	LNPDAAPFVPASK	Harvest Hv	Unclassified	1014
I	2	2	Os09g0125100 protein (*O. sativa*)	35_16653	225	SAGYELPESLSFDDYAESLGK	Harvest Hv	Unclassified	1070
I	2	2	Os09g0125100 protein (*O. sativa*)	35_16653	225	INISTESSSK	Harvest Hv	Unclassified	2715
I	1	6	Os05g0373700 protein (*O. sativa*)	35_16909	95.21	DIELVMAQASVPR	Harvest Hv	Unclassified	878
I	1	6	Os05g0373700 protein (*O. sativa*)	35_16909	86.61	AITGVSR	Harvest Hv	Unclassified	2381
I	2	6	Os05g0373700 protein (*O. sativa*)	35_16909	119.44	AADGDIVSAIMELTN	Harvest Hv	Unclassified	7176
I	2	6	Os05g0373700 protein (*O. sativa*)	35_16909	119.44	SSNSDTYVMFGEAK	Harvest Hv	Unclassified	10052
I	2	6	Os05g0373700 protein (*O. sativa*)	35_16909	119.44	DIELVMAQASVPR	Harvest Hv	Unclassified	14514

I	2	6	Os05g0373700 protein (*O. sativa*)	35_16909	119.44	SVMFVLSKPDVFK	Harvest Hv	Unclassified	22668
I	2	6	Os05g0373700 protein (*O. sativa*)	35_16909	119.44	GRPAMAAAQDDEEVDETGVDK	Harvest Hv	Unclassified	25242
I	2	7	Os05g0373700 protein (*O. sativa*)	35_16909	118.85	DIELVMAQASVPR	Harvest Hv	Unclassified	653
I	2	8	Os05g0373700 protein (*O. sativa*)	35_16909	296.89	AADGDIVSAIMELTN	Harvest Hv	Unclassified	511
I	2	8	Os05g0373700 protein (*O. sativa*)	35_16909	296.89	SSNSDTYVMFGEAK	Harvest Hv	Unclassified	772
I	2	8	Os05g0373700 protein (*O. sativa*)	35_16909	296.89	DIELVMAQASVPR	Harvest Hv	Unclassified	6202
I	2	8	Os05g0373700 protein (*O. sativa*)	35_16909	296.89	GRPAMAAAQDDEEVDETGVDKK	Harvest Hv	Unclassified	6367
I	2	8	Os05g0373700 protein (*O. sativa*)	35_16909	296.89	IEDLSTQLHSQAAEQFK	Harvest Hv	Unclassified	7317
I	2	8	Os05g0373700 protein (*O. sativa*)	35_16909	296.89	SVMFVLSKPDVFK	Harvest Hv	Unclassified	8773
I	1	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	135.31	LDTSEDSSGAVPLLK	Harvest Hv	Protein destination	1150
I	1	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	135.31	FGFSSSTPQQNDK	Harvest Hv	Protein destination	2230
I	1	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	136.05	EVHEAK	Harvest Hv	Protein destination	3810
I	2	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	362.88	TLLEGVDMTDK	Harvest Hv	Protein destination	1025
I	2	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	362.88	VLRPAEVGVTEGGPSEEPEDK	Harvest Hv	Protein destination	1085
I	2	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	362.88	SLLDVADNLAR	Harvest Hv	Protein destination	1189
I	2	2	Putative chaperone GrpE type 2 (*O. sativa*)	35_17646	362.88	LDTSEDSSGAVPLLK	Harvest Hv	Protein destination	1741
I	1	2	Putative chaperonin 21 (O. sativa)	35_1799	250.94	EDDIIGILDTDDVK	Harvest Hv	Protein destination	943
I	1	4	Putative chaperonin 21 (O. sativa)	35_1799	250.94	TPLSITPGSSVLYSK	Harvest Hv	Protein destination	1057
I	1	5	Putative chaperonin 21 (O. sativa)	35_1799	250.94	EKPSVGTVVAVGPGPLGDDGSR	Harvest Hv	Protein destination	2147
I	2	2	Putative chaperonin 21 (O. sativa)	35_1799	228.18	EDDIIGILDTDDVK	Harvest Hv	Protein destination	246
I	2	2	Putative chaperonin 21 (O. sativa)	35_1799	228.18	GSEGEYIVLR	Harvest Hv	Protein destination	624
I	2	2	Putative chaperonin 21 (O. sativa)	35_1799	228.18	EDDIIGILDTDDVKDLKPLSDR	Harvest Hv	Protein destination	1514
I	2	2	Putative chaperonin 21 (O. sativa)	35_1799	228.18	VAESEEETAGGLLLTQMSK	Harvest Hv	Protein destination	2741
I	2	2	Putative chaperonin 21 (O. sativa)	35_1799	228.18	EKPSVGTVVAVGPGPLGDDGSR	Harvest Hv	Protein destination	12441
I	2	4	Putative chaperonin 21 (O. sativa)	35_1799	121.66	TPLSITPGSSVLYSK	Harvest Hv	Protein destination	53
I	2	7	Putative chaperonin 21 (O. sativa)	35_1799	78.51	EKPSVGTVVAVGPGPLGDDGSR	Harvest Hv	Protein destination	3285
I	2	8	Putative chaperonin 21 (O. sativa)	35_1799	129.49	YTSVKPLGDR	Harvest Hv	Protein destination	6105
I	2	8	Putative chaperonin 21 (O. sativa)	35_1799	129.49	GSEGEYIVLR	Harvest Hv	Protein destination	8527
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	91.28	QPYRGGGGR	Harvest Hv	Unclassified	1616
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	190.56	NINEFLKPAEGER	Harvest Hv	Unclassified	5292
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	190.56	RPAAAPAIEDQSQFPTLGGK	Harvest Hv	Unclassified	5709
I	1	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	91.28	AILALK	Harvest Hv	Unclassified	5881
I	1	5	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	162.22	TPEDAPLPEAEK	Harvest Hv	Unclassified	493
I	1	5	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	190.56	SLNINEFLKPAEGER	Harvest Hv	Unclassified	4154
I	2	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	178.06	EGAENAEEEKEAEEDKEMTLEEYEK	Harvest Hv	Unclassified	1579
I	2	2	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	178.06	RPAAAPAIEDQSQFPTLGGK	Harvest Hv	Unclassified	3171
I	2	7	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	315.04	TPEDAPLPEAEK	Harvest Hv	Unclassified	528

I	2	7	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	315.04	SLNINEFLKPAEGER	Harvest Hv	Unclassified	4244
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	224.47	KDAEEVFIK	Harvest Hv	Unclassified	1780
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	224.47	TPEDAPLPEAEK	Harvest Hv	Unclassified	16531
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	224.47	GGYSDGQNTDEFGRPHR	Harvest Hv	Unclassified	21815
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	224.47	SLNINEFLKPAEGER	Harvest Hv	Unclassified	50322
I	2	8	Putative nuclear RNA binding protein A (*O. sativa*)	35_2103	224.47	VKEGAENAEEEKEAEEDKEMTLEEYEK	Harvest Hv	Unclassified	50645
I	1	5	HMG I Y protein HMGa (*T. aestivum*)	35_2226	101.03	YEGLPSAHASLLTANLASMK	Harvest Hv	DNA binding	12606
I	1	6	HMG I Y protein HMGa (*T. aestivum*)	35_2226	210.34	EAESPAAASGSAPAK	Harvest Hv	DNA binding	1318
I	1	6	HMG I Y protein HMGa (*T. aestivum*)	35_2226	234.03	EAESPAAASGSAPAK	Harvest Hv	DNA binding	15919
I	2	4	HMG I Y protein HMGa (*T. aestivum*)	35_2226	211.8	EAESPAAASGSAPAK	Harvest Hv	DNA binding	3495
I	2	4	HMG I Y protein HMGa (*T. aestivum*)	35_2226	211.8	YEGLPSAHASLLTANLASMK	Harvest Hv	DNA binding	15214
I	2	7	HMG I Y protein HMGa (*T. aestivum*)	35_2226	178.54	SAISSYIEEK	Harvest Hv	DNA binding	525
I	2	7	HMG I Y protein HMGa (*T. aestivum*)	35_2226	178.54	YEGLPSAHASLLTANLASMK	Harvest Hv	DNA binding	12874
I	2	8	HMG I Y protein HMGa (*T. aestivum*)	35_2226	238.52	SGDIPPYPEMILAAIEALGDTNGSNK	Harvest Hv	DNA binding	2613
I	2	8	HMG I Y protein HMGa (*T. aestivum*)	35_2226	238.52	ADAVSATPAK	Harvest Hv	DNA binding	12425
I	2	8	HMG I Y protein HMGa (*T. aestivum*)	35_2226	238.52	GRPPKDPMSVAVK	Harvest Hv	DNA binding	15651
I	2	8	HMG I Y protein HMGa (*T. aestivum*)	35_2226	238.52	LAFVK	Harvest Hv	DNA binding	16560
I	2	8	HMG I Y protein HMGa (*T. aestivum*)	35_2226	238.52	SGDIPPYPEMILAAIEALGDTNGSNK	Harvest Hv	DNA binding	50069
I	1	2	Phytepsin precursor (*H. vulgare*)	35_280	302.91	EPGVTFLVAK	Harvest Hv	Protein destination	1073
I	1	2	Phytepsin precursor (*H. vulgare*)	35_280	302.91	ELISAGKDAESAYWELVIK	Harvest Hv	Protein destination	4490
I	1	5	Phytepsin precursor (*H. vulgare*)	35_280	263.99	HYVGEHTYVPVTQK	Harvest Hv	Protein destination	7229
I	2	2	Phytepsin precursor (*H. vulgare*)	35_280	102.21	EPGVTFLVAK	Harvest Hv	Protein destination	1651
I	2	2	Phytepsin precursor (*H. vulgare*)	35_280	102.21	FDGILGLGFK	Harvest Hv	Protein destination	6180
I	2	8	Phytepsin precursor (*H. vulgare*)	35_280	276.85	DQEFIEATKEPGVTFLVAK	Harvest Hv	Protein destination	7259
I	2	8	Phytepsin precursor (*H. vulgare*)	35_280	276.85	EPGVTFLVAK	Harvest Hv	Protein destination	13586
I	1	5	Putative CDR1 (*O. sativa*)	35_3551	183.87	AAVTDPGAVTTPLIPSQVK	Harvest Hv	Protein destination	296
I	1	5	Putative CDR1 (*O. sativa*)	35_3551	183.87	LLPLCFDVSGVR	Harvest Hv	Protein destination	982
I	2	2	Putative CDR1 (*O. sativa*)	35_3551	173.42	DADAQPPGVQFDPSK	Harvest Hv	Protein destination	493
I	2	2	Putative CDR1 (*O. sativa*)	35_3551	173.42	ASSALNFGPR	Harvest Hv	Protein destination	1129
I	2	4	Putative CDR1 (*O. sativa*)	35_3551	603.05	LLPLCFDVSGVR	Harvest Hv	Protein destination	71
I	2	4	Putative CDR1 (*O. sativa*)	35_3551	603.05	SPLIVDSGTTLTFLPEALVDPLVK	Harvest Hv	Protein destination	83
I	2	4	Putative CDR1 (*O. sativa*)	35_3551	603.05	AAVTDPGAVTTPLIPSQVK	Harvest Hv	Protein destination	1339
I	2	4	Putative CDR1 (*O. sativa*)	35_3551	603.05	LVDCDSVACSELPEASCGADSK	Harvest Hv	Protein destination	1374
I	2	8	Putative CDR1 (*O. sativa*)	35_3551	214.47	AYYIVELR	Harvest Hv	Protein destination	7122
I	2	8	Putative CDR1 (*O. sativa*)	35_3551	214.47	LVDCDSVACSELPEASCGADSK	Harvest Hv	Protein destination	28306
I	1	6	Peroxiredoxin (*O. sativa*)	35_35528	176.87	FLADGAAAYTK	Harvest Hv	Disease/Defence	150
I	1	6	Peroxiredoxin (*O. sativa*)	35_35528	176.87	ALGLELDLTEK	Harvest Hv	Disease/Defence	1600

I	2	4	Peroxiredoxin (*O. sativa*)	35_35528	139.21	ALGLELDLTEK	Harvest Hv	Disease/Defence	7002
I	2	4	Peroxiredoxin (*O. sativa*)	35_35528	139.21	VILFGVPGAFTPTCSNQHVPGFITQAEDLK	Harvest Hv	Disease/Defence	27669
I	2	7	Peroxiredoxin (*O. sativa*)	35_35528	152.01	FALLADDLK	Harvest Hv	Disease/Defence	50
I	2	7	Peroxiredoxin (*O. sativa*)	35_35528	152.01	FLADGAAAYTK	Harvest Hv	Disease/Defence	656
I	2	8	Peroxiredoxin (*O. sativa*)	35_35528	113.58	FLADGAAAYTK	Harvest Hv	Disease/Defence	10983
I	2	8	Peroxiredoxin (*O. sativa*)	35_35528	113.58	KVILFGVPGAFTPTCSNQHVPGFITQAEDLK	Harvest Hv	Disease/Defence	28022
I	2	8	Peroxiredoxin (*O. sativa*)	35_35528	113.58	ALGLELDLTEK	Harvest Hv	Disease/Defence	28069
I	1	2	Elongation factor 1 beta (*T. aestivum*)	35_41584	287.05	ALEAHLAGK	Harvest Hv	Protein synthesis	199
I	1	2	Elongation factor 1 beta (*T. aestivum*)	35_41584	125.02	LPSSPDPMAVTFSDLHSADGLK	Harvest Hv	Protein synthesis	18439
I	1	5	Elongation factor 1 beta (*T. aestivum*)	35_41584	287.05	GVQMEGLTWGASK	Harvest Hv	Protein synthesis	562
I	1	5	Elongation factor 1 beta (*T. aestivum*)	35_41584	287.05	WYDAVAAAVSPR	Harvest Hv	Protein synthesis	2110
I	1	6	Elongation factor 1 beta (*T. aestivum*)	35_41584	287.05	TYISGDAITK	Harvest Hv	Protein synthesis	1124
I	2	2	Elongation factor 1 beta (*T. aestivum*)	35_41584	231.54	ALEAHLAGK	Harvest Hv	Protein synthesis	3443
I	2	2	Elongation factor 1 beta (*T. aestivum*)	35_41584	231.54	VFAAVPVKPSAEFPNAAR	Harvest Hv	Protein synthesis	27742
I	1	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432	169.99	FEELNMDLFR	Harvest Hv	Disease/Defence	29917
I	1	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432	946.28	FADAPVQSDIK	Harvest Hv	Disease/Defence	361
I	2	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432	449.24	FADAPVQSDIK	Harvest Hv	Disease/Defence	9506
I	2	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432	449.24	KIEDAVDAAIQWLDANQLGEVDEFEDK	Harvest Hv	Disease/Defence	31427
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432	332.85	FADAPVQSDIK	Harvest Hv	Disease/Defence	316
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_432	332.85	MYQGAGADMPGGMDDDVPAASGGAGPK	Harvest Hv	Disease/Defence	1265
I	1	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	121.33	EEIEKMVQEAEK	Harvest Hv	Disease/Defence	33817
I	1	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	1058.81	FTDSTVQSDIK	Harvest Hv	Disease/Defence	352
I	1	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	449.17	MVQEAEK	Harvest Hv	Disease/Defence	691
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	858.43	VVAGPGDKPMINVQYK	Harvest Hv	Disease/Defence	4869
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	382.55	DAGVIAGINVLR	Harvest Hv	Disease/Defence	2578
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	382.55	FEEMNMDLFR	Harvest Hv	Disease/Defence	2596
I	2	8	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	35_453	382.55	FTDSTVQSDIK	Harvest Hv	Disease/Defence	3729
I	1	4	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	210.63	NILESVGAEADEEK	Harvest Hv	Protein synthesis	749
I	1	5	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	210.63	NILESVGAEADEEKLK	Harvest Hv	Protein synthesis	3305
I	1	6	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	210.63	GKDITEVIAAGR	Harvest Hv	Protein synthesis	1126
I	2	2	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	506.03	DITEVIAAGREK	Harvest Hv	Protein synthesis	1413
I	2	2	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	506.03	GKDITEVIAAGR	Harvest Hv	Protein synthesis	4788
I	2	2	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	506.03	FAAVPSGGGAIAVGAPAAAAGGAAAPAAESK	Harvest Hv	Protein synthesis	27599
I	2	7	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	203.73	NILESVGAEADEEK	Harvest Hv	Protein synthesis	640
I	2	7	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	203.73	FLLAELK	Harvest Hv	Protein synthesis	888

I	2	7	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	203.73	NILESVGAEADEEKLK	Harvest Hv	Protein synthesis	3198
I	2	3	60S acidic ribosomal protein P2B (*Z. mays*)	35_49914	344.06	FAAVPSGGGAIAVGAPAAAAGGAAAPAAESK	Harvest Hv	Protein synthesis	737
I	1	2	Histone H2B 3 (*Z. mays*)	35_50103	230.23	KPVEEEPAAEK	Harvest Hv	DNA binding	5958
I	1	6	Histone H2B 3 (*Z. mays*)	35_50103	177.86	KPVEEEPAAEK	Harvest Hv	DNA binding	2818
I	1	6	Histone H2B 3 (*Z. mays*)	35_50103	158.02	LPSAGK	Harvest Hv	DNA binding	2948
I	2	8	Histone H2B 3 (*Z. mays*)	35_50103	203.91	KPVEEEPAAEK	Harvest Hv	DNA binding	3919
I	2	8	Histone H2B 3 (*Z. mays*)	35_50103	203.91	YNKKPTITSR	Harvest Hv	DNA binding	20451
I	2	8	Histone H2B 3 (*Z. mays*)	35_50103	203.91	AMSIMNSFINDIFEK	Harvest Hv	DNA binding	28534
I	2	8	Histone H2B 3 (*Z. mays*)	35_50103	203.91	LPHPTLIPTPAATYPDPMAPKAEK	Harvest Hv	DNA binding	51084
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	185.64	ELAAAAMAR	Harvest Hv	Metabolism	29660
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	185.64	ANRPYGMDLPGRPTGR	Harvest Hv	Metabolism	32546
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	185.64	FTNGYNLADVISQR	Harvest Hv	Metabolism	32660
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	185.64	EAAAATMK	Harvest Hv	Metabolism	33129
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	185.64	MVTTYIEHIQALYDMGAR	Harvest Hv	Metabolism	33159
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	138.14	LAEAAAATMK	Harvest Hv	Metabolism	33691
I	1	1	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	185.64	ANRPYGMDLPGRPTGR	Harvest Hv	Metabolism	38180
I	1	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	296.92	TQVQYFK	Harvest Hv	Metabolism	1261
I	1	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	104.19	ANRPYGMDLPGRPTGR	Harvest Hv	Metabolism	10153
I	1	4	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	296.92	YGEPVNFATLVTGK	Harvest Hv	Metabolism	932
I	1	6	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	296.92	YASGGSGILDTTGK	Harvest Hv	Metabolism	1586
I	1	6	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	296.92	FTNGYNLADVISQR	Harvest Hv	Metabolism	3372
I	1	6	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	296.92	IGANYASGGSGILDTTGK	Harvest Hv	Metabolism	3921
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	YGEPVNFATLVTGK	Harvest Hv	Metabolism	924
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	TQVQYFK	Harvest Hv	Metabolism	1434
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	IGANYASGGSGILDTTGK	Harvest Hv	Metabolism	3543
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	AADNMICYPSK	Harvest Hv	Metabolism	4199
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	FTNGYNLADVISQR	Harvest Hv	Metabolism	4997
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	LAEAAAATMK	Harvest Hv	Metabolism	5428
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	ILLGLCK	Harvest Hv	Metabolism	5841
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	MVTTYIEHIQALYDMGAR	Harvest Hv	Metabolism	6082
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	MVGILDVPPIGCTPGQR	Harvest Hv	Metabolism	10333
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	YSVAANYNILNEMMDNSLVAGLR	Harvest Hv	Metabolism	12289
I	2	2	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	772.19	SLFLLSGGGNDFSAFDPSTASPQAYVVK	Harvest Hv	Metabolism	15620
I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	IGANYASGGSGILDTTGKGTLTMR	Harvest Hv	Metabolism	1144
I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	AADNMICYPSK	Harvest Hv	Metabolism	7658
I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	GVVAFFYGNGPK	Harvest Hv	Metabolism	14618

I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	LAEAAAATMK	Harvest Hv	Metabolism	16810
I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	SLFLLSGGGNDFSAFDPSTASPQAYVVK	Harvest Hv	Metabolism	16815
I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	MVTTYIEHIQALYDMGAR	Harvest Hv	Metabolism	17293
I	2	8	GDSL like Lipase Acylhydrolase family protein (*O. sativa*)	35_581	325.89	ANRPYGMDLPGRPTGR	Harvest Hv	Metabolism	29162
I	1	2	Nucleoside diphosphate kinase (*L. perenne*)	35_610	209.63	GLIGEVISR	Harvest Hv	Energy metabolism	1623
I	1	3	Nucleoside diphosphate kinase (*L. perenne*)	35_610	209.63	IIGATNPLASEPGTIR	Harvest Hv	Energy metabolism	89
I	2	2	Nucleoside diphosphate kinase (*L. perenne*)	35_610	480.32	GLIGEVISR	Harvest Hv	Energy metabolism	1882
I	2	2	Nucleoside diphosphate kinase (*L. perenne*)	35_610	480.32	SSQHNWIYEA	Harvest Hv	Energy metabolism	2545
I	2	2	Nucleoside diphosphate kinase (*L. perenne*)	35_610	480.32	IIGATNPLASEPGTIR	Harvest Hv	Energy metabolism	27700
I	2	7	Nucleoside diphosphate kinase (*L. perenne*)	35_610	180.52	IIGATNPLASEPGTIR	Harvest Hv	Energy metabolism	452
I	1	2	40S ribosomal protein (*O. sativa*)	35_685	206.19	LDRPDGDEVIPGAEEVAAAE	Harvest Hv	Protein synthesis	9720
I	1	2	40S ribosomal protein (*O. sativa*)	35_685	206.19	LMEVHGDYKEDVGVK	Harvest Hv	Protein synthesis	10040
I	1	3	40S ribosomal protein (*O. sativa*)	35_685	634.54	ATSSIFPLQNVYVR	Harvest Hv	Protein synthesis	122
I	1	4	40S ribosomal protein (*O. sativa*)	35_685	634.54	LDRPDGDEVIPGAEEVAAAE	Harvest Hv	Protein synthesis	572
I	1	5	40S ribosomal protein (*O. sativa*)	35_685	634.54	APLLFTSR	Harvest Hv	Protein synthesis	1169
I	2	2	40S ribosomal protein (*O. sativa*)	35_685	546.23	APLLFTSR	Harvest Hv	Protein synthesis	338
I	2	2	40S ribosomal protein (*O. sativa*)	35_685	546.23	AEDVQGMNVLTNFWGMDFTTDK	Harvest Hv	Protein synthesis	1145
I	2	2	40S ribosomal protein (*O. sativa*)	35_685	546.23	MFAIGFTK	Harvest Hv	Protein synthesis	3135
I	2	7	40S ribosomal protein (*O. sativa*)	35_685	270.87	ATSSIFPLQNVYVR	Harvest Hv	Protein synthesis	37
I	2	8	40S ribosomal protein (*O. sativa*)	35_685	138.6	APLLFTSR	Harvest Hv	Protein synthesis	15679
I	2	8	40S ribosomal protein (*O. sativa*)	35_685	138.6	FIPEVIGK	Harvest Hv	Protein synthesis	28100
I	2	8	40S ribosomal protein (*O. sativa*)	35_685	138.6	LDRPDGDEVIPGAEEVAAAE	Harvest Hv	Protein synthesis	50546
I	1	2	CAA303712 1 protein (*O. sativa*)	35_759	196.99	TTAPIVQQFAR	Harvest Hv	Disease/Defence	3147
I	1	2	CAA303712 1 protein (*O. sativa*)	35_759	196.99	VHAACGPTVSCADISALATR	Harvest Hv	Disease/Defence	5906
I	1	2	CAA303712 1 protein (*O. sativa*)	35_759	196.99	IFFHDCFPQGCDASVYLK	Harvest Hv	Disease/Defence	10320
I	2	2	CAA303712 1 protein (*O. sativa*)	35_759	456.42	TTAPIVQQFAR	Harvest Hv	Disease/Defence	3185
I	2	2	CAA303712 1 protein (*O. sativa*)	35_759	456.42	EVALAAGLLR	Harvest Hv	Disease/Defence	5513
I	2	2	CAA303712 1 protein (*O. sativa*)	35_759	456.42	LQNLDVVTPDLFDNGYYK	Harvest Hv	Disease/Defence	5853
I	2	6	CAA303712 1 protein (*O. sativa*)	35_759	247.3	TTAPIVQQFAR	Harvest Hv	Disease/Defence	17082
I	2	6	CAA303712 1 protein (*O. sativa*)	35_759	247.3	MDDAFSR	Harvest Hv	Disease/Defence	24197
I	2	8	CAA303712 1 protein (*O. sativa*)	35_759	306.94	DAFFAQFAK	Harvest Hv	Disease/Defence	6515
I	2	8	CAA303712 1 protein (*O. sativa*)	35_759	306.94	ALVNSQGVFTSDMVLIK	Harvest Hv	Disease/Defence	14570
I	2	8	CAA303712 1 protein (*O. sativa*)	35_759	306.94	MDDAFSR	Harvest Hv	Disease/Defence	16558
I	2	8	CAA303712 1 protein (*O. sativa*)	35_759	306.94	NCFSPNALR	Harvest Hv	Disease/Defence	17635
I	2	8	CAA303712 1 protein (*O. sativa*)	35_759	306.94	HTTSTMATTGSR	Harvest Hv	Disease/Defence	50379
I	1	2	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	164.99	DINALEQHIK	Harvest Hv	Cell wall	1009
I	1	2	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	164.99	DINALEQHIK	Harvest Hv	Cell wall	1417

I	1	2	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	164.99	TGLPYIWHSK	Harvest Hv	Cell wall	3864
I	1	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	164.99	YVDAVLTIPK	Harvest Hv	Cell wall	145
I	2	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	297.01	DELDIVIPTIR	Harvest Hv	Cell wall	3407
I	2	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	297.01	ASCISFK	Harvest Hv	Cell wall	3813
I	2	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	297.01	GAITTTNSPAVK	Harvest Hv	Cell wall	15764
I	2	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	297.01	NLLSPSTPFFFNTLYDPYR	Harvest Hv	Cell wall	22410
I	2	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	297.01	EGADFVR	Harvest Hv	Cell wall	25586
I	2	6	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	297.01	GTLFPMCGMNLAFDR	Harvest Hv	Cell wall	28241
I	1	2	Dehydroascorbate reductase (*T. aestivum*)	35_861	61.54	AHGPYINGANVSAADLSLAPK	Harvest Hv	Unclassified	5925
I	1	2	Dehydroascorbate reductase (*T. aestivum*)	35_861	61.54	VPETLTSVHAYTEALFSR	Harvest Hv	Unclassified	12711
I	2	2	Dehydroascorbate reductase (*T. aestivum*)	35_861	94.49	VPVFNGGDGK	Harvest Hv	Unclassified	1812
I	2	2	Dehydroascorbate reductase (*T. aestivum*)	35_861	94.49	KVPYEMK	Harvest Hv	Unclassified	10924
I	2	2	Dehydroascorbate reductase (*T. aestivum*)	35_861	94.49	ALVDELQALEEHLK	Harvest Hv	Unclassified	15116
I	2	6	Dehydroascorbate reductase (*T. aestivum*)	35_861	148.89	INPEGKVPVFNGGDGK	Harvest Hv	Unclassified	18450
I	2	6	Dehydroascorbate reductase (*T. aestivum*)	35_861	148.89	VPETLTSVHAYTEALFSRESFVK	Harvest Hv	Unclassified	19647
I	2	6	Dehydroascorbate reductase (*T. aestivum*)	35_861	148.89	ALVDELQALEEHLK	Harvest Hv	Unclassified	21243
I	2	6	Dehydroascorbate reductase (*T. aestivum*)	35_861	148.89	AAVGHPDTLGDCPFSQR	Harvest Hv	Unclassified	27350
I	2	6	Dehydroascorbate reductase (*T. aestivum*)	35_861	148.89	VPVFNGGDGK	Harvest Hv	Unclassified	35111
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2WW49	78.98	ALTVPELTQQMWDAK	Uniref 90	Unclassified	797
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2WW49	78.98	RVSEQFTAMFR	Uniref 90	Unclassified	2092
I	1	5	Putative uncharacterized protein (*O. sativa*)	A2WW49	78.98	AVLMDLEPGTMDSVR	Uniref 90	Unclassified	615
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2WW49	78.98	VNVYYNEASCGR	Uniref 90	Unclassified	463
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2WW49	172.29	AVLMDLEPGTMDSVR	Uniref 90	Unclassified	516
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2WW49	172.29	LAVNLIPFPR	Uniref 90	Unclassified	566
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2WW49	172.29	FWEVVCDEHGIDPTGR	Uniref 90	Unclassified	9267
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2WW49	172.29	YTGNSDLQLERVNVYYNEASCGR	Uniref 90	Unclassified	21383
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2X180	151.75	IEDVTPVPTDSTR	Uniref 90	Unclassified	292
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2X180	151.75	TPGPGAQSALR	Uniref 90	Unclassified	2270
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2X180	144.14	IEDVTPVPTDSTR	Uniref 90	Unclassified	62
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2X180	144.14	TPGPGAQSALR	Uniref 90	Unclassified	3904
I	1	3	Putative uncharacterized protein (*O. sativa*)	A2XF40	665.74	IINEPTAAAIAYGLDK	Uniref 90	Protein destination	511
I	1	4	Putative uncharacterized protein (*O. sativa*)	A2XF40	665.74	TTPSYVAFTDSER	Uniref 90	Protein destination	165
I	1	4	Putative uncharacterized protein (*O. sativa*)	A2XF40	665.74	NAVVTVPAYFNDSQR	Uniref 90	Protein destination	283
I	1	4	Putative uncharacterized protein (*O. sativa*)	A2XF40	665.74	NQVAMNPINTVFDAK	Uniref 90	Protein destination	517
I	1	5	Putative uncharacterized protein (*O. sativa*)	A2XF40	665.74	IINEPTAAAIAYGLDKK	Uniref 90	Protein destination	785
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2XF40	518.65	VEIIANDQGNR	Uniref 90	Protein destination	233
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2XF40	518.65	NQVAMNPINTVFDAK	Uniref 90	Protein destination	3335

I	1	2	Putative uncharacterized protein (*O. sativa*)	A2XHR6	171.25	HTPGTFTNQLQTSFSEPR	Uniref 90	Protein synthesis	2507
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2XHR6	171.25	ESALGNIPTIAFCDTDSPMR	Uniref 90	Protein synthesis	530
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2XHR6	301.97	ESALGNIPTIAFCDTDSPMR	Uniref 90	Protein synthesis	280
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2XHR6	301.97	NCDFQMER	Uniref 90	Protein synthesis	722
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2XHR6	301.97	YVDIGIPANNK	Uniref 90	Protein synthesis	1697
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2XLB7	204.45	FFEVPTGWK	Uniref 90	Unclassified	411
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2XLB7	192.2	EDFGGGHPDPNLTYAK	Uniref 90	Unclassified	1686
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2XLB7	204.45	LSGTGSVGATIR	Uniref 90	Unclassified	2164
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2XLB7	204.45	SMPTSAALDVVAK	Uniref 90	Unclassified	2371
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XLB7	175.48	FFEVPTGWK	Uniref 90	Unclassified	927
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XLB7	175.48	GATIVVSGDGR	Uniref 90	Unclassified	4418
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2XLB7	175.48	KVTVFQQPHYLQNFVQSTFNALPADK	Uniref 90	Unclassified	21234
I	1	2	Histone H2A (*O. sativa*)	A2XLW3	115.38	APVSRSSR	Uniref 90	Unclassified	245
I	1	2	Histone H2A (*O. sativa*)	A2XLW3	115.38	GDEELDTLIK	Uniref 90	Unclassified	1071
I	1	2	Histone H2A (*O. sativa*)	A2XLW3	115.38	HLQLAIR	Uniref 90	Unclassified	1913
I	2	2	Histone H2A (*O. sativa*)	A2XLW3	197.52	GDEELDTLIK	Uniref 90	Unclassified	364
I	2	2	Histone H2A (*O. sativa*)	A2XLW3	197.52	HLQLAIR	Uniref 90	Unclassified	8710
I	1	2	40S ribosomal protein S12 (*O. sativa*)	A2YI73	169.01	VVGCSCVVVK	Uniref 90	Unclassified	3004
I	1	2	40S ribosomal protein S12 (*O. sativa*)	A2YI73	169.01	HAAQLCVLAEDCDQPDYVK	Uniref 90	Unclassified	5204
I	1	4	40S ribosomal protein S12 (*O. sativa*)	A2YI73	164.81	ALCAEHNVHLVTVPSAK	Uniref 90	Unclassified	8673
I	2	2	40S ribosomal protein S12 (*O. sativa*)	A2YI73	169.55	VVGCSCVVVK	Uniref 90	Unclassified	2729
I	2	2	40S ribosomal protein S12 (*O. sativa*)	A2YI73	169.55	HAAQLCVLAEDCDQPDYVK	Uniref 90	Unclassified	4650
I	1	4	Putative uncharacterized protein (*O. sativa*)	A2YLI4	166.88	EIAMLWGEIK	Uniref 90	Unclassified	234
I	1	4	Putative uncharacterized protein (*O. sativa*)	A2YLI4	166.88	MIVSLSYASSR	Uniref 90	Unclassified	263
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2YLI4	166.88	LTVNFVLPYK	Uniref 90	Unclassified	22
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2YLI4	137.02	IMFDPIKVDK	Uniref 90	Unclassified	1820
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2YLI4	137.02	LEYGELTVDR	Uniref 90	Unclassified	3934
I	2	8	Putative uncharacterized protein (*O. sativa*)	A2YLI4	137.02	NSSLLSSLVQEIEHYSSR	Uniref 90	Unclassified	4811
I	1	5	Putative uncharacterized protein (*O. sativa*)	A2YSB2	132.15	GNVTPDAVLQTVSK	Uniref 90	Transport	324
I	1	6	Putative uncharacterized protein (*O. sativa*)	A2YSB2	132.15	VGMSCEGCVGAVK	Uniref 90	Transport	1877
I	2	4	Putative uncharacterized protein (*O. sativa*)	A2YSB2	197.39	VGMSCEGCVGAVK	Uniref 90	Transport	381
I	2	7	Putative uncharacterized protein (*O. sativa*)	A2YSB2	119.8	GNVTPDAVLQTVSK	Uniref 90	Transport	632
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	202.56	VFEVSLADLQNDE	Uniref 90	Unclassified	1751
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	202.56	FIPEVIGK	Uniref 90	Unclassified	2849
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	202.56	VFEVSLADLQNDEDQAYRK	Uniref 90	Unclassified	4311
I	1	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	202.56	MVEIMVNQASSCDLK	Uniref 90	Unclassified	10829
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	405.34	VFEVSLADLQNDEDQAYR	Uniref 90	Unclassified	221

I	2	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	405.34	TCYAQASQIR	Uniref 90	Unclassified	297
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	405.34	TTDNYMLR	Uniref 90	Unclassified	326
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	405.34	FIPEVIGK	Uniref 90	Unclassified	331
I	2	2	Putative uncharacterized protein (*O. sativa*)	A2ZJS3	405.34	WQTLIEAHVDVK	Uniref 90	Unclassified	1842
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3BQX7	321.29	VIEEGLGK	Uniref 90	Protein synthesis	3103
I	1	4	Putative uncharacterized protein (*O. sativa*)	A3BQX7	321.29	EANNFLWPFK	Uniref 90	Protein synthesis	1022
I	1	5	Putative uncharacterized protein (*O. sativa*)	A3BQX7	321.29	VEPYVAYGYPNLK	Uniref 90	Protein synthesis	1006
I	1	5	Putative uncharacterized protein (*O. sativa*)	A3BQX7	321.29	QIFNGVFLK	Uniref 90	Protein synthesis	1486
I	2	2	Putative uncharacterized protein (*O. sativa*)	A3BQX7	150.67	ATINMLR	Uniref 90	Protein synthesis	638
I	2	2	Putative uncharacterized protein (*O. sativa*)	A3BQX7	150.67	GGFYVSPEAK	Uniref 90	Protein synthesis	1073
I	2	2	Putative uncharacterized protein (*O. sativa*)	A3BQX7	150.67	EANNFLWPFK	Uniref 90	Protein synthesis	4966
I	2	4	Putative uncharacterized protein (*O. sativa*)	A3BRX9	204.57	TASVLCLTTVK	Uniref 90	Protein synthesis	1184
I	2	4	Putative uncharacterized protein (*O. sativa*)	A3BRX9	204.57	YGLNHVTYLIEQSK	Uniref 90	Protein synthesis	19974
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3BRY5	310.89	VLAFEAGR	Uniref 90	Protein synthesis	2542
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3C065	146.86	MKETAEAFLGK	Uniref 90	Unclassified	1239
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3C065	146.86	SSGGLSESDIEKMVR	Uniref 90	Unclassified	1418
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3C065	146.86	GVNPDEAVAMGAAIQGGILR	Uniref 90	Unclassified	1424
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3C065	139.91	TAEAFLGK	Uniref 90	Unclassified	3295
I	1	2	Putative uncharacterized protein (*O. sativa*)	A3C065	139.91	NSADTTIYSIEK	Uniref 90	Unclassified	8742
I	1	6	Putative uncharacterized protein (*O. sativa*)	A3C065	146.86	AVITVPAYFNDAQR	Uniref 90	Unclassified	307
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3C065	179.05	GVNPDEAVAMGAAIQGGILR	Uniref 90	Unclassified	4240
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3C065	179.05	IPCVNCLK	Uniref 90	Unclassified	5726
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3C065	179.05	DIDEVLLVGGMTR	Uniref 90	Unclassified	6236
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3C065	179.05	AVITVPAYFNDAQR	Uniref 90	Unclassified	11437
I	2	8	Putative uncharacterized protein (*O. sativa*)	A3C065	179.05	EGLIAVFDLGGGTFDVSILEISNGVFEVK	Uniref 90	Unclassified	51440
I	1	2	EEA1 (*H. vulgare*)	O22491	130.79	SEGDLATDIISVNGR	Uniref 90	Protein destination	1269
I	1	2	EEA1 (*H. vulgare*)	O22491	130.79	ENVIGHCLSSK	Uniref 90	Protein destination	1813
I	1	6	EEA1 (*H. vulgare*)	O22491	130.79	VVCGSPLCVAVR	Uniref 90	Protein destination	11
I	1	6	EEA1 (*H. vulgare*)	O22491	130.79	GVLYVGDFNPPTR	Uniref 90	Protein destination	1581
I	2	8	EEA1 (*H. vulgare*)	O22491	122.19	GVLYVGDFNPPTR	Uniref 90	Protein destination	2366
I	2	8	EEA1 (*H. vulgare*)	O22491	122.19	VVCGSPLCVAVR	Uniref 90	Protein destination	2628
I	2	8	EEA1 (*H. vulgare*)	O22491	122.19	EDGETCLAILDASLDPVLK	Uniref 90	Protein destination	4859
I	1	3	60S ribosomal protein (*P. armeniaca*)	O50003	233.95	VSVVPSAAALVIK	Uniref 90	Protein synthesis	155
I	1	4	60S ribosomal protein (*P. armeniaca*)	O50003	104.1	VTGGEVGAASSLAPK	Uniref 90	Protein synthesis	4740
I	1	6	60S ribosomal protein (*P. armeniaca*)	O50003	233.95	IGPLGLSPK	Uniref 90	Protein synthesis	1618
I	2	2	60S ribosomal protein (*P. armeniaca*)	O50003	127.81	VTGGEVGAASSLAPK	Uniref 90	Protein synthesis	49946
I	2	5	60S ribosomal protein (*P. armeniaca*)	O50003	165.51	VSVVPSAAALVIK	Uniref 90	Protein synthesis	92

I	2	7	60S ribosomal protein (*P. armeniaca*)	O50003	191.7	IGPLGLSPK	Uniref 90	Protein synthesis	635
I	2	7	60S ribosomal protein (*P. armeniaca*)	O50003	191.7	VTGGEVGAASSLAPK	Uniref 90	Protein synthesis	4047
I	1	2	Cp31BHv (*H. vulgare*)	O81988	106.31	AYVGNLPWQAEDSR	Uniref 90	Unclassified	1606
I	1	4	Cp31BHv (*H. vulgare*)	O81988	106.31	VYVGNLPYDVDSER	Uniref 90	Unclassified	629
I	2	2	Cp31BHv (*H. vulgare*)	O81988	114.77	GFGFVTMASK	Uniref 90	Unclassified	1109
I	2	2	Cp31BHv (*H. vulgare*)	O81988	114.77	EDLDSAISALDGQEMDGRPLR	Uniref 90	Unclassified	10720
I	2	8	Cp31BHv (*H. vulgare*)	O81988	156.4	VYVGNLPYDVDSER	Uniref 90	Unclassified	28242
I	1	2	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	714.67	RIEDAIDEAIK	Uniref 90	Disease/Defence	1746
I	1	6	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	307.92	VQQLLQDFFNGK	Uniref 90	Disease/Defence	5574
I	2	2	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	775.85	ATAGDTHLGGEDFDNR	Uniref 90	Disease/Defence	1056
I	2	2	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	775.85	TTPSYVGFTDTER	Uniref 90	Disease/Defence	1500
I	2	2	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	775.85	SINPDEAVAYGAAVQAAILSGEGNEK	Uniref 90	Disease/Defence	6027
I	2	6	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	374.8	CMEPVEK	Uniref 90	Disease/Defence	9635
I	2	6	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	374.8	FEELNMDLFR	Uniref 90	Disease/Defence	19996
I	2	8	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	168.33	FEELNMDLFR	Uniref 90	Disease/Defence	1800
I	2	8	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	168.33	IINEPTAAAIAYGLDKK	Uniref 90	Disease/Defence	3698
I	2	8	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	168.33	ITITNDK	Uniref 90	Disease/Defence	3891
I	2	8	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	168.33	EQVFSTYSDNQPGVLIQVYEGER	Uniref 90	Disease/Defence	8931
I	2	8	Heat shock cognate 70 kDa protein (*P. hybrida*)	P09189	168.33	VEIIANDQGNRTTPSYVGFTDTER	Uniref 90	Disease/Defence	14789
I	1	2	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	134.41	LVGTK	Uniref 90	Protein destination	2736
I	1	2	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	336.38	SHGALSFLK	Uniref 90	Protein destination	6074
I	1	2	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	134.41	LPPDASFPGAQAER	Uniref 90	Protein destination	7441
I	1	2	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	134.41	ISNIIFVDQPTGTGFSYSSDDR	Uniref 90	Protein destination	8567
I	1	2	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	134.41	NDFFITGESYAGHYIPAFASR	Uniref 90	Protein destination	13131
I	1	2	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	134.41	LCGTNGKASCMAAYMVCNTIFNSIMK	Uniref 90	Protein destination	46780
I	1	5	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	336.38	TAESSFLVDDAQAGVLK	Uniref 90	Protein destination	1189
I	1	6	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	336.38	GFAIGNGLTDPAIQYK	Uniref 90	Protein destination	2512
I	2	8	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	141.25	TAESSFLVDDAQAGVLK	Uniref 90	Protein destination	1053
I	2	8	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	141.25	NDFFITGESYAGHYIPAFASR	Uniref 90	Protein destination	3974
I	2	8	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	141.25	GFAIGNGLTDPAIQYK	Uniref 90	Protein destination	20224
I	2	8	Serine carboxypeptidase 3 precursor (*H. vulgare*)	P21529	141.25	ISNIIFVDQPTGTGFSYSSDDRDTR	Uniref 90	Protein destination	22605
I	1	1	Luminal binding protein 2 precursor (*Z. mays*)	P24067	99.22	INDAVVTVPAYFNDAQR	Uniref 90	Disease/Defence	28136
I	1	1	Luminal binding protein 2 precursor (*Z. mays*)	P24067	99.22	NGHVEIIANDQGNR	Uniref 90	Disease/Defence	29015
I	1	1	Luminal binding protein 2 precursor (*Z. mays*)	P24067	183.44	DILLLDVAPLTLGIETVGGVMTK	Uniref 90	Disease/Defence	38729
I	1	1	Luminal binding protein 2 precursor (*Z. mays*)	P24067	99.22	NQLETYVYNMK	Uniref 90	Disease/Defence	45211
I	1	1	Luminal binding protein 2 precursor (*Z. mays*)	P24067	134.22	LKEVEAVCNPIVSAVYQR	Uniref 90	Disease/Defence	46474
I	1	2	Luminal binding protein 2 precursor (*Z. mays*)	P24067	370.24	EAEEFAEEDKK	Uniref 90	Disease/Defence	382

I	1	2	Luminal binding protein 2 precursor (*Z. mays*)	P24067	134.22	INDAVVTVPAYFNDAQR	Uniref 90	Disease/Defence	12847
I	1	5	Luminal binding protein 2 precursor (*Z. mays*)	P24067	370.24	INDAVVTVPAYFNDAQR	Uniref 90	Disease/Defence	661
I	1	5	Luminal binding protein 2 precursor (*Z. mays*)	P24067	352.93	NQLETYVYNMK	Uniref 90	Disease/Defence	2077
I	1	5	Luminal binding protein 2 precursor (*Z. mays*)	P24067	370.24	FEELNNDLFR	Uniref 90	Disease/Defence	3378
I	1	5	Luminal binding protein 2 precursor (*Z. mays*)	P24067	352.93	LKEVEAVCNPIVSAVYQR	Uniref 90	Disease/Defence	7207
I	1	5	Luminal binding protein 2 precursor (*Z. mays*)	P24067	99.22	VEIESLFDGTDFSEPLTR	Uniref 90	Disease/Defence	24493
I	1	6	Luminal binding protein 2 precursor (*Z. mays*)	P24067	370.24	EVEAVCNPIVSAVYQR	Uniref 90	Disease/Defence	2156
I	2	2	Luminal binding protein 2 precursor (*Z. mays*)	P24067	458.27	FEELNNDLFR	Uniref 90	Disease/Defence	491
I	2	2	Luminal binding protein 2 precursor (*Z. mays*)	P24067	458.27	VEIESLFDGTDFSEPLTR	Uniref 90	Disease/Defence	1077
I	2	2	Luminal binding protein 2 precursor (*Z. mays*)	P24067	458.27	NQLETYVYNMK	Uniref 90	Disease/Defence	1323
I	2	2	Luminal binding protein 2 precursor (*Z. mays*)	P24067	458.27	LSQEEIDR	Uniref 90	Disease/Defence	1989
I	2	8	Luminal binding protein 2 precursor (*Z. mays*)	P24067	348.02	EVEAVCNPIVSAVYQR	Uniref 90	Disease/Defence	25
I	2	8	Luminal binding protein 2 precursor (*Z. mays*)	P24067	348.02	DAGVIAGLNVAR	Uniref 90	Disease/Defence	292
I	2	8	Luminal binding protein 2 precursor (*Z. mays*)	P24067	348.02	EAEEFAEEDKK	Uniref 90	Disease/Defence	3710
I	2	8	Luminal binding protein 2 precursor (*Z. mays*)	P24067	348.02	INDAVVTVPAYFNDAQR	Uniref 90	Disease/Defence	4744
I	2	8	Luminal binding protein 2 precursor (*Z. mays*)	P24067	348.02	VEIESLFDGTDFSEPLTR	Uniref 90	Disease/Defence	28345
I	1	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	661.98	NSLENYAYNMRNTVK	Uniref 90	Disease/Defence	2294
I	1	5	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	661.98	MVNHFVHEFK	Uniref 90	Disease/Defence	341
I	1	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	353.05	MVQEAEK	Uniref 90	Disease/Defence	691
I	1	6	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	661.98	EIAEAFLGSTVK	Uniref 90	Disease/Defence	1809
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	DAGVISGLNVMR	Uniref 90	Disease/Defence	9138
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	EQVFSTYSDNQPGVLIQVFEGER	Uniref 90	Disease/Defence	13218
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	EFAAEEISSMVLTK	Uniref 90	Disease/Defence	19086
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	NTVK	Uniref 90	Disease/Defence	21927
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	ELEGICNPIIAKMYQGAGGDAGVPMDDDA	Uniref 90	Disease/Defence	32034
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	QATKDAGVISGLNVMR	Uniref 90	Disease/Defence	32551
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	TTPSYVGFTDTER	Uniref 90	Disease/Defence	32836
I	2	1	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	453.93	FELSVIPPAPR	Uniref 90	Disease/Defence	37364
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	250.87	IEDAVDQAISWLESNQLAEVDEFEDK	Uniref 90	Disease/Defence	9269
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	250.87	STVHDVVLVGGSTR	Uniref 90	Disease/Defence	9433
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	250.87	ATAGDTHLGGEDFDNR	Uniref 90	Disease/Defence	18403
I	2	2	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	250.87	IPKVQQVAMTNFFNGK	Uniref 90	Disease/Defence	29177
I	1	2	14 3 3 like protein A (*H. vulgare*)	P29305	149.54	SAQDIALADLPTTHPIR	Uniref 90	Disease/Defence	2654
I	1	2	14 3 3 like protein A (*H. vulgare*)	P29305	149.54	EAAENTLVAYK	Uniref 90	Disease/Defence	4657
I	1	6	14 3 3 like protein A (*H. vulgare*)	P29305	98.29	TADVGELTVEER	Uniref 90	Disease/Defence	4323
I	2	6	14 3 3 like protein A (*H. vulgare*)	P29305	644.26	TADVGELTVEER	Uniref 90	Disease/Defence	213
I	2	6	14 3 3 like protein A (*H. vulgare*)	P29305	644.26	GNEAYVASIK	Uniref 90	Disease/Defence	410

I	2	6	14 3 3 like protein A (*H. vulgare*)	P29305	644.26	QAFDEAIAELDSLGEESYK	Uniref 90	Disease/Defence	1392
I	2	6	14 3 3 like protein A (*H. vulgare*)	P29305	644.26	EAAENTLVAYK	Uniref 90	Disease/Defence	1439
I	2	6	14 3 3 like protein A (*H. vulgare*)	P29305	644.26	EENVYMAK	Uniref 90	Disease/Defence	2059
I	2	6	14 3 3 like protein A (*H. vulgare*)	P29305	334.44	EENVYMAK	Uniref 90	Disease/Defence	15146
I	2	1	14 3 3 like protein A (*H. vulgare*)	P29305	334.44	SAQDIALADLPTTHPIR	Uniref 90	Disease/Defence	18187
I	2	1	14 3 3 like protein A (*H. vulgare*)	P29305	334.44	KEAAENTLVAYK	Uniref 90	Disease/Defence	22615
I	2	1	14 3 3 like protein A (*H. vulgare*)	P29305	334.44	STAEATREENVYMAK	Uniref 90	Disease/Defence	24862
I	2	4	14 3 3 like protein A (*H. vulgare*)	P29305	450.13	SAQDIALADLPTTHPIR	Uniref 90	Disease/Defence	1823
I	2	4	14 3 3 like protein A (*H. vulgare*)	P29305	450.13	LLDSHLVPSATAAESK	Uniref 90	Disease/Defence	5356
I	2	2	14 3 3 like protein A (*H. vulgare*)	P29305	356.56	DNLTLWTSDNAEEGGDEIK	Uniref 90	Disease/Defence	3699
I	2	2	14 3 3 like protein A (*H. vulgare*)	P29305	356.56	LLDSHLVPSATAAESK	Uniref 90	Disease/Defence	11427
I	2	2	14 3 3 like protein A (*H. vulgare*)	P29305	356.56	GNEAYVASIK	Uniref 90	Disease/Defence	13921
I	2	2	14 3 3 like protein A (*H. vulgare*)	P29305	356.56	TADVGELTVEER	Uniref 90	Disease/Defence	16561
I	2	2	14 3 3 like protein A (*H. vulgare*)	P29305	356.56	EAAENTLVAYK	Uniref 90	Disease/Defence	20758
I	1	4	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	216.42	AVCMISNSTSVAEVFSR	Uniref 90	Cell wall	609
I	1	6	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	216.42	AVFVDLEPTVIDEVR	Uniref 90	Cell wall	117
I	1	6	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	188.72	RTIQFVDWCPTGFK	Uniref 90	Cell wall	7377
I	2	2	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	283.14	FDLMYAK	Uniref 90	Cell wall	711
I	2	2	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	283.14	TIQFVDWCPTGFK	Uniref 90	Cell wall	1121
I	2	2	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	283.14	AVFVDLEPTVIDEVR	Uniref 90	Cell wall	1212
I	2	2	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	283.14	IHFMLSSYAPVISAEK	Uniref 90	Cell wall	17285
I	2	2	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	283.14	SLSIERPTYTNLNRLVSQVISSLTASLR	Uniref 90	Cell wall	50046
I	1	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	158.91	IMQAQTLSDASK	Uniref 90	Protein destination	668
I	1	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	158.91	LVSLDEYISR	Uniref 90	Protein destination	869
I	1	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	158.91	SPFLEQLTK	Uniref 90	Protein destination	2218
I	1	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	300.59	LGAVPHGLSTDSEVVQR	Uniref 90	Protein destination	3164
I	1	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	300.59	LVYQTALMESGFNLPDPK	Uniref 90	Protein destination	3489
I	1	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	300.59	VFISDEFDDLLPK	Uniref 90	Protein destination	14502
I	1	6	Endoplasmin homolog precursor (*H. vulgare*)	P36183	158.91	ELISNASDALDK	Uniref 90	Protein destination	1016
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	LVSLDEYISR	Uniref 90	Protein destination	63
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	IMQAQTLSDASK	Uniref 90	Protein destination	515
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	SLDLSPDAAVEEEEEVEEPEVEEK	Uniref 90	Protein destination	563
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	LGAVPHGLSTDSEVVQR	Uniref 90	Protein destination	1458
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	ILSIR	Uniref 90	Protein destination	2329
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	EVTEEEYAK	Uniref 90	Protein destination	2768
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	LHNTPCVVVTSK	Uniref 90	Protein destination	2903
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	DIFYLTGSSK	Uniref 90	Protein destination	3520

I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	ISNRLHNTPCVVVTSK	Uniref 90	Protein destination	5182
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	ALDTEGIDSVK	Uniref 90	Protein destination	6479
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	YGWSSNMEK	Uniref 90	Protein destination	8887
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	FYHSLAK	Uniref 90	Protein destination	17067
I	2	2	Endoplasmin homolog precursor (*H. vulgare*)	P36183	476.94	RVFISDEFDDLLPK	Uniref 90	Protein destination	51058
I	1	4	Histone H4 (*A. thaliana*)	P59259	650.93	TAMDVVYALK	Uniref 90	DNA binding	908
I	1	7	Histone H4 (*A. thaliana*)	P59259	650.93	DNIQGITKPAIR	Uniref 90	DNA binding	40
I	1	7	Histone H4 (*A. thaliana*)	P59259	650.93	FLENVIR	Uniref 90	DNA binding	2987
I	2	6	Histone H4 (*A. thaliana*)	P59259	124.06	ISGLIYEETR	Uniref 90	DNA binding	27616
I	2	6	Histone H4 (*A. thaliana*)	P59259	124.06	TLYGFGG	Uniref 90	DNA binding	49677
I	2	4	Histone H4 (*A. thaliana*)	P59259	484.6	TVTAMDVVYALKR	Uniref 90	DNA binding	4181
I	2	4	Histone H4 (*A. thaliana*)	P59259	484.6	KTVTAMDVVYALK	Uniref 90	DNA binding	4393
I	2	4	Histone H4 (*A. thaliana*)	P59259	484.6	IFLENVIR	Uniref 90	DNA binding	19728
I	2	4	Histone H4 (*A. thaliana*)	P59259	484.6	TVTAMDVVYALK	Uniref 90	DNA binding	27578
I	2	4	Histone H4 (*A. thaliana*)	P59259	484.6	DNIQGITKPAIR	Uniref 90	DNA binding	49648
I	1	2	Os07g0173500 protein (*O. sativa*)	Q0D8A3	168.48	LRDDLER	Uniref 90	Unclassified	3431
I	1	4	Os07g0173500 protein (*O. sativa*)	Q0D8A3	168.48	VPDWFLNR	Uniref 90	Unclassified	581
I	2	6	Os07g0173500 protein (*O. sativa*)	Q08479	194.02	GFILDGFPR	Uniref 90	Unclassified	380
I	2	6	Os07g0173500 protein (*O. sativa*)	Q08479	194.02	VLNFAIDDAILEER	Uniref 90	Unclassified	4860
I	1	2	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	772.31	PAYFNDSQR	Uniref 90	Disease/Defence	1177
I	1	5	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	772.31	VQQLLQDFFNGK	Uniref 90	Disease/Defence	4100
I	1	6	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	772.31	NEPTAAAIAYGLDKK	Uniref 90	Disease/Defence	1105
I	2	1	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	384.87	GEEKQFAAEEISSMVLIK	Uniref 90	Disease/Defence	19556
I	2	1	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	384.87	TTPSYVGFTDSER	Uniref 90	Disease/Defence	25531
I	2	1	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	384.87	IEDAIDQAIQWLDGNQLAEADEFDDK	Uniref 90	Disease/Defence	29791
I	2	2	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	202.6	NINPDEAVAYGAAVQAAILSGEGNEK	Uniref 90	Disease/Defence	9785
I	2	2	Heat shock cognate 70 kDa protein (*O. sativa*)	Q2QZ41	202.6	DAGVIAGLNVMRIINEPTAAAIAYGLDK	Uniref 90	Disease/Defence	19089
I	1	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	118.32	VVQSMTTLISGL	Uniref 90	Metabolism	1906
I	1	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	118.32	GFVISDWQGIDR	Uniref 90	Metabolism	3396
I	1	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	118.32	ATIFPHNVGLGATR	Uniref 90	Metabolism	6682
I	1	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	118.32	IGQMTQIERENATAEAMSK	Uniref 90	Metabolism	9111
I	1	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	118.32	VVQSMTTLISGLQGDVPAGSEGRPYVGGSK	Uniref 90	Metabolism	15118
I	1	6	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	178.33	TAGTTILSAIK	Uniref 90	Metabolism	359
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	GDVPAGSEGRPYVGGSK	Uniref 90	Metabolism	94
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	IGQMTQIER	Uniref 90	Metabolism	263
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	FTMGLFESPYADPSLVGELGK	Uniref 90	Metabolism	2691

I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	STVDPSTEVVFSENPDSAAVDSGK	Uniref 90	Metabolism	3658
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	GFVISDWQGIDR	Uniref 90	Metabolism	4868
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	ATIFPHNVGLGATR	Uniref 90	Metabolism	6275
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	SADQLPMNVGDK	Uniref 90	Metabolism	8013
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	VVQSMTTLISGLQGDVPAGSEGRPYVGGSK	Uniref 90	Metabolism	8828
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	ATGIPYAFAPCIAVCR	Uniref 90	Metabolism	14442
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	HYDPLFPFGFGLTTEAK	Uniref 90	Metabolism	20809
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	CYESYSEDPKVVQSMTTLISGLQGDVPAGSEGRPYVGGSK	Uniref 90	Metabolism	21769
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	ATGIPYAFAPCIAVCR	Uniref 90	Metabolism	28465
I	2	2	Beta D glucan exohydrolase isoenzyme ExoII (*H. vulgare*)	Q42835	249.18	YFIGSVLSGGGSVPSPQASAAAWQSMVNEMQK	Uniref 90	Metabolism	29130
I	1	2	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	109.68	PVFNGGDGK	Uniref 90	Unclassified	2490
I	1	2	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	109.68	GVEVCVKAAVGHPDTLGDCPFSQR	Uniref 90	Unclassified	5048
I	1	2	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	109.68	VPVFNGGDGK	Uniref 90	Unclassified	6211
I	1	4	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	109.68	YPTPSLVTPPEYASVGSK	Uniref 90	Unclassified	313
I	1	6	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	109.68	VPVFNGGDGK	Uniref 90	Unclassified	2177
I	2	4	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	225.98	YPTPSLVTPPEYASVGSK	Uniref 90	Unclassified	835
I	2	4	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	225.98	AAVGHPDTLGDCPFSQR	Uniref 90	Unclassified	1860
I	2	4	Dehydroascorbate reductase (*O. sativa*)	Q65XA0	225.98	VLLTLEEK	Uniref 90	Unclassified	3281
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	NTLQGLAAR	Uniref 90	DNA binding	2052
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	TYHMIDEDEPILEK	Uniref 90	DNA binding	4988
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	MYEPLYSK	Uniref 90	DNA binding	5106
I	1	2	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	116.06	AALEAK	Uniref 90	DNA binding	19384
I	2	6	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	164.32	MYEPLYSK	Uniref 90	DNA binding	709
I	2	6	Nucleosome assembly protein 1 like protein 2 (*O. sativa*)	Q70Z20	164.32	TYHMIDEDEPILEK	Uniref 90	DNA binding	3738
I	1	2	Putative sex determination protein tasselseed 2 (*O. sativa*)	Q7XAN5	129.87	AALYLASDEAK	Uniref 90	Metabolism	1242
I	1	2	Putative sex determination protein tasselseed 2 (*O. sativa*)	Q7XAN5	129.87	YVNGHNLVVDGGFTSHK	Uniref 90	Metabolism	10180
I	2	6	Putative sex determination protein tasselseed 2 (*O. sativa*)	Q7XAN5	192.31	AALYLASDEAK	Uniref 90	Metabolism	444
I	2	6	Putative sex determination protein tasselseed 2 (*O. sativa*)	Q7XAN5	192.31	VAVITGGASGIGK	Uniref 90	Metabolism	6018
I	1	2	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	127.51	LNDAEIAKK	Uniref 90	Unclassified	855
I	1	4	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	127.51	NPDTLKK	Uniref 90	Unclassified	2273
I	1	5	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	127.51	CIELDPTFSK	Uniref 90	Unclassified	931
I	1	6	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	127.51	LNDAEIAKK	Uniref 90	Unclassified	162
I	2	6	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	217.96	LNDAEIAKK	Uniref 90	Unclassified	385
I	2	1	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	410.3	MAADPTTRPYLDQPDFMRMLR	Uniref 90	Unclassified	11084

I	2	1	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	410.3	ASRGELSQEELQER	Uniref 90	Unclassified	13201
I	2	1	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	410.3	SAAYASLHRYPEALADAER	Uniref 90	Unclassified	13845
I	2	1	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	410.3	EFPAFSHPPESSRTVEIAR	Uniref 90	Unclassified	18280
I	2	1	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	410.3	TVALRPDWAK	Uniref 90	Unclassified	27172
I	2	1	OSJNBa0091D06 14 protein (*O. sativa*)	Q7XQQ8	410.3	GELSQEELQER	Uniref 90	Unclassified	31777
I	1	1	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	213.65	FHDLDDYLLK	Uniref 90	Disease/Defence	34497
I	1	2	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	113.54	ASEEVPDPDVIK	Uniref 90	Disease/Defence	14235
I	1	2	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	113.54	VELVVEVK	Uniref 90	Disease/Defence	25264
I	1	3	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	273.86	ASEEVPDPDVIK	Uniref 90	Disease/Defence	53
I	1	3	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	273.86	YTEGVPMVTFAK	Uniref 90	Disease/Defence	74
I	1	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	273.86	TFHDLDDYLLKN	Uniref 90	Disease/Defence	3883
I	1	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	206.21	TFHDLDDYLLK	Uniref 90	Disease/Defence	4764
I	1	5	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	273.86	SIETVEGDGK	Uniref 90	Disease/Defence	1004
I	1	6	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	213.65	TFHDLDDYLLK	Uniref 90	Disease/Defence	24761
I	2	6	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	136.98	ASEEVPDPDVIKETAAK	Uniref 90	Disease/Defence	3924
I	2	6	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	136.98	VELVVEVK	Uniref 90	Disease/Defence	5432
I	2	6	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	136.98	IFPEQYK	Uniref 90	Disease/Defence	15251
I	2	6	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	136.98	TFHDLDDYLLK	Uniref 90	Disease/Defence	27768
I	2	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	508.69	ASEEVPDPDVIK	Uniref 90	Disease/Defence	230
I	2	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	508.69	YTEGVPMVTFAK	Uniref 90	Disease/Defence	733
I	2	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	508.69	SIETVEGDGK	Uniref 90	Disease/Defence	2186
I	2	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	508.69	TFHDLDDYLLKN	Uniref 90	Disease/Defence	5134
I	2	4	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	508.69	TFHDLDDYLLK	Uniref 90	Disease/Defence	6722
I	2	2	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	112.74	EKVEVADDEK	Uniref 90	Disease/Defence	7634
I	2	2	OSJNBb0048E02 12 protein (*O. sativa*)	Q7XUY5	112.74	SIETVEGDGK	Uniref 90	Disease/Defence	19268
I	1	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	106.76	STYQVAALPLNAR	Uniref 90	Unclassified	85
I	1	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	106.76	FVSESVEEQTEQVMK	Uniref 90	Unclassified	464
I	1	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	106.76	AAATPAAELR	Uniref 90	Unclassified	1366
I	2	6	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	134.46	STYQVAALPLNAR	Uniref 90	Unclassified	181
I	2	6	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	134.46	FVSESVEEQTEQVMK	Uniref 90	Unclassified	1153
I	2	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	287.01	APAALGPYSQAIK	Uniref 90	Unclassified	203
I	2	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	287.01	YFPAPAPAR	Uniref 90	Unclassified	2531
I	2	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	287.01	ASGASYSSVVK	Uniref 90	Unclassified	3593
I	2	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	287.01	TTIMLADLQDFK	Uniref 90	Unclassified	6184
I	2	2	Putative translational inhibitor protein (*O. sativa*)	Q8H4B9	287.01	MAWTAAAATVTRAAATPAAELR	Uniref 90	Unclassified	28378
I	1	5	Ascorbate peroxidase (*H. vulgare*)	Q945R5	169.94	EGLLQLPTDK	Uniref 90	Disease/Defence	309
I	1	5	Ascorbate peroxidase (*H. vulgare*)	Q945R5	169.94	VLLTDPAFRPLVDK	Uniref 90	Disease/Defence	4024

I	2	6	Ascorbate peroxidase (*H. vulgare*)	Q945R5	189.02	EGLLQLPTDK	Uniref 90	Disease/Defence	586
I	2	6	Ascorbate peroxidase (*H. vulgare*)	Q945R5	189.02	CYPTVSDEYLAAVAK	Uniref 90	Disease/Defence	1270
I	2	6	Ascorbate peroxidase (*H. vulgare*)	Q945R5	189.02	LPDATQGSDHLR	Uniref 90	Disease/Defence	2398
I	2	6	Ascorbate peroxidase (*H. vulgare*)	Q945R5	189.02	VLLTDPAFRPLVDK	Uniref 90	Disease/Defence	4419
I	2	2	Ascorbate peroxidase (*H. vulgare*)	Q945R5	154.34	LSELGFGEASEGCC	Uniref 90	Disease/Defence	703
I	2	2	Ascorbate peroxidase (*H. vulgare*)	Q945R5	154.34	CPAELAHGANAGLDIAVR	Uniref 90	Disease/Defence	6522
I	2	2	Ascorbate peroxidase (*H. vulgare*)	Q945R5	154.34	LAWHSAGTFDVATK	Uniref 90	Disease/Defence	7237
I	2	2	Ascorbate peroxidase (*H. vulgare*)	Q945R5	154.34	EGLLQLPTDK	Uniref 90	Disease/Defence	13837
I	2	2	Ascorbate peroxidase (*H. vulgare*)	Q945R5	154.34	QVFSTQMGLSDQDIVALSGGHTLGR	Uniref 90	Disease/Defence	14578
I	2	2	Ascorbate peroxidase (*H. vulgare*)	Q945R5	154.34	YAADEDAFFADYAEAHLK	Uniref 90	Disease/Defence	16544
I	1	6	Probable ubiquitin fold modifier 1 precursor (*O. sativa*)	Q94DM8	75.02	VFSVPEAAPFTAVLK	Uniref 90	Protein destination	723
I	1	6	Probable ubiquitin fold modifier 1 precursor (*O. sativa*)	Q94DM8	75.02	VPPQTSAIITNDGVGINPQQSAGNVFLK	Uniref 90	Protein destination	2418
I	2	5	Probable ubiquitin fold modifier 1 precursor (*O. sativa*)	Q94DM8	144.14	VFSVPEAAPFTAVLK	Uniref 90	Protein destination	1445
I	2	5	Probable ubiquitin fold modifier 1 precursor (*O. sativa*)	Q94DM8	144.14	VPPQTSAIITNDGVGINPQQSAGNVFLK	Uniref 90	Protein destination	3085
I	1	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	179.91	MEGLLWGASK	Uniref 90	Protein synthesis	2704
I	1	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	110.94	SSVLLDVKPWDDETDMVK	Uniref 90	Protein synthesis	5961
I	1	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	110.94	KLDGYLLSR	Uniref 90	Protein synthesis	6108
I	1	6	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	179.91	LSGVTAPGQGVK	Uniref 90	Protein synthesis	261
I	2	6	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	299.36	LSGVTAPGQGVK	Uniref 90	Protein synthesis	370
I	2	6	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	299.36	MEGLLWGASK	Uniref 90	Protein synthesis	1111
I	2	6	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	299.36	SSVLLDVKPWDDETDMVK	Uniref 90	Protein synthesis	2306
I	2	6	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	299.36	SYISGYQASK	Uniref 90	Protein synthesis	3882
I	2	6	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	299.36	LMPVGYGIK	Uniref 90	Protein synthesis	27710
I	2	4	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	91.92	LMPVGYGIK	Uniref 90	Protein synthesis	574
I	2	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	97.28	SYISGYQASK	Uniref 90	Protein synthesis	3174
I	2	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	97.28	MAATFNVNAEAGLK	Uniref 90	Protein synthesis	6315
I	2	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	97.28	MEGLLWGASK	Uniref 90	Protein synthesis	11307
I	2	2	Putative elongation factor 1 beta (*H. vulgare*)	Q9M3U8	97.28	SSVLLDVKPWDDETDMVK	Uniref 90	Protein synthesis	16137
I	1	2	GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6	110.83	PTTSPLSIEK	Uniref 90	Disease/Defence	350
I	1	5	GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6	110.83	YAPTTSPLSIEK	Uniref 90	Disease/Defence	251
I	1	6	GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6	110.83	VDVNGDNVAPVYK	Uniref 90	Disease/Defence	1045
I	2	6	GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6	152.27	GSLFGDNIK	Uniref 90	Disease/Defence	623
I	2	6	GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6	152.27	VDVNGDNVAPVYK	Uniref 90	Disease/Defence	752
I	2	6	GPX12Hv glutathione peroxidase like protein (*H. vulgare*)	Q9SME6	152.27	FLVDKDGNVVDR	Uniref 90	Disease/Defence	2068
I	1	4	ATP synthase subunit (*Z. mays*)	35_14757	464.31	EGVQSFQGVLDGK	Uniref 90	Transport	290
I	1	5	ATP synthase subunit (*Z. mays*)	35_14757	181.44	AAAYASSAAAEAAPVTPPPTSDK	Uniref 90	Transport	7163
I	2	6	ATP synthase subunit (*Z. mays*)	35_14757	80.74	VLNTGSPITVPVGR	Harvest Hv	Transport	267

I	2	1	ATP synthase subunit (*Z. mays*)	35_14757	225.01	FTQANSEVSALLGR	Harvest Hv	Transport	8691
I	2	1	ATP synthase subunit (*Z. mays*)	35_14757	225.01	AHGGFSVFAGVGER	Harvest Hv	Transport	9002
I	2	1	ATP synthase subunit (*Z. mays*)	35_14757	225.01	SKPSLPAMATRR	Harvest Hv	Transport	13785
I	2	1	ATP synthase subunit (*Z. mays*)	35_14757	225.01	QISELGIYPAVDPLDSTSR	Harvest Hv	Transport	23418
I	2	1	ATP synthase subunit (*Z. mays*)	35_14757	225.01	IINVIGEPIDHK	Harvest Hv	Transport	29350
I	2	1	ATP synthase subunit (*Z. mays*)	35_14757	225.01	MLSPHVLGQEHYNTAR	Harvest Hv	Transport	37375
I	1	4	ATP synthase subunit (*Z. mays*)	P19023	437.2	VLNTGSPITVPVGR	Harvest Hv	Transport	170
I	1	6	ATP synthase subunit (*Z. mays*)	P19023	437.2	TIAMDGTEGLVR	Harvest Hv	Transport	770
I	2	2	ATP synthase subunit (*Z. mays*)	P19023	304.33	TIAMDGTEGLVR	Harvest Hv	Transport	1899
I	2	2	ATP synthase subunit (*Z. mays*)	P19023	304.33	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	Harvest Hv	Transport	51054
I	1	4	Enolase 2 (*Z. mays*)	P42895	504.89	DPTAQTEIDNFMVQQLDGTK	Uniref 90	Energy metabolism	333
I	1	5	Enolase 2 (*Z. mays*)	P42895	128.2	QLVLPVPAFNVINGGSHAGNK	Uniref 90	Energy metabolism	7349
I	1	6	Enolase 2 (*Z. mays*)	P42895	181.25	TAIEK	Uniref 90	Energy metabolism	996
I	1	6	Enolase 2 (*Z. mays*)	P42895	504.89	IEEELGAIAVYAGAK	Uniref 90	Energy metabolism	2265
I	1	6	Enolase 2 (*Z. mays*)	P42895	181.25	AGASIK	Uniref 90	Energy metabolism	5016
I	2	6	Enolase 2 (*Z. mays*)	P42895	381.66	DPTAQTEIDNFMVQQLDGTK	Uniref 90	Energy metabolism	243
I	2	6	Enolase 2 (*Z. mays*)	P42895	381.66	VNQIGSVTESIEAVK	Uniref 90	Energy metabolism	1107
I	2	6	Enolase 2 (*Z. mays*)	P42895	381.66	YGQDATNVGDEGGFAPNIQENK	Uniref 90	Energy metabolism	1178
I	2	6	Enolase 2 (*Z. mays*)	P42895	381.66	SCNALLLK	Uniref 90	Energy metabolism	1540
I	2	6	Enolase 2 (*Z. mays*)	P42895	381.66	AAVPSGASTGVYEALELR	Uniref 90	Energy metabolism	2199
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	EGLELLK	Uniref 90	Energy metabolism	1003
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	NEWGWCK	Uniref 90	Energy metabolism	1737
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	LAMQEFMILPTGAASFK	Uniref 90	Energy metabolism	3787
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	IEEELGAIAVYAGAK	Uniref 90	Energy metabolism	4483
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	FRAPVEPY	Uniref 90	Energy metabolism	7951
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	RAGWGVMTSHR	Uniref 90	Energy metabolism	9941
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	AAVPSGASTGVYEALELR	Uniref 90	Energy metabolism	16179
I	2	2	Enolase 2 (*Z. mays*)	P42895	234.32	DPTAQTEIDNFMVQQLDGTK	Uniref 90	Energy metabolism	27994
I	1	2	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	673.76	KPWNLSFSFGR	Harvest Hv	Energy metabolism	1564
I	1	6	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	170.02	GGKPFVDILK	Harvest Hv	Energy metabolism	4251
I	2	6	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	511.78	FASINVENVEDNRR	Harvest Hv	Energy metabolism	1005
I	2	6	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	511.78	EGNVLPGIK	Harvest Hv	Energy metabolism	2379
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	VDKGTVELAGTNGETTTQGFDDLGK	Harvest Hv	Energy metabolism	43595
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	ALQQSTLK	Harvest Hv	Energy metabolism	50981
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	YYEAGAR	Harvest Hv	Energy metabolism	51938
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	ALNDQHVLLEGTLLKPNMVTPGSDAK	Harvest Hv	Energy metabolism	52506

I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	CAYVTEMVLAACYK	Harvest Hv	Energy metabolism	52745
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	NAAYIGTPGK	Harvest Hv	Energy metabolism	57309
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	FASINVENVEDNR	Harvest Hv	Energy metabolism	57913
I	2	1	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	201.4	FASINVENVEDNRR	Harvest Hv	Energy metabolism	59787
I	2	2	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	258.93	GGKPFVDILK	Harvest Hv	Energy metabolism	11274
I	2	2	Fructose bisphosphate aldolase (*O. sativa*)	35_14100	258.93	EGNVLPGIK	Harvest Hv	Energy metabolism	13226
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	258.97	LGAAHLGLGDAASAAAAYEK	Harvest Hv	Unclassified	7448
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	311.76	QVLMDFQENPR	Harvest Hv	Unclassified	7852
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	258.97	RPPSGGADAIGQMFQGPELWTK	Harvest Hv	Unclassified	12990
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	311.76	FEEAAGHFSDAIALAPANHVLYSNR	Harvest Hv	Unclassified	15523
I	1	4	Putative stress induced protein sti1 (*O. sativa*)	35_15495	258.97	QSKAMQDPEIQNILTDPIMR	Harvest Hv	Unclassified	12384
I	1	5	Putative stress induced protein sti1 (*O. sativa*)	35_15495	159.46	LDPNNQELLDGIR	Harvest Hv	Unclassified	254
I	1	5	Putative stress induced protein sti1 (*O. sativa*)	35_15495	159.46	AMELDDEDISYLTNR	Harvest Hv	Unclassified	3325
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	DLEQQEYYDPK	Harvest Hv	Unclassified	509
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	GLALDPSNEGLK	Harvest Hv	Unclassified	589
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	LINAGIVQTR	Harvest Hv	Unclassified	936
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	FDECIADCDK	Harvest Hv	Unclassified	1029
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	AYLDQPDFMQMLR	Harvest Hv	Unclassified	1486
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	GDISQEDLQEK	Harvest Hv	Unclassified	1746
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	LGAAHLGLGDAASAAAAYEK	Harvest Hv	Unclassified	11998
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	35_15495	982.27	RPPSGGADAIGQMFQGPELWTK	Harvest Hv	Unclassified	15606
I	2	5	Putative stress induced protein sti1 (*O. sativa*)	35_15495	179.15	RPPSGGADAIGQMFQGPELWTK	Harvest Hv	Unclassified	27733
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	LDPNNQELLDGIR	Harvest Hv	Unclassified	5655
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	GRICPPPPSR	Harvest Hv	Unclassified	9087
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	QQPETKAR	Harvest Hv	Unclassified	10156
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	QQKYPEAIK	Harvest Hv	Unclassified	10442
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	GYSRLGAAHLGLGDAASAAAAYEK	Harvest Hv	Unclassified	12152
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	AYLDQPDFMQMLR	Harvest Hv	Unclassified	15250
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	CVQQINK	Harvest Hv	Unclassified	16918
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	GLALDPSNEGLKAGLADAK	Harvest Hv	Unclassified	17434
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	SAALASIHR	Harvest Hv	Unclassified	25764
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	ICPPPPSR	Harvest Hv	Unclassified	28502
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	GLALDPSNEGLK	Harvest Hv	Unclassified	28790
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	MMQVLSLMLNIK	Harvest Hv	Unclassified	29949
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	KGAVQFFMK	Harvest Hv	Unclassified	30104
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	35_15495	523.04	FEEAAGHFSDAIALAPANHVLYSNR	Harvest Hv	Unclassified	32811
I	2	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	350.11	EMEPEPQPEPMEVSDEDKEK	Harvest Hv	Unclassified	392

I	2	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	350.11	AAVYIEMGK	Harvest Hv	Unclassified	3025
I	2	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	350.11	IQTPQDSDFPQSSSPSQPPPQQQR	Harvest Hv	Unclassified	4846
I	2	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	350.11	LGAAHLGLGDAASAAAAYEK	Harvest Hv	Unclassified	15736
I	2	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	350.11	IASDPATR	Harvest Hv	Unclassified	17125
I	2	2	Putative stress induced protein sti1 (*O. sativa*)	35_15495	350.11	FEEAAGHFSDAIALAPANHVLYSNR	Harvest Hv	Unclassified	49991
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	146.92	GNAAFSAGR	Uniref 90	Unclassified	5329
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	146.92	IASDPTTR	Uniref 90	Unclassified	5370
I	1	2	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	146.92	GLALDPTNEGLK	Uniref 90	Unclassified	6444
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	529.4	AMELDDEDISYLTNR	Uniref 90	Unclassified	70
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	529.4	LGAMPEGLK	Uniref 90	Unclassified	520
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	529.4	AMQDPEIQNILTDPIMR	Uniref 90	Unclassified	1103
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	529.4	CIELDPTFSK	Uniref 90	Unclassified	1630
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	529.4	DFETAIQHYTK	Uniref 90	Unclassified	2090
I	2	6	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	529.4	DYDIAIETFQK	Uniref 90	Unclassified	4829
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	345.6	EQKYPDAVK	Uniref 90	Unclassified	7819
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	345.6	GNAAFSAGR	Uniref 90	Unclassified	9106
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	345.6	AYLEQPDFMQMLR	Uniref 90	Unclassified	11866
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	345.6	AMQDPEIQNILTDPIMR	Uniref 90	Unclassified	14678
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	345.6	TSKDYDIAIETFQK	Uniref 90	Unclassified	29921
I	2	1	Putative stress induced protein sti1 (*O. sativa*)	Q6H660	345.6	HDPNNPELLDGVK	Uniref 90	Unclassified	31351
I	1	5	Putative disulfide isomerase (*O. sativa*)	35_15052	242.93	TAEALTEYVNSEAATNVK	Harvest Hv	Disease/Defence	114
I	1	5	Putative disulfide isomerase (*O. sativa*)	35_15052	181.96	QDEGVVIANLDADKYTSLAEK	Harvest Hv	Disease/Defence	3177
I	1	5	Putative disulfide isomerase (*O. sativa*)	35_15052	181.96	NILSAFSS	Harvest Hv	Disease/Defence	3522
I	2	6	Putative disulfide isomerase (*O. sativa*)	35_15052	220.34	NILSAFSS	Harvest Hv	Disease/Defence	120
I	2	6	Putative disulfide isomerase (*O. sativa*)	35_15052	220.34	DLDDFVK	Harvest Hv	Disease/Defence	400
I	2	6	Putative disulfide isomerase (*O. sativa*)	35_15052	220.34	ADEFAIK	Harvest Hv	Disease/Defence	1740
I	2	5	Putative disulfide isomerase (*O. sativa*)	35_15052	997.68	SLAPIYEK	Harvest Hv	Disease/Defence	1030
I	2	5	Putative disulfide isomerase (*O. sativa*)	35_15052	997.68	TAEALTEYVNSEAATNVK	Harvest Hv	Disease/Defence	1047
I	2	5	Putative disulfide isomerase (*O. sativa*)	35_15052	997.68	IAAVPSSVVVLTEENFDSVVLDETK	Harvest Hv	Disease/Defence	3454
I	2	5	Putative disulfide isomerase (*O. sativa*)	35_15052	997.68	GALVEFYAPWCGHCK	Harvest Hv	Disease/Defence	7035
I	2	4	Putative disulfide isomerase (*O. sativa*)	35_15052	265.04	IYVNVAK	Harvest Hv	Disease/Defence	893
I	2	4	Putative disulfide isomerase (*O. sativa*)	35_15052	265.04	QDEGVVIANLDADKYTSLAEK	Harvest Hv	Disease/Defence	3393
I	2	2	Putative disulfide isomerase (*O. sativa*)	35_15052	562.11	GQLTSEAGLVASLDALVK	Harvest Hv	Disease/Defence	2936
I	2	2	Putative disulfide isomerase (*O. sativa*)	35_15052	562.11	YTSLAEK	Harvest Hv	Disease/Defence	6127
I	2	2	Putative disulfide isomerase (*O. sativa*)	35_15052	562.11	AGEEYEAGR	Harvest Hv	Disease/Defence	11020
I	2	2	Putative disulfide isomerase (*O. sativa*)	35_15052	562.11	IAAVPSSVVVLTEENFDSVVLDETK	Harvest Hv	Disease/Defence	20199
I	2	2	Putative disulfide isomerase (*O. sativa*)	35_15052	562.11	GALVEFYAPWCGHCK	Harvest Hv	Disease/Defence	20443

I	1	5	Putative disulfide isomerase (*O. sativa*)	Q75M08	164.96	YGVSGFPTLK	Uniref 90	Disease/Defence	322
I	1	6	Putative disulfide isomerase (*O. sativa*)	Q75M08	164.96	QDEGVVIANLDADK	Uniref 90	Disease/Defence	1157
I	2	4	Putative disulfide isomerase (*O. sativa*)	Q75M08	216.66	YGVSGFPTLK	Uniref 90	Disease/Defence	208
I	2	4	Putative disulfide isomerase (*O. sativa*)	Q75M08	216.66	YGVSGYPTIQWFPK	Uniref 90	Disease/Defence	644
I	2	2	Putative disulfide isomerase (*O. sativa*)	Q75M08	210.55	LAPEYEK	Uniref 90	Disease/Defence	2433
I	2	2	Putative disulfide isomerase (*O. sativa*)	Q75M08	210.55	YGVSGFPTLK	Uniref 90	Disease/Defence	5009
I	2	2	Putative disulfide isomerase (*O. sativa*)	Q75M08	210.55	KLAPEYEK	Uniref 90	Disease/Defence	6261
I	2	2	Putative disulfide isomerase (*O. sativa*)	Q75M08	210.55	QDEGVVIANLDADK	Uniref 90	Disease/Defence	11837
I	2	2	Putative disulfide isomerase (*O. sativa*)	Q75M08	210.55	IAAVPSSVVVLTPETFDSVVLDETK	Uniref 90	Disease/Defence	17582
I	2	2	Putative disulfide isomerase (*O. sativa*)	Q75M08	210.55	DVLVEFYAPWCGHCK	Uniref 90	Disease/Defence	21466
I	1	2	P0402A09 25 protein (*O. sativa*)	35_1149	103.72	FQASPAVIK	Harvest Hv	Unclassified	351
I	1	2	P0402A09 25 protein (*O. sativa*)	35_1149	100.59	EAFELVSGEVSK	Harvest Hv	Unclassified	15697
I	1	2	P0402A09 25 protein (*O. sativa*)	35_1149	100.59	AALQEAYSTPIPALDILAERPPVK	Harvest Hv	Unclassified	24767
I	1	6	P0402A09 25 protein (*O. sativa*)	35_1149	103.72	EAFELVSGEVSK	Harvest Hv	Unclassified	1638
I	2	2	P0402A09 25 protein (*O. sativa*)	35_1149	150.51	EAFELVSGEVSK	Harvest Hv	Unclassified	1297
I	2	2	P0402A09 25 protein (*O. sativa*)	35_1149	150.51	AALQEAYSTPIPALDILAERPPVK	Harvest Hv	Unclassified	3697
I	2	2	P0402A09 25 protein (*O. sativa*)	35_1149	150.51	YGALVSVVSFVLGFIYLVASPSKSSGSK	Harvest Hv	Unclassified	29380
II	1	9	Putative avenin like (*A. cylindrica*)	35_14422	141.3	CQAVCSVAQVIMR	Harvest Hv	Protein destination	10142
II	1	9	Putative avenin like (*A. cylindrica*)	35_14422	141.3	QQCCQPLAQISEQAR	Harvest Hv	Protein destination	12684
II	2	10	Putative avenin like (*A. cylindrica*)	35_14422	293.43	QQQGQSFSQPQQQQSQSFGQPQQQVPVEIIR	Harvest Hv	Protein destination	10284
II	2	10	Putative avenin like (*A. cylindrica*)	35_14422	293.43	CQAVCSVAQVIMR	Harvest Hv	Protein destination	12979
II	2	10	Putative avenin like (*A. cylindrica*)	35_14422	293.43	QQCCQPLAQISEQAR	Harvest Hv	Protein destination	19792
II	2	9	Putative avenin like (*A. cylindrica*)	35_14422	223.23	CQAVCSVAQVIMR	Harvest Hv	Protein destination	49699
II	1	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	508.84	SHIDPNVMEAK	Harvest Hv	Metabolism	7581
II	1	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	508.84	HAALFTSTLLSR	Harvest Hv	Metabolism	19171
II	1	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	137.52	VAGVITNWASASMNQDIK	Harvest Hv	Metabolism	46103
II	1	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	508.42	ALGQPNDIDEQR	Harvest Hv	Metabolism	4147
II	1	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	508.84	MLPTFGATIISGQK	Harvest Hv	Metabolism	7126
II	1	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	508.84	MLPTFGATIISGQK	Harvest Hv	Metabolism	12620
II	1	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	137.52	DPSVNIAIVER	Harvest Hv	Metabolism	16014
II	2	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	263.18	VLDVNTAEDAIVSLTR	Harvest Hv	Metabolism	14920
II	2	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	263.18	MLPTFGATIISGQK	Harvest Hv	Metabolism	14939
II	2	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	263.18	IVVSSCGHEGLFSADGLK	Harvest Hv	Metabolism	19791
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	SHIDPNVMEAK	Harvest Hv	Metabolism	1707
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	LLAQPNVK	Harvest Hv	Metabolism	4600
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	VAGVITNWASASMNQDIK	Harvest Hv	Metabolism	8169

II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	DPSVNIAIVER	Harvest Hv	Metabolism	10458
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	ALGQPNDIDEQR	Harvest Hv	Metabolism	10629
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	RYMTDMIADVNTDVIIIGTGSAGLSCAYELSK	Harvest Hv	Metabolism	10837
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	SVSPGGSGWLGSQLFSAMVVR	Harvest Hv	Metabolism	12714
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	VLDVNTAEDAIVSLTR	Harvest Hv	Metabolism	15196
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	MLPTFGATIISGQK	Harvest Hv	Metabolism	49742
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	IVVSSCGHEGLFSADGLK	Harvest Hv	Metabolism	49778
II	2	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_320	1384.91	HAALFTSTLLSR	Harvest Hv	Metabolism	49864
II	1	9	Hordoindoline b (*H. vulgare*)	35_50624	107.85	CCQQLSQIAPHCR	Harvest Hv	Disease/Defence	7742
II	1	9	Hordoindoline b (*H. vulgare*)	35_50624	107.85	DYVMER	Harvest Hv	Disease/Defence	14366
II	1	9	Hordoindoline b (*H. vulgare*)	35_50624	107.85	CNMGVDCR	Harvest Hv	Disease/Defence	45937
II	2	9	Hordoindoline b (*H. vulgare*)	35_50624	193.12	CNMGVDCR	Harvest Hv	Disease/Defence	10497
II	2	9	Hordoindoline b (*H. vulgare*)	35_50624	193.12	DFPVTWPTK	Harvest Hv	Disease/Defence	12827
II	2	9	Hordoindoline b (*H. vulgare*)	35_50624	193.12	LGGIFGIGGGAVFK	Harvest Hv	Disease/Defence	15794
II	1	10	BTI CMe4 protein precursor (*H. vulgare*)	O49863	219.83	CCDELSAIPAYCR	Uniref 90	Protein destination	3167
II	1	10	BTI CMe4 protein precursor (*H. vulgare*)	O49863	219.83	QTSYAANLVTPQECNLWTIHGSPSCPELQPGYGVVSS	Uniref 90	Protein destination	7211
II	2	10	BTI CMe4 protein precursor (*H. vulgare*)	O49863	195.79	QTSYAANLVTPQECNLWTIHGSPSCPELQPGYGVVSS	Uniref 90	Protein destination	14951
II	2	10	BTI CMe4 protein precursor (*H. vulgare*)	O49863	195.79	CAALRIIMDGIVTWQGVFGAYFK	Uniref 90	Protein destination	49692
II	1	10	Trypsin inhibitor CMe precursor (*H. vulgare*)	P01086	196.25	VVSQICHQGPR	Uniref 90	Disease/Defence	24376
II	1	10	Trypsin inhibitor CMe precursor (*H. vulgare*)	P01086	196.25	TYVVSQICHQGPR	Uniref 90	Disease/Defence	44835
II	2	10	Trypsin inhibitor CMe precursor (*H. vulgare*)	P01086	114.15	TYVVSQICHQGPR	Uniref 90	Disease/Defence	49643
II	2	8	Trypsin inhibitor CMe precursor (*H. vulgare*)	P01086	372.12	CCDELSAIPAYCR	Uniref 90	Disease/Defence	2250
II	2	8	Trypsin inhibitor CMe precursor (*H. vulgare*)	P01086	372.12	TYVVSQICHQGPR	Uniref 90	Disease/Defence	5067
II	1	8	Purothionin II (*H. vulgare*)	P01545	500.07	LALVSNSDEPDTVK	Uniref 90	Disease/Defence	3034
II	1	8	Purothionin II (*H. vulgare*)	P01545	500.07	ASMCDYMVNAAADDEEMK	Uniref 90	Disease/Defence	7064
II	1	10	Purothionin II (*H. vulgare*)	P01545	500.07	CPTGFPK	Uniref 90	Disease/Defence	7098
II	2	10	Purothionin II (*H. vulgare*)	P01545	897.16	LALVSNSDEPDTVK	Uniref 90	Disease/Defence	1689
II	2	10	Purothionin II (*H. vulgare*)	P01545	897.16	ASMCDYMVNAAADDEEMK	Uniref 90	Disease/Defence	2233
II	2	10	Purothionin II (*H. vulgare*)	P01545	897.16	NCYNLCR	Uniref 90	Disease/Defence	2883
II	2	10	Purothionin II (*H. vulgare*)	P01545	897.16	YCNLGCR	Uniref 90	Disease/Defence	2922
II	2	10	Purothionin II (*H. vulgare*)	P01545	897.16	CPTGFPK	Uniref 90	Disease/Defence	5149
II	2	10	Purothionin II (*H. vulgare*)	P01545	897.16	LCAGVCR	Uniref 90	Disease/Defence	10314
II	1	8	B3 hordein (*H. vulgare*)	P06471	344.61	TLPTMCSVNVPLYR	Uniref 90	Protein destination	2969
II	1	8	B3 hordein (*H. vulgare*)	P06471	344.61	SQMLQQSSCHVLQQQCCQQLPQIPEQLR	Uniref 90	Protein destination	8770

II	1	10	B3 hordein (*H. vulgare*)	P06471	344.61	TLPTMCSVNVPLYR	Uniref 90	Protein destination	8660
II	2	8	B3 hordein (*H. vulgare*)	P06471	337.53	TLPTMCSVNVPLYR	Uniref 90	Protein destination	705
II	2	8	B3 hordein (*H. vulgare*)	P06471	337.53	IVPLAIDTR	Uniref 90	Protein destination	1629
II	1	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	211.28	ITPYGVAPSDK	Uniref 90	Protein destination	3292
II	1	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	114.39	ADANYYVLSANR	Uniref 90	Protein destination	7560
II	1	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	211.28	HVITGPVKDPSPSGR	Uniref 90	Protein destination	19550
II	2	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	721.81	ITPYGVAPSDK	Uniref 90	Protein destination	314
II	2	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	721.81	ADANYYVLSANR	Uniref 90	Protein destination	1391
II	2	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	721.81	LMSCGDWCQDLGVFR	Uniref 90	Protein destination	15152
II	2	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	721.81	YSGAEVHEYK	Uniref 90	Protein destination	15375
II	2	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	721.81	HVITGPVK	Uniref 90	Protein destination	15523
II	2	9	Alpha amylase subtilisin inhibitor precursor (*H. vulgare*)	P07596	721.81	AYTTCLQSTEWHIDSELAAGR	Uniref 90	Protein destination	19916
II	1	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	477.69	DYVLQQTCAVFTPGSK	Uniref 90	Protein destination	3027
II	1	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	477.69	LPEWMTSAELNYPGQPYLAK	Uniref 90	Protein destination	12363
II	1	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	256.31	LLVAPGQCNLATIHNVR	Uniref 90	Protein destination	44553
II	1	9	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	477.69	YFMALPVPSQPVDPSTGNVGQSGLMDLPGCPR	Uniref 90	Protein destination	7562
II	1	9	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	477.69	LLVAPGQCNLATIHNVR	Uniref 90	Protein destination	13201
II	1	10	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	477.69	LYCCQELAEIPQQCR	Uniref 90	Protein destination	3090
II	2	10	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	247.6	LPEWMTSAELNYPGQPYLAK	Uniref 90	Protein destination	5109
II	2	10	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	247.6	YCPAVEQPLWI	Uniref 90	Protein destination	6742
II	2	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	1318.46	YFMALPVPSQPVDPSTGNVGQSGLMDLPGCPR	Uniref 90	Protein destination	2285
II	2	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	1318.46	LYCCQELAEIPQQCR	Uniref 90	Protein destination	2829
II	2	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	1318.46	DYVLQQTCAVFTPGSK	Uniref 90	Protein destination	2835
II	2	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	1318.46	LLVAPGQCNLATIHNVR	Uniref 90	Protein destination	5066
II	2	8	Alpha amylase trypsin inhibitor CMd precursor (*H. vulgare*)	P11643	1318.46	LPEWMTSAELNYPGQPYLAK	Uniref 90	Protein destination	5078
II	1	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	SVYAALGVGGGPEEVFPGCQK	Uniref 90	Disease/Defence	4723
II	1	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	LLVAGVPALCNVPIPNEAAGTR	Uniref 90	Disease/Defence	7041
II	1	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	CGDLGSMLR	Uniref 90	Disease/Defence	7061
II	1	9	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	PALCNVPIPNEAAGTR	Uniref 90	Disease/Defence	5989
II	1	9	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	CGDLGSMLR	Uniref 90	Disease/Defence	15078
II	1	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	VPEDVLR	Uniref 90	Disease/Defence	4757
II	1	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	653.15	DCCQEVANISNEWCR	Uniref 90	Disease/Defence	8452
II	1	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	69.16	GVCYWSASTDT	Uniref 90	Disease/Defence	24597
II	2	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	293.38	VPEDVLR	Uniref 90	Disease/Defence	2899
II	2	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	293.38	LECVGNR	Uniref 90	Disease/Defence	3969

II	2	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	293.38	GVCYWSASTDT	Uniref 90	Disease/Defence	13010
II	2	10	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	293.38	SVYAALGVGGGPEEVFPGCQK	Uniref 90	Disease/Defence	19783
II	2	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	1119.95	LLVAGVPALCNVPIPNEAAGTR	Uniref 90	Disease/Defence	1619
II	2	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	1119.95	CGDLGSMLR	Uniref 90	Disease/Defence	2243
II	2	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	1119.95	DCCQEVANISNEWCR	Uniref 90	Disease/Defence	2275
II	2	8	Alpha amylase inhibitor BDAI 1 precursor (*H. vulgare*)	P13691	1119.95	SVYAALGVGGGPEEVFPGCQK	Uniref 90	Disease/Defence	13075
II	1	8	Alpha amylase inhibitor BMAI 1 precursor (*H. vulgare*)	P16968	335.03	SQCAGGQVVESIQK	Uniref 90	Disease/Defence	3011
II	1	10	Alpha amylase inhibitor BMAI 1 precursor (*H. vulgare*)	P16968	335.03	ELGVALADDK	Uniref 90	Disease/Defence	7201
II	2	10	Alpha amylase inhibitor BMAI 1 precursor (*H. vulgare*)	P16968	286.31	SQCAGGQVVESIQK	Uniref 90	Disease/Defence	1650
II	2	8	Alpha amylase inhibitor BMAI 1 precursor (*H. vulgare*)	P16968	279.3	ELGVALADDK	Uniref 90	Disease/Defence	1644
II	2	8	Alpha amylase inhibitor BMAI 1 precursor (*H. vulgare*)	P16968	279.3	ATVAEVFPGCR	Uniref 90	Disease/Defence	3854
II	1	9	Beta hordothionin, Acidic protein (*H. vulgare*)	P21742	257.56	LALVSNSDEPDTIDYCNLGCR	Uniref 90	Disease/Defence	5924
II	1	9	Beta hordothionin, Acidic protein (*H. vulgare*)	P21742	257.56	CPSSFPK	Uniref 90	Disease/Defence	12758
II	2	9	Beta hordothionin, Acidic protein (*H. vulgare*)	P21742	293.74	LALVSNSDEPDTIDYCNLGCR	Uniref 90	Disease/Defence	10418
II	2	9	Beta hordothionin, Acidic protein (*H. vulgare*)	P21742	293.74	CPSSFPK	Uniref 90	Disease/Defence	10489
II	1	10	Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041	139.03	CCQELDEAPQHCR	Uniref 90	Disease/Defence	7073
II	1	10	Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041	230.73	CCQELDEAPQHCR	Uniref 90	Disease/Defence	16286
II	1	10	Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041	230.73	SHPDWSVLK	Uniref 90	Disease/Defence	24548
II	2	10	Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041	317.81	SHPDWSVLK	Uniref 90	Disease/Defence	12993
II	2	10	Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041	317.81	VLVTPGQCNVLTVHNAPYCLGLDI	Uniref 90	Disease/Defence	27587
II	2	8	Alpha amylase trypsin inhibitor CMa precursor (*H. vulgare*)	P28041	217.87	CCQELDEAPQHCR	Uniref 90	Disease/Defence	5085
II	1	10	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	165.22	QQCCGELANIPQQCR	Uniref 90	Protein destination	3328
II	1	10	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	165.22	EVQMDFVR	Uniref 90	Protein destination	7275
II	2	10	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	328.38	SRPDQSGLMELPGCPR	Uniref 90	Protein destination	14883
II	2	10	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	328.38	QQCCGELANIPQQCR	Uniref 90	Protein destination	49642
II	2	9	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	164.35	SRPDQSGLMELPGCPR	Uniref 90	Protein destination	20752
II	2	8	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	614.79	EVQMDFVR	Uniref 90	Protein destination	192
II	2	8	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	614.79	DYVEQQACR	Uniref 90	Protein destination	2869
II	2	8	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	614.79	QQCCGELANIPQQCR	Uniref 90	Protein destination	10239
II	2	8	Alpha amylase trypsin inhibitor CMb precursor (*H. vulgare*)	P32936	614.79	SRPDQSGLMELPGCPR	Uniref 90	Protein destination	13086
II	1	9	Gamma hordein 3 (*H. vulgare*)	P80198	95.4	EFLLQQCTLDEK	Uniref 90	Protein destination	3194
II	1	10	Gamma hordein 3 (*H. vulgare*)	P80198	95.4	QQCCQQLANINEQSR	Uniref 90	Protein destination	8444
II	2	9	Gamma hordein 3 (*H. vulgare*)	P80198	299.95	EFLLQQCTLDEK	Uniref 90	Protein destination	959
II	2	9	Gamma hordein 3 (*H. vulgare*)	P80198	299.95	QQCCQQLANINEQSR	Uniref 90	Protein destination	19850
II	1	9	Grain softness protein (*H. vulgare*)	Q0GIL0	215.81	SCEEVQDQCCQQLR	Uniref 90	Unclassified	8046
II	1	10	Grain softness protein (*H. vulgare*)	Q0GIL0	215.81	LNSCSDYVMDR	Uniref 90	Unclassified	7144
II	2	10	Grain softness protein (*H. vulgare*)	Q0GIL0	214.49	LNSCSDYVMDR	Uniref 90	Unclassified	10310

II	2	9	Grain softness protein (*H. vulgare*)	Q0GIL0	394.05	SCEEVQDQCCQQLR	Uniref 90	Unclassified	10360
II	2	9	Grain softness protein (*H. vulgare*)	Q0GIL0	394.05	DMLLSWVFPR	Uniref 90	Unclassified	50421
II	1	9	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	146.36	CCQQLSQIAPQCR	Uniref 90	Disease/Defence	5914
II	1	10	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	146.36	LGGIFGIGGGDVFK	Uniref 90	Disease/Defence	12495
II	2	10	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	80.72	LGGIFGIGGGDVFK	Uniref 90	Disease/Defence	12947
II	2	9	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	447.75	DFPLTWPTK	Uniref 90	Disease/Defence	10339
II	2	9	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	447.75	DYVMER	Uniref 90	Disease/Defence	10381
II	2	9	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	447.75	CCQQLSQIAPQCR	Uniref 90	Disease/Defence	10384
II	2	9	Hordoindoline B1 precursor (*H. vulgare*)	Q9FSI9	447.75	LGGIFGIGGGDVFK	Uniref 90	Disease/Defence	19822
II	1	10	Serpin Z4 (*H. vulgare*)	P06293	226.13	LSIAHQTR	Uniref 90	Disease/Defence	29074
II	1	9	Serpin Z4 (*H. vulgare*)	P06293	140.93	QYISSSDNLK	Uniref 90	Disease/Defence	5967
II	1	9	Serpin Z4 (*H. vulgare*)	P06293	172.97	LSIAHQTR	Uniref 90	Disease/Defence	9946
II	1	9	Serpin Z4 (*H. vulgare*)	P06293	140.93	LSTEPEFIENHIPK	Uniref 90	Disease/Defence	15321
II	1	9	Serpin Z4 (*H. vulgare*)	P06293	172.97	TEPEFIENHIPK	Uniref 90	Disease/Defence	19730
II	1	9	Serpin Z4 (*H. vulgare*)	P06293	226.13	QILPPGSVDNTTK	Uniref 90	Disease/Defence	45505
II	1	10	Serpin Z4 (*H. vulgare*)	P06293	226.13	DQLVAILGDGGAGDAK	Uniref 90	Disease/Defence	15879
II	2	9	Serpin Z4 (*H. vulgare*)	P06293	579.01	ELNALAEQVVQFVLANESSTGGPR	Uniref 90	Disease/Defence	7302
II	2	9	Serpin Z4 (*H. vulgare*)	P06293	579.01	DQLVAILGDGGAGDAK	Uniref 90	Disease/Defence	11924
II	2	9	Serpin Z4 (*H. vulgare*)	P06293	579.01	TLEAVGQVNSWVEQVTTGLIK	Uniref 90	Disease/Defence	15398
II	2	9	Serpin Z4 (*H. vulgare*)	P06293	579.01	LSTEPEFIENHIPK	Uniref 90	Disease/Defence	49758
II	1	8	Gamma hordein 1 precursor (*H. vulgare*)	35_69	569.2	DVVQPQQLAQMEAIR	Harvest Hv	Protein destination	7058
II	1	9	Gamma hordein 1 precursor (*H. vulgare*)	35_69	569.2	IVQQSNCQVMQEQCCLQLAQIPEQYK	Harvest Hv	Protein destination	7615
II	1	10	Gamma hordein 1 precursor (*H. vulgare*)	35_69	569.2	QGVQIVQQQPQPQEVGQCVLVQGR	Harvest Hv	Protein destination	7111
II	2	10	Gamma hordein 1 precursor (*H. vulgare*)	35_69	850.64	DVVQPQQLAQMEAIR	Harvest Hv	Protein destination	6747
II	2	10	Gamma hordein 1 precursor (*H. vulgare*)	35_69	850.64	APFFSLVNAGML	Harvest Hv	Protein destination	6793
II	2	9	Gamma hordein 1 precursor (*H. vulgare*)	35_69	493.53	IVQQSNCQVMQEQCCLQLAQIPEQYK	Harvest Hv	Protein destination	5387
II	2	9	Gamma hordein 1 precursor (*H. vulgare*)	35_69	493.53	CTTIDSIVHAIFLQQGQR	Harvest Hv	Protein destination	10466
II	2	9	Gamma hordein 1 precursor (*H. vulgare*)	35_69	493.53	APFFSLVNAGML	Harvest Hv	Protein destination	49759
II	2	9	Gamma hordein 1 precursor (*H. vulgare*)	35_69	493.53	SLVLQSVPAMCNFNVPPNCSTMR	Harvest Hv	Protein destination	49893
II	1	10	Alanine aminotransferase 2 (*H. vulgare*)	P52894	148.68	DAIASGIASR	Uniref 90	Metabolism	28277
II	1	10	Alanine aminotransferase 2 (*H. vulgare*)	P52894	148.68	ATGAYSHSQGIK	Uniref 90	Metabolism	34082
II	1	9	Alanine aminotransferase 2 (*H. vulgare*)	P52894	278.04	TLFSADSISR	Uniref 90	Metabolism	6698
II	1	9	Alanine aminotransferase 2 (*H. vulgare*)	P52894	278.04	ALVVINPGNPTGQVLAEENQYDIVK	Uniref 90	Metabolism	7432
II	1	9	Alanine aminotransferase 2 (*H. vulgare*)	P52894	278.04	ASDESYASYK	Uniref 90	Metabolism	11088
II	1	9	Alanine aminotransferase 2 (*H. vulgare*)	P52894	278.04	CTILPQEDKIPAVISR	Uniref 90	Metabolism	13102
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	DAIASGIASR	Uniref 90	Metabolism	4014
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	EVLALCDHPDLLQR	Uniref 90	Metabolism	4476

II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	ASDESYASYK	Uniref 90	Metabolism	11950
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	ATGAYSHSQGIK	Uniref 90	Metabolism	13340
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	IASVNLCSNITGQILASLVMNPPKASDESYASYK	Uniref 90	Metabolism	16819
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	ALVVINPGNPTGQVLAEENQYDIVK	Uniref 90	Metabolism	16994
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	SLGYGEEDLPLVSYQSVSK	Uniref 90	Metabolism	17800
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	TLFSADSISR	Uniref 90	Metabolism	22050
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	FTVFHEAFMSEYRD	Uniref 90	Metabolism	30720
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	MAATVAVDNLNPK	Uniref 90	Metabolism	32450
II	2	8	Alanine aminotransferase 2 (*H. vulgare*)	P52894	443.69	GYYGECGK	Uniref 90	Metabolism	34786
mixed	1	5	Alpha amylase trypsin inhibitor CMb (*H. vulgare*)	35_111	109.75	KSRPDQSGLMELPGCPR	Harvest Hv	Protein destination	1112
mixed	1	6	Alpha amylase trypsin inhibitor CMb (*H. vulgare*)	35_111	109.75	DYVEQQACRIEMPGPPYLAK	Harvest Hv	Protein destination	987
mixed	2	9	Alpha amylase trypsin inhibitor CMb (*H. vulgare*)	35_111	188.53	ILVTPGFCNLTTVHNTPFCLAMDESQWN	Harvest Hv	Protein destination	27827
mixed	2	1	Alpha amylase trypsin inhibitor CMb (*H. vulgare*)	35_111	505.45	IEMPGPPYLAK	Harvest Hv	Protein destination	2281
mixed	1	2	Lactoylglutathione lyase (*O. sativa*)	35_118	181.14	VVLVDYADFLK	Harvest Hv	Metabolism	954
mixed	1	2	Lactoylglutathione lyase (*O. sativa*)	35_118	181.14	GNAYAQVAIGTDDVYK	Harvest Hv	Metabolism	1063
mixed	1	2	Lactoylglutathione lyase (*O. sativa*)	35_118	181.14	SAEAVLEWPK	Harvest Hv	Metabolism	6258
mixed	1	9	Lactoylglutathione lyase (*O. sativa*)	35_118	181.14	CYTECFGMK	Harvest Hv	Metabolism	2382
mixed	2	2	Lactoylglutathione lyase (*O. sativa*)	35_118	396.07	VVLVDYADFLK	Harvest Hv	Metabolism	557
mixed	2	2	Lactoylglutathione lyase (*O. sativa*)	35_118	396.07	AIMFYEK	Harvest Hv	Metabolism	1084
mixed	2	2	Lactoylglutathione lyase (*O. sativa*)	35_118	396.07	ISGVTTGMATGSEAGK	Harvest Hv	Metabolism	6575
mixed	2	2	Lactoylglutathione lyase (*O. sativa*)	35_118	396.07	SAEAVLEWPK	Harvest Hv	Metabolism	11149
mixed	2	2	Lactoylglutathione lyase (*O. sativa*)	35_118	396.07	GNAYAQVAIGTDDVYKSAEAVELVTK	Harvest Hv	Metabolism	50773
mixed	1	2	Putative legumin (*O. sativa*)	35_1242	158.54	GTCGIVLPEATK	Harvest Hv	Protein destination	5727
mixed	1	9	Putative legumin (*O. sativa*)	35_1242	158.54	LSLAAGGMSLPSYSDSAK	Harvest Hv	Protein destination	401
mixed	1	9	Putative legumin (*O. sativa*)	35_1242	158.54	VVVLNTVNLPLVK	Harvest Hv	Protein destination	1671
mixed	1	9	Putative legumin (*O. sativa*)	35_1242	154.45	AISPEVLEASFNTTPEMEK	Harvest Hv	Protein destination	4762
mixed	2	1	Putative legumin (*O. sativa*)	35_1242	276.43	AISPEVLEASFNTTPEMEK	Harvest Hv	Protein destination	6482
mixed	2	1	Putative legumin (*O. sativa*)	35_1242	276.43	ANQPPSLIDRSAAMAVDLTPR	Harvest Hv	Protein destination	18328
mixed	2	2	Putative legumin (*O. sativa*)	35_1242	146.69	VVVLNTVNLPLVK	Harvest Hv	Protein destination	423
mixed	1	9	Elongation factor 1 alpha (*A. thaliana*)	35_13730	195.06	SRYDEIVK	Harvest Hv	Protein synthesis	10792
mixed	1	9	Elongation factor 1 alpha (*A. thaliana*)	35_13730	195.06	QMICCCNK	Harvest Hv	Protein synthesis	10942
mixed	2	2	Elongation factor 1 alpha (*A. thaliana*)	35_13730	207.9	YSCTVIDAPGHR	Harvest Hv	Protein synthesis	3444
mixed	2	2	Elongation factor 1 alpha (*A. thaliana*)	35_13730	207.9	QMICCCNK	Harvest Hv	Protein synthesis	3958
mixed	2	2	Elongation factor 1 alpha (*A. thaliana*)	35_13730	207.9	VETGVIKPGMVVTFGPTGLTTEVK	Harvest Hv	Protein synthesis	28766
mixed	1	2	Lipoxygenase 2 (*H. vulgare*)	35_14193	99.82	HSSDEVYLGQHDTPAWTSDAK	Harvest Hv	Metabolism	6395
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	35_14193	176.92	LEGIEK	Harvest Hv	Metabolism	163

mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	35_14193	176.92	YDVYNDLGDSR	Harvest Hv	Metabolism	649
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	35_14193	176.92	STLDPSK	Harvest Hv	Metabolism	3260
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	35_14193	768.06	QSDFLGYTLK	Harvest Hv	Metabolism	739
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	35_14193	453.7	GVTCQLISSTNVDHNNGGR	Harvest Hv	Metabolism	19261
mixed	1	10	Lipoxygenase 2 (*H. vulgare*)	35_14193	768.06	LLPLVQNVYVPR	Harvest Hv	Metabolism	527
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	35_14193	495.63	NALDFNDFGATVMDGVTELLGR	Harvest Hv	Metabolism	24526
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	35_14193	495.63	ALVDGIIPAIR	Harvest Hv	Metabolism	33884
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	35_14193	495.63	AKMFGVGGIVSDLTGGLR	Harvest Hv	Metabolism	36185
mixed	1	5	Malate dehydrogenase (*O. sativa*)	35_14420	93.05	NAIIWGNHSSSQYPDVNHATVK	Harvest Hv	Energy metabolism	7234
mixed	1	5	Malate dehydrogenase (*O. sativa*)	35_14420	93.05	GVVATTDPVEACTGVNVAVMVGGFPR	Harvest Hv	Energy metabolism	12461
mixed	1	6	Malate dehydrogenase (*O. sativa*)	35_14420	583.56	ASALEAHAAPNCK	Harvest Hv	Energy metabolism	1659
mixed	1	6	Malate dehydrogenase (*O. sativa*)	35_14420	183.47	MELVDAAFPLLK	Harvest Hv	Energy metabolism	1984
mixed	1	6	Malate dehydrogenase (*O. sativa*)	35_14420	583.56	SQASALEAHAAPNCK	Harvest Hv	Energy metabolism	2157
mixed	1	6	Malate dehydrogenase (*O. sativa*)	35_14420	183.47	ALAYSCLE	Harvest Hv	Energy metabolism	12616
mixed	2	9	Malate dehydrogenase (*O. sativa*)	35_14420	1138.32	ALGQISER	Harvest Hv	Energy metabolism	1597
mixed	2	9	Malate dehydrogenase (*O. sativa*)	35_14420	1138.32	SQASALEAHAAPNCK	Harvest Hv	Energy metabolism	4839
mixed	2	9	Malate dehydrogenase (*O. sativa*)	35_14420	1138.32	NISCLTR	Harvest Hv	Energy metabolism	6104
mixed	2	9	Malate dehydrogenase (*O. sativa*)	35_14420	1138.32	NAIIWGNHSSSQYPDVNHATVK	Harvest Hv	Energy metabolism	27630
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	35_14479	205.35	VVHGIDVFDPK	Harvest Hv	Metabolism	15458
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	35_14479	205.35	NMTGLVEMYGK	Harvest Hv	Metabolism	47333
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	EQLVDEHASSK	Harvest Hv	Metabolism	4065
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	HQLLAEFDALFESDK	Harvest Hv	Metabolism	16651
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	DSVGGQYESHIAFTLPDLYR	Harvest Hv	Metabolism	16759
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	DEHASSK	Harvest Hv	Metabolism	23120
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	AMAAKLTR	Harvest Hv	Metabolism	26166
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	VDEHASSK	Harvest Hv	Metabolism	31268
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	EQLVDEHASSK	Harvest Hv	Metabolism	33248
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	35_14479	418.54	LVDEHASSK	Harvest Hv	Metabolism	36656
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	35_14479	885.4	KAEEYLVSIPEDTPSSEFNHR	Harvest Hv	Metabolism	7071
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	35_14479	885.4	FNIVSPGADMTVYFPYTETDKR	Harvest Hv	Metabolism	27752
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	35_14479	885.4	EMQTKPDLIIGNYSDGNLVATLLAHK	Harvest Hv	Metabolism	27840
mixed	1	9	Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	120.98	VAVVCGYGDVGK	Harvest Hv	Metabolism	1532
mixed	1	9	Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	178.63	VPDPESTDNPEFK	Harvest Hv	Metabolism	2285
mixed	2	2	Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	114.11	VPDPESTDNPEFK	Harvest Hv	Metabolism	91
mixed	2	2	Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	114.11	LVGVSEETTTGVK	Harvest Hv	Metabolism	1522
mixed	2	2	Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	114.11	VAVVCGYGDVGK	Harvest Hv	Metabolism	1636
mixed	2	2	Adenosylhomocysteinase 1 (*A. thaliana*)	35_14558	114.11	IAASSLSPLLAR	Harvest Hv	Metabolism	6353

mixed	1	2	60S acidic ribosomal protein (*O. sativa*)	35_14696	137.68	VLIAVADNVGSK	Harvest Hv	Protein synthesis	19245
mixed	1	4	60S acidic ribosomal protein (*O. sativa*)	35_14696	404.17	FAVAAPAAAASGGAAAAAPK	Harvest Hv	Protein synthesis	733
mixed	1	9	60S acidic ribosomal protein (*O. sativa*)	35_14696	57.5	FAVAAPAAAASGGAAAAAPK	Harvest Hv	Protein synthesis	46275
mixed	2	6	60S acidic ribosomal protein (*O. sativa*)	35_14696	680.57	FAVAAPAAAASGGAAAAAPK	Harvest Hv	Protein synthesis	617
mixed	2	6	60S acidic ribosomal protein (*O. sativa*)	35_14696	680.57	VLIAVADNVGSK	Harvest Hv	Protein synthesis	3110
mixed	2	2	60S acidic ribosomal protein (*O. sativa*)	35_14696	299.83	VLIAVADNVGSK	Harvest Hv	Protein synthesis	5094
mixed	2	2	60S acidic ribosomal protein (*O. sativa*)	35_14696	299.83	FAVAAPAAAASGGAAAAAPK	Harvest Hv	Protein synthesis	8433
mixed	1	6	ATP synthase subunit beta (*Z. mays*)	35_14758	504.87	SISELGIYPAVDPLDSTSR	Harvest Hv	Transport	1263
mixed	1	9	ATP synthase subunit beta (*Z. mays*)	35_14758	70.78	SISELGIYPAVDPLDSTSR	Harvest Hv	Transport	14593
mixed	2	1	ATP synthase subunit beta (*Z. mays*)	35_14758	266.72	ALSSLLRSASR	Harvest Hv	Transport	15128
mixed	2	1	ATP synthase subunit beta (*Z. mays*)	35_14758	266.72	AAAYASAAAAEAPAPADKLPPTSDK	Harvest Hv	Transport	23063
mixed	2	2	ATP synthase subunit beta (*Z. mays*)	35_14758	489.72	SISELGIYPAVDPLDSTSR	Harvest Hv	Transport	483
mixed	2	2	ATP synthase subunit beta (*Z. mays*)	35_14758	489.72	IINVIGEPIDHK	Harvest Hv	Transport	715
mixed	1	9	Protein Z (*H. vulgare*)	35_14790	172.6	LSIAHQTR	Harvest Hv	Disease/Defence	9946
mixed	1	9	Protein Z (*H. vulgare*)	35_14790	172.6	TEPEFIENHIPK	Harvest Hv	Disease/Defence	19730
mixed	1	10	Protein Z (*H. vulgare*)	35_14790	132.53	LASAISSNPER	Harvest Hv	Disease/Defence	3570
mixed	2	1	Protein Z (*H. vulgare*)	35_14790	180.31	LNSTTAQRTTTPAMATTLATDVR	Harvest Hv	Disease/Defence	8447
mixed	2	1	Protein Z (*H. vulgare*)	35_14790	180.31	ISYQFEASSLLR	Harvest Hv	Disease/Defence	17815
mixed	2	1	Protein Z (*H. vulgare*)	35_14790	180.31	QYISSSDNLK	Harvest Hv	Disease/Defence	20960
mixed	2	1	Protein Z (*H. vulgare*)	35_14790	180.31	QTVEVGR	Harvest Hv	Disease/Defence	25946
mixed	2	1	Protein Z (*H. vulgare*)	35_14790	180.31	QILPPGSVDNTTK	Harvest Hv	Disease/Defence	28838
mixed	2	2	Protein Z (*H. vulgare*)	35_14790	139.97	AAGNVAFSPLSLHVALSLITAGAGGATR	Harvest Hv	Disease/Defence	6581
mixed	2	9	Protein Z (*H. vulgare*)	35_14790	687.7	LASAISSNPER	Harvest Hv	Disease/Defence	5032
mixed	1	2	Adenosine kinase (*Z. mays*)	35_14937	337.04	ISQLPLASGK	Harvest Hv	Metabolism	52
mixed	1	2	Adenosine kinase (*Z. mays*)	35_14937	337.04	GNVEYIAGGATQNSIR	Harvest Hv	Metabolism	1621
mixed	1	6	Adenosine kinase (*Z. mays*)	35_14937	337.04	IAVITQGADPVVVAEDGK	Harvest Hv	Metabolism	528
mixed	1	6	Adenosine kinase (*Z. mays*)	35_14937	337.04	LNNAILAEDK	Harvest Hv	Metabolism	1055
mixed	1	6	Adenosine kinase (*Z. mays*)	35_14937	337.04	SLIANLSAANCYK	Harvest Hv	Metabolism	1286
mixed	1	6	Adenosine kinase (*Z. mays*)	35_14937	337.04	VLPYADYIFGNETEAR	Harvest Hv	Metabolism	7415
mixed	1	9	Adenosine kinase (*Z. mays*)	35_14937	74.29	IAVITQGADPVVVAEDGK	Harvest Hv	Metabolism	46493
mixed	1	9	Adenosine kinase (*Z. mays*)	35_14937	74.29	HLPMYDELSSK	Harvest Hv	Metabolism	48249
mixed	2	6	Adenosine kinase (*Z. mays*)	35_14937	183.3	TFPVILLPK	Harvest Hv	Metabolism	150
mixed	2	6	Adenosine kinase (*Z. mays*)	35_14937	183.3	IAVITQGADPVVVAEDGK	Harvest Hv	Metabolism	627
mixed	2	1	Adenosine kinase (*Z. mays*)	35_14937	201.8	VAQWMLQTPGATSYMGCIGK	Harvest Hv	Metabolism	51494
mixed	2	1	Adenosine kinase (*Z. mays*)	35_14937	201.8	RMAASNLEGVLLGMGNPLLDISAVVDEAFLAK	Harvest Hv	Metabolism	52087
mixed	2	1	Adenosine kinase (*Z. mays*)	35_14937	201.8	IAVITQGADPVVVAEDGK	Harvest Hv	Metabolism	52308

mixed	2	1	Adenosine kinase (*Z. mays*)	35_14937	201.8	VAQWMLQTPGATSYMGCIGK	Harvest Hv	Metabolism	56756
mixed	2	1	Adenosine kinase (*Z. mays*)	35_14937	201.8	GNVEYIAGGATQNSIR	Harvest Hv	Metabolism	71963
mixed	2	2	Adenosine kinase (*Z. mays*)	35_14937	132.6	LNNAILAEDK	Harvest Hv	Metabolism	171
mixed	2	2	Adenosine kinase (*Z. mays*)	35_14937	132.6	ISQLPLASGK	Harvest Hv	Metabolism	571
mixed	2	2	Adenosine kinase (*Z. mays*)	35_14937	132.6	YIFGNETEAR	Harvest Hv	Metabolism	3160
mixed	1	2	Phosphoglucomutase (*B. inermis*)	35_15040	478.8	DTTPYEGQKPGTSGLR	Harvest Hv	Metabolism	1313
mixed	1	2	Phosphoglucomutase (*B. inermis*)	35_15040	138.69	FGGGHPDPNLTYAK	Harvest Hv	Metabolism	4017
mixed	1	2	Phosphoglucomutase (*B. inermis*)	35_15040	174.22	TSNGEPPEFGAAADGDADRNMVLGK	Harvest Hv	Metabolism	7595
mixed	1	5	Phosphoglucomutase (*B. inermis*)	35_15040	478.8	EIQPAVADVVSADEFEYKDPVDGSVSK	Harvest Hv	Metabolism	141
mixed	1	6	Phosphoglucomutase (*B. inermis*)	35_15040	478.8	ESSDALSPLVDVALK	Harvest Hv	Metabolism	575
mixed	1	6	Phosphoglucomutase (*B. inermis*)	35_15040	478.8	IFVDELGASESSLLNCVPK	Harvest Hv	Metabolism	848
mixed	1	6	Phosphoglucomutase (*B. inermis*)	35_15040	478.8	YDYENVDAEAAK	Harvest Hv	Metabolism	1051
mixed	1	6	Phosphoglucomutase (*B. inermis*)	35_15040	138.69	EDFGGGHPDPNLTYAK	Harvest Hv	Metabolism	1686
mixed	1	9	Phosphoglucomutase (*B. inermis*)	35_15040	138.69	YNMENGGPAPESVTDK	Harvest Hv	Metabolism	1996
mixed	1	9	Phosphoglucomutase (*B. inermis*)	35_15040	138.69	EDFGGGHPDPNLTYAK	Harvest Hv	Metabolism	2961
mixed	1	9	Phosphoglucomutase (*B. inermis*)	35_15040	129.81	SMPTSAALDVVAK	Harvest Hv	Metabolism	3391
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	ELMANLVK	Harvest Hv	Metabolism	1031
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	TIFDFESIK	Harvest Hv	Metabolism	2226
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	DAVQIIAK	Harvest Hv	Metabolism	4400
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	LLASPKFSFCFDGLHGVAGAYAK	Harvest Hv	Metabolism	5136
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	LVTVEDIVLQHWGTYGR	Harvest Hv	Metabolism	9926
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	IQEYTGR	Harvest Hv	Metabolism	9988
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	VWVGQDSLLSTPAVSAIIR	Harvest Hv	Metabolism	12185
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	AQRPGAVVTAADMVFSVTK	Harvest Hv	Metabolism	15618
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	EIQPAVADVVSADEFEYKDPVDGSVSK	Harvest Hv	Metabolism	17455
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	VWVGQDSLLSTPAVSAIIR	Harvest Hv	Metabolism	18609
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	IFVDELGASESSLLNCVPK	Harvest Hv	Metabolism	21556
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	EDFGGGHPDPNLTYAK	Harvest Hv	Metabolism	22029
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	FSFCFDGLHGVAGAYAK	Harvest Hv	Metabolism	22517
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	VSADEFEYKDPVDGSVSK	Harvest Hv	Metabolism	29248
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	DPVDGSVSK	Harvest Hv	Metabolism	33135
mixed	2	1	Phosphoglucomutase (*B. inermis*)	35_15040	453.5	IYIEQYEKDSSK	Harvest Hv	Metabolism	37619
mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	DTTPYEGQKPGTSGLR	Harvest Hv	Metabolism	391
mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	DAVQIIAK	Harvest Hv	Metabolism	794
mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	IFVDELGASESSLLNCVPK	Harvest Hv	Metabolism	1955
mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	YDYENVDAEAAK	Harvest Hv	Metabolism	2313
mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	EIQPAVADVVSADEFEYKDPVDGSVSK	Harvest Hv	Metabolism	2703

mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	VWVGQDSLLSTPAVSAIIR	Harvest Hv	Metabolism	3270
mixed	2	2	Phosphoglucomutase (*B. inermis*)	35_15040	361.23	LLASPKFSFCFDGLHGVAGAYAK	Harvest Hv	Metabolism	11052
mixed	2	9	Phosphoglucomutase (*B. inermis*)	35_15040	105.06	ESSDALSPLVDVALK	Harvest Hv	Metabolism	668
mixed	1	1	Os01g0663400 protein (*O. sativa*)	35_15471	212.79	ICPSIGLCIQNGTQGVSFGIR	Harvest Hv	Protein destination	34378
mixed	1	9	Os01g0663400 protein (*O. sativa*)	35_15471	606.32	LESLPDVAFTIGGK	Harvest Hv	Protein destination	5095
mixed	1	9	Os01g0663400 protein (*O. sativa*)	35_15471	606.32	LCDYIPSPMGESSVDCK	Harvest Hv	Protein destination	6494
mixed	1	9	Os01g0663400 protein (*O. sativa*)	35_15471	274.77	EGAEGHVVALK	Harvest Hv	Protein destination	8100
mixed	1	9	Os01g0663400 protein (*O. sativa*)	35_15471	606.32	QFALKPEEYILK	Harvest Hv	Protein destination	13010
mixed	1	9	Os01g0663400 protein (*O. sativa*)	35_15471	606.32	QFALKPEEYILK	Harvest Hv	Protein destination	15403
mixed	1	9	Os01g0663400 protein (*O. sativa*)	35_15471	212.79	EGAEGHVVALK	Harvest Hv	Protein destination	46251
mixed	1	10	Os01g0663400 protein (*O. sativa*)	35_15471	606.32	ILQLMLDGIDPTK	Harvest Hv	Protein destination	4792
mixed	1	10	Os01g0663400 protein (*O. sativa*)	35_15471	606.32	IGAPGILSQECK	Harvest Hv	Protein destination	12519
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	AVASQYGQR	Harvest Hv	Protein destination	7680
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	GNVEPVWYNMVNQHLVGSPIFSFWFNR	Harvest Hv	Protein destination	12019
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	EGAEGHVVALK	Harvest Hv	Protein destination	13518
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	RLESLPDVAFTIGGK	Harvest Hv	Protein destination	21809
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	FDGILGLGFK	Harvest Hv	Protein destination	23037
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	HGLVYNSAAHVPK	Harvest Hv	Protein destination	23472
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	RLESLPDVAFTIGGK	Harvest Hv	Protein destination	25945
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	LESLPDVAFTIGGK	Harvest Hv	Protein destination	28362
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	HADNGQGGEIVFGGIDPK	Harvest Hv	Protein destination	30869
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	YINKLCDYIPSPMGESSVDCK	Harvest Hv	Protein destination	31271
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	CFLSIACYLHASYKASK	Harvest Hv	Protein destination	32529
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	310.85	LCDYIPSPMGESSVDCKR	Harvest Hv	Protein destination	37955
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	SNDAMCHVCEMAVMWAK	Harvest Hv	Protein destination	44138
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	LCDYIPSPMGESSVDCK	Harvest Hv	Protein destination	51957
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	LESLPDVAFTIGGK	Harvest Hv	Protein destination	52330
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	CAAIADSGTSLLVGPTAIIAQINEK	Harvest Hv	Protein destination	52919
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	SNDAMCHVCEMAVMWAK	Harvest Hv	Protein destination	53725
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	ICPSIGLCIQNGTQGVSFGIR	Harvest Hv	Protein destination	59124
mixed	2	1	Os01g0663400 protein (*O. sativa*)	35_15471	151.47	CFLSIACYLHASYK	Harvest Hv	Protein destination	65520
mixed	2	9	Os01g0663400 protein (*O. sativa*)	35_15471	618.18	IGAPGILSQECK	Harvest Hv	Protein destination	6942
mixed	2	9	Os01g0663400 protein (*O. sativa*)	35_15471	618.18	HADNGQGGEIVFGGIDPK	Harvest Hv	Protein destination	15644
mixed	2	9	Os01g0663400 protein (*O. sativa*)	35_15471	618.18	QFALKPEEYILK	Harvest Hv	Protein destination	19928
mixed	2	9	Os01g0663400 protein (*O. sativa*)	35_15471	618.18	CAAIADSGTSLLVGPTAIIAQINEK	Harvest Hv	Protein destination	19967
mixed	2	9	Os01g0663400 protein (*O. sativa*)	35_15471	618.18	RLESLPDVAFTIGGK	Harvest Hv	Protein destination	27743
mixed	2	9	Os01g0663400 protein (*O. sativa*)	35_15471	618.18	ILQLMLDGIDPTK	Harvest Hv	Protein destination	50082

mixed	1	5	Members 73 frame 3 forw	35_15733	138.82	INLENVPGVEPLLTDNER	Harvest Hv	Unclassified	4058
mixed	1	5	Members 73 frame 3 forw	35_15733	138.82	CVDAADYNAIECR	Harvest Hv	Unclassified	4211
mixed	2	2	Members 73 frame 3 forw	35_15733	107.49	CVDAADYNAIECR	Harvest Hv	Unclassified	4438
mixed	2	2	Members 73 frame 3 forw	35_15733	107.49	ATSLMVEACKNASGESDDPDVTQELCLSTFQSDNR	Harvest Hv	Unclassified	51189
mixed	2	9	Members 73 frame 3 forw	35_15733	127.35	INLENVPGVEPLLTDNER	Harvest Hv	Unclassified	4874
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	273.89	FAVGTEAVAK	Harvest Hv	Energy metabolism	953
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	273.89	KADDVIGPEVEK	Harvest Hv	Energy metabolism	3826
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	170.84	FAVGTEAVAK	Harvest Hv	Energy metabolism	7483
mixed	1	5	Phosphoglycerate kinase (*T. aestivum*)	35_19	273.89	ELDYLDGAVSNPK	Harvest Hv	Energy metabolism	1709
mixed	1	9	Phosphoglycerate kinase (*T. aestivum*)	35_19	170.84	SVGDLTAADLEGK	Harvest Hv	Energy metabolism	6944
mixed	1	9	Phosphoglycerate kinase (*T. aestivum*)	35_19	273.89	FYKEEEK	Harvest Hv	Energy metabolism	7298
mixed	2	5	Phosphoglycerate kinase (*T. aestivum*)	35_19	302.87	SVGDLTAADLEGK	Harvest Hv	Energy metabolism	695
mixed	2	5	Phosphoglycerate kinase (*T. aestivum*)	35_19	302.87	LASLADLFVNDAFGTAHR	Harvest Hv	Energy metabolism	10746
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	KADDVIGPEVEK	Harvest Hv	Energy metabolism	38165
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	GVTTIIGGGDSVAAVEK	Harvest Hv	Energy metabolism	52855
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	RPFAAIVGGSK	Harvest Hv	Energy metabolism	53605
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	GVSLLLPSDVVIADK	Harvest Hv	Energy metabolism	53638
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	CDILLLGGGMIFTFYKAQGLSVGSSLVEEDK	Harvest Hv	Energy metabolism	53735
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	TFNDALDTTQTIIWNGPMGVFEFDK	Harvest Hv	Energy metabolism	54336
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	AHASTEGVTK	Harvest Hv	Energy metabolism	54545
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	FLKPSVAGFLLQK	Harvest Hv	Energy metabolism	61576
mixed	2	1	Phosphoglycerate kinase (*T. aestivum*)	35_19	301.65	VGVADVMSHISTGGGASLELLEGK	Harvest Hv	Energy metabolism	67228
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	540.84	ELDYLDGAVSNPK	Harvest Hv	Energy metabolism	411
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	540.84	FAPDANSQTVAASAIPDGWMGLDIGPDSVK	Harvest Hv	Energy metabolism	2172
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	540.84	ADDVIGPEVEK	Harvest Hv	Energy metabolism	3295
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	540.84	LVADLANGAVLLLENVR	Harvest Hv	Energy metabolism	11942
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	540.84	VGVADVMSHISTGGGASLELLEGK	Harvest Hv	Energy metabolism	16358
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	35_19	540.84	LASLADLFVNDAFGTAHR	Harvest Hv	Energy metabolism	21514
mixed	1	9	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	87.81	ELGIGVVPYSPLAR	Harvest Hv	Disease/Defence	6283
mixed	1	9	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	87.81	LGTQGLEVSR	Harvest Hv	Disease/Defence	6998
mixed	1	9	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	87.81	AAVESIPSGSLLSK	Harvest Hv	Disease/Defence	8252
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	EDLEEISAAVPAGDVAGSR	Harvest Hv	Disease/Defence	5359
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	LGTQGLEVSR	Harvest Hv	Disease/Defence	9238
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	LAVDYIDLYFLHR	Harvest Hv	Disease/Defence	9255

mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	HQGDDVVPIPGTTK	Harvest Hv	Disease/Defence	9620
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	VIGILEPYSWR	Harvest Hv	Disease/Defence	10030
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	DIEEDITPLCR	Harvest Hv	Disease/Defence	10477
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	YVGLSEASADTIR	Harvest Hv	Disease/Defence	11582
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	AAVESIPSGSLLSK	Harvest Hv	Disease/Defence	12601
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	YTGENLEKNK	Harvest Hv	Disease/Defence	14449
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	IDQSVPIEETMGELK	Harvest Hv	Disease/Defence	14809
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	LEMLSTK	Harvest Hv	Disease/Defence	17294
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	IGFGCMGLTGVYNDPVPEDAGVAIIR	Harvest Hv	Disease/Defence	28743
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	YGCTPAQLALAWVLHQGDDVVPIPGTTK	Harvest Hv	Disease/Defence	30286
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	CGIAGFDAGGLCVK	Harvest Hv	Disease/Defence	33734
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	YGCTPAQLALAWVLH	Harvest Hv	Disease/Defence	33757
mixed	2	1	Auxin induced protein PCNT115 (*O. sativa*)	35_2241	358.08	ELGIGVVPYSPLAR	Harvest Hv	Disease/Defence	34348
mixed	1	4	Osr40g2 protein (*O. sativa*)	35_268	371.59	LVPFNPAYEDASVLWTESK	Harvest Hv	Unclassified	1380
mixed	1	10	Osr40g2 protein (*O. sativa*)	35_268	371.59	DEEGMPAFALVNK	Harvest Hv	Unclassified	477
mixed	2	2	Osr40g2 protein (*O. sativa*)	35_268	107.23	DGEVVLAPVNPK	Harvest Hv	Unclassified	2292
mixed	2	2	Osr40g2 protein (*O. sativa*)	35_268	107.23	FSTTVKDEEGMPAFALVNK	Harvest Hv	Unclassified	8568
mixed	2	9	Osr40g2 protein (*O. sativa*)	35_268	464.62	LVPFNPAYEDASVLWTESK	Harvest Hv	Unclassified	943
mixed	2	9	Osr40g2 protein (*O. sativa*)	35_268	464.62	DEEGMPAFALVNK	Harvest Hv	Unclassified	1560
mixed	2	9	Osr40g2 protein (*O. sativa*)	35_268	464.62	DGEVVLAPVNPK	Harvest Hv	Unclassified	2486
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_373	128.58	VENLYEGPLDDVYANAIR	Harvest Hv	Protein synthesis	8397
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_373	128.58	EGALAEENMR	Harvest Hv	Protein synthesis	10334
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_373	122.77	VMQTWLPASR	Harvest Hv	Protein synthesis	13553
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_373	122.77	NMSVIAHVDHGK	Harvest Hv	Protein synthesis	16622
mixed	2	1	Elongation factor 2 (*B. vulgaris*)	35_373	358.14	GFVQFCYEPIK	Harvest Hv	Protein synthesis	3953
mixed	2	1	Elongation factor 2 (*B. vulgaris*)	35_373	358.14	NMSVIAHVDHGK	Harvest Hv	Protein synthesis	9097
mixed	2	1	Elongation factor 2 (*B. vulgaris*)	35_373	358.14	VENLYEGPLDDVYANAIR	Harvest Hv	Protein synthesis	14660
mixed	2	1	Elongation factor 2 (*B. vulgaris*)	35_373	358.14	VMQTWLPASR	Harvest Hv	Protein synthesis	14996
mixed	2	1	Elongation factor 2 (*B. vulgaris*)	35_373	358.14	VRIMGPNFVPGQK	Harvest Hv	Protein synthesis	32088
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_373	272.89	VMQTWLPASR	Harvest Hv	Protein synthesis	891
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_373	272.89	TVIWMGK	Harvest Hv	Protein synthesis	1404
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_373	272.89	GGGQVIPTAR	Harvest Hv	Protein synthesis	1542
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_373	272.89	LAKSDPMVLCSIEESGEHIIAGAGELHLEICLK	Harvest Hv	Protein synthesis	17941
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_373	272.89	NCDPDGPLMLYVSK	Harvest Hv	Protein synthesis	23479
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_373	272.89	EVDACPIR	Harvest Hv	Protein synthesis	28299
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_393	106.57	EQMTPLSDFEDKL	Harvest Hv	Protein synthesis	2659

mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_393	106.57	NCDPDGPLMLYVSK	Harvest Hv	Protein synthesis	3794
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_393	115.69	IRPVLTVNK	Harvest Hv	Protein synthesis	5793
mixed	1	9	Elongation factor 2 (*B. vulgaris*)	35_393	106.57	IMGPNFVPGQK	Harvest Hv	Protein synthesis	45474
mixed	2	1	Elongation factor 2 (*B. vulgaris*)	35_393	360.15	MDRCFLELQVEGEEAYQTFSR	Harvest Hv	Protein synthesis	29392
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_393	278.81	EQMTPLSDFEDKL	Harvest Hv	Protein synthesis	2127
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_393	278.81	ILSEEFGWDK	Harvest Hv	Protein synthesis	2645
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_393	278.81	LLEPVYLVEIQAPENALGGIYGVLNQK	Harvest Hv	Protein synthesis	5175
mixed	2	2	Elongation factor 2 (*B. vulgaris*)	35_393	278.81	LYMEARPLEEGLAEAIDDGRIGPR	Harvest Hv	Protein synthesis	21204
mixed	1	2	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	148.51	IVVSSCGHEGLFSADGLK	Harvest Hv	Metabolism	2899
mixed	1	9	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	327.17	IVVSSCGHEGLFSADGLK	Harvest Hv	Metabolism	25436
mixed	1	10	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	148.51	LEDIGTINTVPGMK	Harvest Hv	Metabolism	1364
mixed	2	1	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	188.28	ALHPATVLVSTSNGDTVDA	Harvest Hv	Metabolism	49152
mixed	2	1	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	188.28	HAALFTSTLLSR	Harvest Hv	Metabolism	51539
mixed	2	1	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	188.28	HAALFTSTLLSR	Harvest Hv	Metabolism	54438
mixed	2	1	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	188.28	VLDVNTAEDAIVSLTR	Harvest Hv	Metabolism	54782
mixed	2	1	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	188.28	IVVSSCGHEGLFSADGLKR	Harvest Hv	Metabolism	56568
mixed	2	1	Thiamine biosynthetic enzyme (*O. sativa*)	35_50571	188.28	RLEDIGTINTVPGMK	Harvest Hv	Metabolism	59991
mixed	1	2	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	192.74	MLVIGSEAPFK	Harvest Hv	Translation	986
mixed	1	6	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	192.74	YQEENTVSYVTLNK	Harvest Hv	Translation	190
mixed	1	9	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	192.74	NPLDLLPPSK	Harvest Hv	Translation	892
mixed	1	9	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	192.74	QAEVVPSVQK	Harvest Hv	Translation	1714
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	MVLDDWK	Harvest Hv	Translation	3986
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	GDNLLWGGSLIEYAR	Harvest Hv	Translation	5258
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	SNFHDVAVK	Harvest Hv	Translation	6399
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	NFEMGVSNK	Harvest Hv	Translation	7609
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	VEQWMDFAATEVDPNIAR	Harvest Hv	Translation	8126
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	YFWTMVNQPNFK	Harvest Hv	Translation	9850
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	RVEAMIEDLEPFEGQSLLDAK	Harvest Hv	Translation	23646
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	ILTKTFTSEFPHVER	Harvest Hv	Translation	37013
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	279.97	ALIAAEYCGVK	Harvest Hv	Translation	37159
mixed	2	1	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	374.49	YQEENTVSYVTLNK	Harvest Hv	Translation	209
mixed	2	2	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	374.49	QAEVVPSVQK	Harvest Hv	Translation	473
mixed	2	2	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	374.49	VEAMIEDLEPFEGQSLLDAK	Harvest Hv	Translation	774
mixed	2	2	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	374.49	TFTSEFPHVER	Harvest Hv	Translation	1530
mixed	2	2	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	374.49	NFEMGVSNK	Harvest Hv	Translation	2606
mixed	2	9	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	233.31	VPVLETPDGAVFESNAIAR	Harvest Hv	Translation	482
mixed	2	9	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	233.31	MLVIGSEAPFK	Harvest Hv	Translation	599

mixed	1	9	RNA binding protein Rp120 (*O. sativa*)	35_617	78.47	GFAVANK	Harvest Hv	Unclassified	1643
mixed	1	9	RNA binding protein Rp120 (*O. sativa*)	35_617	78.47	TNVGSVLLESGLAK	Harvest Hv	Unclassified	4579
mixed	1	9	RNA binding protein Rp120 (*O. sativa*)	35_617	78.47	GGEPLPNVSELIR	Harvest Hv	Unclassified	6549
mixed	1	9	RNA binding protein Rp120 (*O. sativa*)	35_617	78.47	REDNKPENFAR	Harvest Hv	Unclassified	8994
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	VDYTAPNIGR	Harvest Hv	Unclassified	6366
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	INVAELLLSR	Harvest Hv	Unclassified	7761
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	LAASTASTEVPPDR	Harvest Hv	Unclassified	8707
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	GGEPLPNVSELIR	Harvest Hv	Unclassified	12112
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	DLPPSAIGELSGFDAK	Harvest Hv	Unclassified	22064
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	GEIVLAQFSVDNSWNR	Harvest Hv	Unclassified	24051
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	AEIPPEKSITLSYLMAPR	Harvest Hv	Unclassified	25202
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	IPDAHVLTRAEK	Harvest Hv	Unclassified	32566
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	VVATEVLGGGK	Harvest Hv	Unclassified	34201
mixed	2	1	RNA binding protein Rp120 (*O. sativa*)	35_617	492.47	IWENYVEGEEVTNGSASESK	Harvest Hv	Unclassified	36461
mixed	1	9	Putative ketol acid reductoisomerase (*O. sativa*)	35_730	134.63	VGAAMPSLDFDTAVFNK	Harvest Hv	Metabolism	1078
mixed	1	9	Putative ketol acid reductoisomerase (*O. sativa*)	35_730	136.91	STVEGITGIISK	Harvest Hv	Metabolism	50342
mixed	2	2	Putative ketol acid reductoisomerase (*O. sativa*)	35_730	195.5	VGAAMPSLDFDTAVFNK	Harvest Hv	Metabolism	1853
mixed	2	2	Putative ketol acid reductoisomerase (*O. sativa*)	35_730	195.5	STVEGITGIISK	Harvest Hv	Metabolism	3673
mixed	1	2	Putative uncharacterized protein (*O. sativa*)	A2XUU7	631.77	LEKPASYDQIK	Uniref 90	Metabolism	2701
mixed	1	2	Putative uncharacterized protein (*O. sativa*)	A2XUU7	631.77	AASFNIIPSSTGAAK	Uniref 90	Metabolism	3871
mixed	1	3	Putative uncharacterized protein (*O. sativa*)	A2XUU7	631.77	AGIALNDNFVK	Uniref 90	Metabolism	197
mixed	1	5	Putative uncharacterized protein (*O. sativa*)	A2XUU7	631.77	VPTVDVSVVDLTVR	Uniref 90	Metabolism	531
mixed	1	6	Putative uncharacterized protein (*O. sativa*)	A2XUU7	631.77	TLLFGEK	Uniref 90	Metabolism	558
mixed	1	7	Putative uncharacterized protein (*O. sativa*)	A2XUU7	215.35	AASFNIIPSSTGAAK	Uniref 90	Metabolism	39
mixed	2	10	Putative uncharacterized protein (*O. sativa*)	A2XUU7	201.02	AASFNIIPSSTGAAK	Uniref 90	Metabolism	567
mixed	2	6	Putative uncharacterized protein (*O. sativa*)	A2XUU7	150.86	VPTVDVSVVDLTVR	Uniref 90	Metabolism	3169
mixed	2	6	Putative uncharacterized protein (*O. sativa*)	A2XUU7	150.86	VALQSDDVELVAVNDPFITTDYMICEFGIWISVCRPVDQIVIDMSSDAFAHAK	Uniref 90	Metabolism	49881
mixed	2	9	Putative uncharacterized protein (*O. sativa*)	A2XUU7	213.49	TLLFGEK	Uniref 90	Metabolism	336
mixed	2	9	Putative uncharacterized protein (*O. sativa*)	A2XUU7	213.49	AGIALNDNFVK	Uniref 90	Metabolism	680
mixed	1	5	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	282.87	ELISNSSDALDK	Uniref 90	Unclassified	1957
mixed	1	6	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	282.87	SDLVNNLGTIAR	Uniref 90	Unclassified	634
mixed	1	6	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	282.87	GIVDSEDLPLNISR	Uniref 90	Unclassified	681
mixed	1	9	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	282.87	SGDELTSLK	Uniref 90	Unclassified	1020
mixed	2	6	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	315.78	GIVDSEDLPLNISR	Uniref 90	Unclassified	125
mixed	2	1	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	420.76	ELISNSSDALDK	Uniref 90	Unclassified	277
mixed	2	2	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	420.76	FESLTDK	Uniref 90	Unclassified	841

mixed	2	2	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	420.76	SDLVNNLGTIAR	Uniref 90	Unclassified	1239
mixed	2	2	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	420.76	TMEINPENAIMDELR	Uniref 90	Unclassified	1291
mixed	2	2	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	420.76	DSSMAGYMSSK	Uniref 90	Unclassified	8522
mixed	1	2	Enolase (*O. sativa*)	A3AG33	338.76	PSGASTGVYEALELR	Uniref 90	Unclassified	1727
mixed	1	4	Enolase (*O. sativa*)	A3AG33	338.76	VNQIGSVTESIEAVK	Uniref 90	Unclassified	262
mixed	1	4	Enolase (*O. sativa*)	A3AG33	338.76	AAVPSGASTGVYEALELR	Uniref 90	Unclassified	325
mixed	1	5	Enolase (*O. sativa*)	A3AG33	338.76	YGQDATNVGDEGGFAPNIQENK	Uniref 90	Unclassified	102
mixed	2	9	Enolase (*O. sativa*)	A3AG33	170.88	SFVSEYPIVSIEDPFDQDDWVHYAK	Uniref 90	Unclassified	7018
mixed	2	9	Enolase (*O. sativa*)	A3AG33	170.88	VNQIGSVTESIEAVK	Uniref 90	Unclassified	15910
mixed	1	9	Orthophosphate dikinase precursor (*O. sativa*)	O24612	228.58	CRDGAAAAGR	Uniref 90	Energy metabolism	6244
mixed	1	9	Orthophosphate dikinase precursor (*O. sativa*)	O24612	332.79	LGDPARPLLLSVR	Uniref 90	Energy metabolism	19571
mixed	1	9	Orthophosphate dikinase precursor (*O. sativa*)	O24612	332.79	GDPARPLLLSVR	Uniref 90	Energy metabolism	26009
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	SGAAVSMPGMMDTVLNLGLNDEVAAGLAAKSGDR	Uniref 90	Energy metabolism	13186
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	LGDPARPLLLSVR	Uniref 90	Energy metabolism	21970
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	SGAAVSMPGMMDTVLNLGL	Uniref 90	Energy metabolism	23175
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	SGAAVSMPGMMDTVLNLGLNDEVAAGLAAK	Uniref 90	Energy metabolism	26694
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	GMMDTVLNLGLNDEVAAGLAAK	Uniref 90	Energy metabolism	29279
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	IVVIEDKALHEGEWLSLNGSTGEVIIGK	Uniref 90	Energy metabolism	30987
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	IALDMVNEGLVER	Uniref 90	Energy metabolism	33885
mixed	2	1	Orthophosphate dikinase precursor (*O. sativa*)	O24612	428.89	DVYVEAKGEPFPSDPK	Uniref 90	Energy metabolism	34496
mixed	1	4	Ribosomal protein L25 (*Z. mays*)	O81229	314.66	PDYDALDVANK	Uniref 90	Protein synthesis	241
mixed	1	4	Ribosomal protein L25 (*Z. mays*)	O81229	314.66	YPLTTESAMK	Uniref 90	Protein synthesis	600
mixed	1	5	Ribosomal protein L25 (*Z. mays*)	O81229	314.66	LDQYQILK	Uniref 90	Protein synthesis	236
mixed	1	9	Ribosomal protein L25 (*Z. mays*)	O81229	314.66	LTPDYDALDVANK	Uniref 90	Protein synthesis	2652
mixed	1	7	Ribosomal protein L25 (*Z. mays*)	O81229	125.31	LTPDYDALDVANK	Uniref 90	Protein synthesis	42
mixed	2	6	Ribosomal protein L25 (*Z. mays*)	O81229	428.33	LDQYQILK	Uniref 90	Protein synthesis	806
mixed	2	6	Ribosomal protein L25 (*Z. mays*)	O81229	428.33	MYDIQAK	Uniref 90	Protein synthesis	3820
mixed	2	6	Ribosomal protein L25 (*Z. mays*)	O81229	428.33	LTPDYDALDVANK	Uniref 90	Protein synthesis	6771
mixed	2	6	Ribosomal protein L25 (*Z. mays*)	O81229	428.33	YPLTTESAMK	Uniref 90	Protein synthesis	12725
mixed	2	3	Ribosomal protein L25 (*Z. mays*)	O81229	113.51	YPLTTESAMK	Uniref 90	Protein synthesis	307
mixed	2	4	Ribosomal protein L25 (*Z. mays*)	O81229	170.84	MYDIQAK	Uniref 90	Protein synthesis	593
mixed	2	4	Ribosomal protein L25 (*Z. mays*)	O81229	170.84	LDQYQILK	Uniref 90	Protein synthesis	610
mixed	2	4	Ribosomal protein L25 (*Z. mays*)	O81229	170.84	NKLDQYQILK	Uniref 90	Protein synthesis	10337
mixed	2	7	Ribosomal protein L25 (*Z. mays*)	O81229	160.30	LTPDYDALDVANK	Uniref 90	Protein synthesis	1660
mixed	1	1	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	158.64	NPEEIPWAAAGAEYVVESTGVFTDK	Uniref 90	Energy metabolism	47652

mixed	1	4	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	850.48	GILGYVDEDLVSTDFQGDSR	Uniref 90	Energy metabolism	1389
mixed	1	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	158.64	GILGYVDEDLVSTDFQGDSR	Uniref 90	Energy metabolism	25302
mixed	1	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	158.64	AAIKEESEGNLK	Uniref 90	Energy metabolism	46404
mixed	1	10	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	850.48	DAPMFVCGVNEK	Uniref 90	Energy metabolism	268
mixed	2	6	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	214.74	EVAVFGCR	Uniref 90	Energy metabolism	1480
mixed	2	2	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	249.69	EVAVFGCR	Uniref 90	Energy metabolism	4498
mixed	2	2	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	249.69	YDTVHGQWK	Uniref 90	Energy metabolism	4760
mixed	2	2	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	249.69	NPEEIPWAAAGAEYVVESTGVFTDK	Uniref 90	Energy metabolism	11266
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	DAPMFVCGVNEK	Uniref 90	Energy metabolism	154
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	VLPELNGK	Uniref 90	Energy metabolism	1639
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	AAIKEESEGNLK	Uniref 90	Energy metabolism	1654
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	VIISAPSK	Uniref 90	Energy metabolism	1662
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	GILGYVDEDLVSTDFQGDSR	Uniref 90	Energy metabolism	3176
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	LVSWYDNEWGYSTR	Uniref 90	Energy metabolism	11800
mixed	2	9	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	860.04	NPEEIPWAAAGAEYVVESTGVFTDKDK	Uniref 90	Energy metabolism	12422
mixed	1	6	Subtilisin chymotrypsin inhibitor CI 1A (*H. vulgare*)	P16062	88.09	TSWPEVVGMSAEK	Uniref 90	Disease/Defence	647
mixed	1	10	Subtilisin chymotrypsin inhibitor CI 1A (*H. vulgare*)	P16062	88.09	YPEPTEGSIGASSAK	Uniref 90	Disease/Defence	4772
mixed	2	10	Subtilisin chymotrypsin inhibitor CI 1A (*H. vulgare*)	P16062	85.19	YPEPTEGSIGASSAK	Uniref 90	Disease/Defence	4067
mixed	2	9	Subtilisin chymotrypsin inhibitor CI 1A (*H. vulgare*)	P16062	78.35	TSWPEVVGMSAEK	Uniref 90	Disease/Defence	1914
mixed	2	9	Subtilisin chymotrypsin inhibitor CI 1A (*H. vulgare*)	P16062	78.35	DKPNAQVEVIPVDAMVHLNFDPNR	Uniref 90	Disease/Defence	27852
mixed	1	9	Sucrose synthase 2 (*O. sativa*)	P31924	295.99	AMENEMLLR	Uniref 90	Metabolism	3130
mixed	1	9	Sucrose synthase 2 (*O. sativa*)	P31924	295.99	DKEEQAEFK	Uniref 90	Metabolism	10858
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	LMTLTGVYGFWKYVSNLER	Uniref 90	Metabolism	7657
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	DKEEQAEFK	Uniref 90	Metabolism	19546
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	YLEMLYALK	Uniref 90	Metabolism	24440
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	ESMYPLLNFLR	Uniref 90	Metabolism	28458
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	NLTGLVELYGR	Uniref 90	Metabolism	29673
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	CQEDPSHWTK	Uniref 90	Metabolism	35188
mixed	2	1	Sucrose synthase 2 (*O. sativa*)	P31924	271.55	TMASTVPLAVEGEPSNK	Uniref 90	Metabolism	36778
mixed	2	9	Sucrose synthase 2 (*O. sativa*)	P31924	296.49	SIGNGVQFLNR	Uniref 90	Metabolism	1230
mixed	2	9	Sucrose synthase 2 (*O. sativa*)	P31924	296.49	VVHGIDVFDPK	Uniref 90	Metabolism	6948
mixed	2	9	Sucrose synthase 2 (*O. sativa*)	P31924	296.49	AMENEMLLR	Uniref 90	Metabolism	8034
mixed	2	9	Sucrose synthase 2 (*O. sativa*)	P31924	296.49	WISAQMNR	Uniref 90	Metabolism	10612
mixed	2	9	Sucrose synthase 2 (*O. sativa*)	P31924	296.49	SLSALQGALR	Uniref 90	Metabolism	50413
mixed	1	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	206.96	VTYPIMADPDR	Uniref 90	Disease/Defence	12865
mixed	1	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	206.96	LSFLYPSCTGR	Uniref 90	Disease/Defence	13231
mixed	1	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	206.96	QLNMVDPDEKDAQGQLPSR	Uniref 90	Disease/Defence	14803

mixed	1	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	154.76	MFPQGFETADLPSKK	Uniref 90	Disease/Defence	26348
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	QLNMVDPDEK	Uniref 90	Disease/Defence	9371
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	DIEAYKPGSK	Uniref 90	Disease/Defence	13648
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	DAQGQLPSR	Uniref 90	Disease/Defence	13791
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	TLHIVGPDK	Uniref 90	Disease/Defence	16486
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	NMDEVVR	Uniref 90	Disease/Defence	16901
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	MPGLTIGDTVPNLELDSTHGK	Uniref 90	Disease/Defence	22058
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	MFPQGFETADLPSK	Uniref 90	Disease/Defence	26202
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	KMFPQGFETADLPSK	Uniref 90	Disease/Defence	28990
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	VATPANWKPGECVVIAPGVSDEEAKK	Uniref 90	Disease/Defence	29151
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	DIEAYKPGSKVTYPIMADPDR	Uniref 90	Disease/Defence	36530
mixed	2	1	1 Cys peroxiredoxin (*H. vulgare*)	P52572	334.49	VATPANWKPGECVVIAPGVSDEEAK	Uniref 90	Disease/Defence	37614
mixed	2	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	584.02	VTYPIMADPDR	Uniref 90	Disease/Defence	7581
mixed	2	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	584.02	AVDSLLTAAK	Uniref 90	Disease/Defence	12220
mixed	2	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	584.02	LLGISCDDVQSHK	Uniref 90	Disease/Defence	15305
mixed	2	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	584.02	LSFLYPSCTGR	Uniref 90	Disease/Defence	16013
mixed	2	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	584.02	VATPANWKPGECVVIAPGVSDEEAK	Uniref 90	Disease/Defence	20041
mixed	2	9	1 Cys peroxiredoxin (*H. vulgare*)	P52572	584.02	PGLTIGDTVPNLELDSTHGK	Uniref 90	Disease/Defence	50327
mixed	1	1	Embryo globulin (*H. vulgare*)	Q03678	309.65	AQDQDEGFVAGPEQQSR	Uniref 90	Protein destination	29046
mixed	1	1	Embryo globulin (*H. vulgare*)	Q03678	309.65	GGHSLQQCVQR	Uniref 90	Protein destination	29338
mixed	1	1	Embryo globulin (*H. vulgare*)	Q03678	309.65	LRPFDQVSR	Uniref 90	Protein destination	34348
mixed	1	9	Embryo globulin (*H. vulgare*)	Q03678	343.93	SFHALANQDVR	Uniref 90	Protein destination	2159
mixed	1	9	Embryo globulin (*H. vulgare*)	Q03678	309.65	DTFNLLEQRPK	Uniref 90	Protein destination	8215
mixed	1	9	Embryo globulin (*H. vulgare*)	Q03678	309.65	ALRPFDQVSR	Uniref 90	Protein destination	19591
mixed	1	9	Embryo globulin (*H. vulgare*)	Q03678	343.93	AQDQDEGFVAGPEQQSR	Uniref 90	Protein destination	27538
mixed	1	9	Embryo globulin (*H. vulgare*)	Q03678	309.65	EGDVIVAPAGSIMHLANTDGR	Uniref 90	Protein destination	45617
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	EGDVIVAPAGSIMHLANTDGR	Uniref 90	Protein destination	4057
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	VAIMEVNPR	Uniref 90	Protein destination	10577
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	DTFNLLEQRPK	Uniref 90	Protein destination	20350
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	GGHSLQQCVQR	Uniref 90	Protein destination	20703
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	SFHALANQDVR	Uniref 90	Protein destination	28014
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	AQDQDEGFVAGPEQQSR	Uniref 90	Protein destination	50497
mixed	2	9	Embryo globulin (*H. vulgare*)	Q03678	694.76	ALRPFDQVSR	Uniref 90	Protein destination	50576
mixed	1	2	Non specific lipid transfer protein (*H. vulgare*)	Q42848	267.86	EASAALSCGQVDSK	Uniref 90	Transport	1005
mixed	1	4	Non specific lipid transfer protein (*H. vulgare*)	Q42848	267.86	LAPCVAYVTGR	Uniref 90	Transport	1825
mixed	1	5	Non specific lipid transfer protein (*H. vulgare*)	Q42848	267.86	ECCSGVQGLNGLAR	Uniref 90	Transport	201
mixed	1	6	Non specific lipid transfer protein (*H. vulgare*)	Q42848	267.86	ECCSGVQGLNGLAR	Uniref 90	Transport	1439

mixed	1	10	Non specific lipid transfer protein (*H. vulgare*)	Q42848	267.86	CGVSVPFPISMSTDCNK	Uniref 90	Transport	782
mixed	2	5	Non specific lipid transfer protein (*H. vulgare*)	Q42848	160.49	ECCSGVQGLNGLAR	Uniref 90	Transport	384
mixed	2	3	Non specific lipid transfer protein (*H. vulgare*)	Q42848	203.9	CGVSVPFPISMSTDCNK	Uniref 90	Transport	840
mixed	2	4	Non specific lipid transfer protein (*H. vulgare*)	Q42848	103.25	LAPCVAYVTGR	Uniref 90	Transport	1729
mixed	1	5	Cytoplasmatic ribosomal protein S13 (*T. aestivum*)	Q5XUU9	316.59	DQHGIPLVK	Uniref 90	Protein synthesis	1415
mixed	1	7	Cytoplasmatic ribosomal protein S13 (*T. aestivum*)	Q5XUU9	316.59	TAVADVDELITK	Uniref 90	Protein synthesis	23
mixed	2	3	Cytoplasmatic ribosomal protein S13 (*T. aestivum*)	Q5XUU9	154.07	TAVADVDELITK	Uniref 90	Protein synthesis	809
mixed	2	9	Cytoplasmatic ribosomal protein S13 (*T. aestivum*)	Q5XUU9	129.04	TAVADVDELITK	Uniref 90	Protein synthesis	12292
mixed	1	5	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	222.11	SGDVSALQIGVK	Uniref 90	Protein Destination	88
mixed	1	5	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	222.11	GTLTDGTVFDSSYER	Uniref 90	Protein Destination	466
mixed	1	5	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	222.11	GDPIEFELGTGQVIK	Uniref 90	Protein Destination	760
mixed	2	6	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	142.82	GWDQGILGMCIGEK	Uniref 90	Protein Destination	5886
mixed	2	5	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	477.08	SGDVSALQIGVK	Uniref 90	Protein Destination	304
mixed	2	5	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	477.08	GTLTDGTVFDSSYER	Uniref 90	Protein Destination	1045
mixed	2	5	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	477.08	GDPIEFELGTGQVIK	Uniref 90	Protein Destination	4436
mixed	2	2	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	133.35	SDEDVADSDL	Uniref 90	Protein Destination	1642
mixed	2	2	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	133.35	YKPESCSISAHK	Uniref 90	Protein Destination	7136
mixed	2	2	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	133.35	GWDQGILGMCIGEK	Uniref 90	Protein Destination	16083
mixed	2	2	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	133.35	GDPIEFELGTGQVIK	Uniref 90	Protein Destination	16734
mixed	2	2	Peptidyl prolyl cis trans isomerase (*H. vulgare*)	Q70YJ6	133.35	LGYGDQGSPPTIPGGATLIFDTELVAVNGEPSSK	Uniref 90	Protein Destination	28408
mixed	1	2	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	225.21	LIDIPVSNCLNSNVSK	Uniref 90	Metabolism	4389
mixed	1	2	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	225.21	DALIPSGTVI	Uniref 90	Metabolism	4597
mixed	1	9	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	225.21	VLSETGGIPIGIGK	Uniref 90	Metabolism	210
mixed	1	9	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	225.21	IINVDDIQEASR	Uniref 90	Metabolism	321
mixed	1	9	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	110.26	LIDIPVSNCLNSNVSK	Uniref 90	Metabolism	569
mixed	1	10	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	225.21	ETDADITVAALPMDEER	Uniref 90	Metabolism	984
mixed	2	1	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	422.88	ETDADITVAALPMDEER	Uniref 90	Metabolism	8740
mixed	2	1	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	422.88	DNFPSANDFGSEVIPGATEIGMR	Uniref 90	Metabolism	14243
mixed	2	1	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	422.88	NSQTCLDPDASTSVLGIILGGGAGTR	Uniref 90	Metabolism	30029
mixed	2	1	Glucose 1 phosphate adenylyltransferase (*H. vulgare*)	Q8HS72	422.88	VLSETGGIPIGIGK	Uniref 90	Metabolism	34061
mixed	1	2	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	155.74	VYPMESYQEAR	Uniref 90	Metabolism	1054
mixed	1	4	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	155.74	VLMGYVGEVDSK	Uniref 90	Metabolism	1060
mixed	1	5	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	155.74	VIGSTVPVLDGEALSMR	Uniref 90	Metabolism	928
mixed	1	5	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	145.89	GLDGGLHTSFCQDELR	Uniref 90	Metabolism	8187
mixed	1	9	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	155.74	SSDNSSEMLHVLK	Uniref 90	Metabolism	2737
mixed	2	6	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	182.51	VIGSTVPVLDGEALSMR	Uniref 90	Metabolism	282

mixed	2	6	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	182.51	VYPMESYQEAR	Uniref 90	Metabolism	1528
mixed	2	6	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	182.51	VLMGYVGEVDSK	Uniref 90	Metabolism	2789
mixed	2	2	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	279.55	VYLFNNATGASVTAER	Uniref 90	Metabolism	9015
mixed	2	2	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	279.55	TNLLLWPVEEIETLR	Uniref 90	Metabolism	9518
mixed	2	2	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	279.55	GALGPFGLLVLAAGDR	Uniref 90	Metabolism	12902
mixed	2	2	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	279.55	GWASIQSVPR	Uniref 90	Metabolism	22237
mixed	2	2	Sucrose fructan 6 fructosyltransferase (*H. vulgare*)	Q96466	279.55	GLDGGLHTSFCQDELR	Uniref 90	Metabolism	28482
mixed	1	4	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	634.72	SDIDIVSNASCTTNCLAPLAK	Uniref 90	Metabolism	215
mixed	1	9	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	634.72	KVIISAPSK	Uniref 90	Metabolism	639
mixed	2	1	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	214.6	SDIDIVSNASCTTNCLAPLAK	Uniref 90	Metabolism	21873
mixed	2	1	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	214.6	LVSWYDNEWGYSTR	Uniref 90	Metabolism	25406
mixed	2	1	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	214.6	KVIISAPSK	Uniref 90	Metabolism	29117
mixed	2	1	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	214.6	GILGYVDEDLVSTDFQGDNRSSIFDAK	Uniref 90	Metabolism	29335
mixed	2	1	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	214.6	VINDRFGIVEGLMTTVHAMTATQK	Uniref 90	Metabolism	29413
mixed	2	2	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	167.49	SDIDIVSNASCTTNCLAPLAK	Uniref 90	Metabolism	966
mixed	2	2	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	167.49	FGIVEGLMTTVHAMTATQK	Uniref 90	Metabolism	20680
mixed	2	9	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	553.65	AGIALNDHFVK	Uniref 90	Metabolism	2158
mixed	2	9	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	553.65	KVIISAPSK	Uniref 90	Metabolism	3292
mixed	2	9	Cytosolic glyceraldehyde 3 phosphate dehydrogenase GAPDH (*T. aestivum*)	Q9M4V4	553.65	EYKSDIDIVSNASCTTNCLAPLAK	Uniref 90	Metabolism	50361
mixed	1	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	88.7	GEEFPVENYIVK	Uniref 90	Disease/Defence	1995
mixed	1	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	88.7	CDVVVINTPLTEK	Uniref 90	Disease/Defence	7643
mixed	2	1	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	489.1	CDVVVINTPLTEK	Uniref 90	Disease/Defence	11429
mixed	2	1	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	489.1	EGELASQYK	Uniref 90	Disease/Defence	14459
mixed	2	1	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	489.1	NFLPGYQQVVK	Uniref 90	Disease/Defence	22548
mixed	2	1	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	489.1	GEWNVAGIAHR	Uniref 90	Disease/Defence	29292

mixed	2	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	267.71	NFLPGYQQVVK	Uniref 90	Disease/Defence	3577
mixed	2	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	267.71	CDVVVINTPLTEK	Uniref 90	Disease/Defence	5357
mixed	2	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	267.71	GEEFPVENYIVK	Uniref 90	Disease/Defence	5879
mixed	2	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	267.71	LQINPELEK	Uniref 90	Disease/Defence	5945
mixed	2	9	Formate dehydrogenase mitochondrial precursor (*H. vulgare*)	Q9ZRI8	267.71	FEEDLDAMLPK	Uniref 90	Disease/Defence	28056
mixed	1	2	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	151.41	VALEACVQAR	Uniref 90	Energy metabolism	6357
mixed	1	4	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	218.57	FEFEPVDTIDK	Uniref 90	Energy metabolism	75
mixed	1	5	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	151.41	WSPELAAACEVWK	Uniref 90	Energy metabolism	1636
mixed	1	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	151.41	FEFEPVDTIDKK	Uniref 90	Energy metabolism	2424
mixed	2	1	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	345.81	VSPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR	Uniref 90	Energy metabolism	21750
mixed	2	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	35_136	322.77	FEFEPVDTIDK	Uniref 90	Energy metabolism	1280
mixed	1	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	208.84	GGLDFTKDDENVNSQPFMR	Uniref 90	Energy metabolism	6455
mixed	1	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	208.84	DDENVNSQPFMR	Uniref 90	Energy metabolism	7972
mixed	1	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	208.84	VALEACVQAR	Uniref 90	Energy metabolism	24819
mixed	2	1	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	211.55	LTYYTPEYETK	Uniref 90	Energy metabolism	4169
mixed	2	1	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	211.55	DRFLFCAEAIYK	Uniref 90	Energy metabolism	14154
mixed	2	1	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	211.55	GGLDFTKDDENVNSQPFMR	Uniref 90	Energy metabolism	17327
mixed	2	1	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	211.55	SQAETGEIK	Uniref 90	Energy metabolism	17401
mixed	2	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	247.48	LTYYTPEYETK	Uniref 90	Energy metabolism	1128
mixed	2	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	247.48	TFQGPPHGIQVER	Uniref 90	Energy metabolism	4969
mixed	2	9	Ribulose bisphosphate carboxylase large chain precursor (*A. thaliana*)	O03042	247.48	NEGRDLAVEGNEIIR	Uniref 90	Energy metabolism	49950

mixed	1	1	Phosphoglycerate kinase (*T. aestivum*)	P12783	105.11	PTDVVVADK	Uniref 90	Energy metabolism	29363
mixed	1	1	Phosphoglycerate kinase (*T. aestivum*)	P12783	105.11	EEEKNDPEFAK	Uniref 90	Energy metabolism	39426
mixed	1	1	Phosphoglycerate kinase (*T. aestivum*)	P12783	105.11	LLLPTDVVVADK	Uniref 90	Energy metabolism	45515
mixed	1	1	Phosphoglycerate kinase (*T. aestivum*)	P12783	105.11	LAAALPDGGVLLLENVR	Uniref 90	Energy metabolism	50151
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	LPTDVVVADK	Uniref 90	Energy metabolism	618
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	186.55	KPFAAIVGGSK	Uniref 90	Energy metabolism	3352
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	186.55	LASVADLYVNDAFGTAHR	Uniref 90	Energy metabolism	7654
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	186.55	FLRPSVAGFLMQK	Uniref 90	Energy metabolism	10426
mixed	1	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	186.55	SLVEEDKLELATSLIETAK	Uniref 90	Energy metabolism	12833
mixed	1	4	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	GVTTIIGGGDSVAAVEK	Uniref 90	Energy metabolism	335
mixed	1	4	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	LLLPTDVVVADK	Uniref 90	Energy metabolism	720
mixed	1	5	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	ELDYLVGAVANPK	Uniref 90	Energy metabolism	346
mixed	1	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	ADLNVPLDDAQK	Uniref 90	Energy metabolism	106
mixed	1	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	TFAEALDTTK	Uniref 90	Energy metabolism	300
mixed	1	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	484.69	LAAALPDGGVLLLENVR	Uniref 90	Energy metabolism	1568
mixed	1	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	188.19	FAAGTDAIAK	Uniref 90	Energy metabolism	2994
mixed	1	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	188.19	FYKEEEK	Uniref 90	Energy metabolism	7298
mixed	1	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	188.19	KPFAAIVGGSK	Uniref 90	Energy metabolism	10638
mixed	1	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	188.19	SVGTLGEADLK	Uniref 90	Energy metabolism	48392
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	ADLNVPLDDAQK	Uniref 90	Energy metabolism	78
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	FAAGTDAIAK	Uniref 90	Energy metabolism	665
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	TFAEALDTTK	Uniref 90	Energy metabolism	687
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	GVTTIIGGGDSVAAVEK	Uniref 90	Energy metabolism	746
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	ELDYLVGAVANPK	Uniref 90	Energy metabolism	1134
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	SVGTLGEADLK	Uniref 90	Energy metabolism	1418
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	SVGTLGEADLK	Uniref 90	Energy metabolism	2150
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	TVIWNGPMGVFEFEK	Uniref 90	Energy metabolism	3499
mixed	2	6	Phosphoglycerate kinase (*T. aestivum*)	P12783	865.9	LASVADLYVNDAFGTAHR	Uniref 90	Energy metabolism	10750
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	QLAELTGK	Uniref 90	Energy metabolism	4228
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	IVPATAIPDGWMGLDVGPDSIK	Uniref 90	Energy metabolism	5446
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	SVGTLGEADLK	Uniref 90	Energy metabolism	6423
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	TFAEALDTTK	Uniref 90	Energy metabolism	8125
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	FAAGTDAIAK	Uniref 90	Energy metabolism	8188
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	FAADAESK	Uniref 90	Energy metabolism	11408
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	KPFAAIVGGSK	Uniref 90	Energy metabolism	14594
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	LASVADLYVNDAFGTAHR	Uniref 90	Energy metabolism	21645
mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	ADLNVPLDDAQK	Uniref 90	Energy metabolism	28181

mixed	2	2	Phosphoglycerate kinase (*T. aestivum*)	P12783	634.77	FLRPSVAGFLMQK	Uniref 90	Energy metabolism	28459
mixed	2	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	205.49	FLRPSVAGFLMQK	Uniref 90	Energy metabolism	19935
mixed	2	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	205.49	IVPATAIPDGWMGLDVGPDSIK	Uniref 90	Energy metabolism	20186
mixed	2	9	Phosphoglycerate kinase (*T. aestivum*)	P12783	205.49	ELDYLVGAVANPK	Uniref 90	Energy metabolism	20674
mixed	1	1	Elongation factor 1 alpha (*A. thaliana*)	35_13677	127.48	MIPTKPMVVETFATYPPLGR	Harvest Hv	Protein synthesis	29494
mixed	1	1	Elongation factor 1 alpha (*A. thaliana*)	35_13677	163.31	QMICCCNK	Harvest Hv	Protein synthesis	37111
mixed	1	6	Elongation factor 1 alpha (*A. thaliana*)	35_13677	88.12	MIPTKPMVVETFATYPPLGR	Harvest Hv	Protein synthesis	8050
mixed	1	9	Elongation factor 1 alpha (*A. thaliana*)	35_13677	290.77	GFVASNSK	Harvest Hv	Protein synthesis	5518
mixed	1	9	Elongation factor 1 alpha (*A. thaliana*)	35_13677	127.48	STNLDWYK	Harvest Hv	Protein synthesis	19410
mixed	1	9	Elongation factor 1 alpha (*A. thaliana*)	35_13677	127.48	ARYEEIVK	Harvest Hv	Protein synthesis	48800
mixed	1	10	Elongation factor 1 alpha (*A. thaliana*)	35_13677	127.48	VETGVIKPGMVVTFGPTGLTTEVK	Harvest Hv	Protein synthesis	24364
mixed	2	10	Elongation factor 1 alpha (*A. thaliana*)	35_13677	278.16	MIPTKPMVVETFATYPPLGR	Harvest Hv	Protein synthesis	10292
mixed	2	10	Elongation factor 1 alpha (*A. thaliana*)	35_13677	278.16	VETGVIKPGMVVTFGPTGLTTEVK	Harvest Hv	Protein synthesis	10293
mixed	2	6	Elongation factor 1 alpha (*A. thaliana*)	35_13677	312.16	VETGVIKPGMVVTFGPTGLTTEVK	Harvest Hv	Protein synthesis	15325
mixed	1	1	Beta amylase (*H. vulgare*)	35_14441	882.84	CDPDIFYTDGHGTR	Harvest Hv	Metabolism	39009
mixed	1	9	Beta amylase (*H. vulgare*)	35_14441	882.84	DVGTCDPDIFYTDGHGTR	Harvest Hv	Metabolism	14098
mixed	1	9	Beta amylase (*H. vulgare*)	35_14441	882.84	GPTGGMGGQAEDPTSGMGGELPATM	Harvest Hv	Metabolism	25170
mixed	1	10	Beta amylase (*H. vulgare*)	35_14441	882.84	DVGTCDPDIFYTDGHGTR	Harvest Hv	Metabolism	15938
mixed	1	10	Beta amylase (*H. vulgare*)	35_14441	882.84	LSNQLVEGQNYANFK	Harvest Hv	Metabolism	24445
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	ASINFTCAEMR	Harvest Hv	Metabolism	6769
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	SGPEISIEMILQAAQPK	Harvest Hv	Metabolism	7399
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	SAVQMYADYMTSFR	Harvest Hv	Metabolism	13900
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	NIEYLTLGVDNQPLFHGR	Harvest Hv	Metabolism	20784
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	NARPHGINQSGPPEHK	Harvest Hv	Metabolism	27103
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	DSEQSSQAMSAPEELVQQVLSAGWR	Harvest Hv	Metabolism	28558
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	GPTGGMGGQAEDPTSGMGGELPATM	Harvest Hv	Metabolism	29044
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	EGLNVACENALPRYDPTAYNTILR	Harvest Hv	Metabolism	34219
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	SGPEISIEMILQAA	Harvest Hv	Metabolism	36057
mixed	2	1	Beta amylase (*H. vulgare*)	35_14441	380.05	GNYVQVYVMLPLDAVSVNNR	Harvest Hv	Metabolism	36344
mixed	2	9	Beta amylase (*H. vulgare*)	35_14441	756.64	LSNQLVEGQNYANFK	Harvest Hv	Metabolism	12154
mixed	2	9	Beta amylase (*H. vulgare*)	35_14441	756.64	DVGTCDPDIFYTDGHGTR	Harvest Hv	Metabolism	20107
mixed	1	1	Beta amylase (*H. vulgare*)	P16098	665.76	DFLDAGVIVDIEVGLGPAGEMR	Uniref 90	Metabolism	30405
mixed	1	9	Beta amylase (*H. vulgare*)	P16098	665.76	AAAAAVGHPEWEFPNDVGQYNDTPER	Uniref 90	Metabolism	45995
mixed	1	10	Beta amylase (*H. vulgare*)	P16098	665.76	YDPTAYNTILR	Uniref 90	Metabolism	8624
mixed	1	10	Beta amylase (*H. vulgare*)	P16098	665.76	ASINFTCAEMR	Uniref 90	Metabolism	15904
mixed	1	10	Beta amylase (*H. vulgare*)	P16098	665.76	EGLNVACENALPR	Uniref 90	Metabolism	16170
mixed	1	10	Beta amylase (*H. vulgare*)	P16098	665.76	DPYVDPMAPLPR	Uniref 90	Metabolism	16228

mixed	2	9	Beta amylase (*H. vulgare*)	P16098	488.71	DPYVDPMAPLPR	Uniref 90	Metabolism	7076
mixed	2	9	Beta amylase (*H. vulgare*)	P16098	488.71	EGLNVACENALPR	Uniref 90	Metabolism	20293
mixed	2	9	Beta amylase (*H. vulgare*)	P16098	488.71	ASINFTCAEMR	Uniref 90	Metabolism	20511
mixed	2	9	Beta amylase (*H. vulgare*)	P16098	488.71	AAAAAVGHPEWEFPNDVGQYNDTPER	Uniref 90	Metabolism	27729
mixed	2	9	Beta amylase (*H. vulgare*)	P16098	488.71	GPTGGMGGQAEDPTSGIGGELPATM	Uniref 90	Metabolism	50458
mixed	1	2	Sucrose synthase 1 (*O. sativa*)	P30298	218.99	SLASAVPLAVDGESTSK	Uniref 90	Metabolism	202
mixed	1	4	Sucrose synthase 1 (*O. sativa*)	P30298	218.99	FQELGLEKGWGDCAK	Uniref 90	Metabolism	510
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	218.99	SIGNGVQFLNR	Uniref 90	Metabolism	515
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	YAPFEDILR	Uniref 90	Metabolism	5059
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	PFEDILR	Uniref 90	Metabolism	5102
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	WISAQMNR	Uniref 90	Metabolism	6708
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	PDAVGTTCGQR	Uniref 90	Metabolism	7616
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	LGVTQCTIAHALEK	Uniref 90	Metabolism	9554
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	230.64	TKYPNSDIYLDK	Uniref 90	Metabolism	10671
mixed	1	9	Sucrose synthase 1 (*O. sativa*)	P30298	230.64	NMTGLVEMYGK	Uniref 90	Metabolism	47333
mixed	1	10	Sucrose synthase 1 (*O. sativa*)	P30298	218.99	QQGLDITPK	Uniref 90	Metabolism	1541
mixed	1	10	Sucrose synthase 1 (*O. sativa*)	P30298	360.33	SIGNGVQFLNR	Uniref 90	Metabolism	1847
mixed	1	10	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	LLPDAVGTTCGQR	Uniref 90	Metabolism	3458
mixed	1	10	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	VVHGIDVFDPK	Uniref 90	Metabolism	5386
mixed	1	10	Sucrose synthase 1 (*O. sativa*)	P30298	384.56	FNIVSPGADMSVYFPYTEADK	Uniref 90	Metabolism	8471
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	P30298	356.95	NKPIIFSMAR	Uniref 90	Metabolism	1425
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	P30298	356.95	GTTMMLNDR	Uniref 90	Metabolism	1774
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	P30298	356.95	DREEQAEFK	Uniref 90	Metabolism	10117
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	P30298	356.95	NMTGLVEMYGK	Uniref 90	Metabolism	13732
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	P30298	356.95	LLPDAVGTTCGQR	Uniref 90	Metabolism	18695
mixed	2	1	Sucrose synthase 1 (*O. sativa*)	P30298	356.95	YPNSDIYLDK	Uniref 90	Metabolism	23494
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	ALENEMLLR	Uniref 90	Metabolism	787
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	QQGLDITPK	Uniref 90	Metabolism	1474
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	YAPFEDILR	Uniref 90	Metabolism	1497
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	LLPDAVGTTCGQR	Uniref 90	Metabolism	1512
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	NMTGLVEMYGK	Uniref 90	Metabolism	11835
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	VIGTEHTDILR	Uniref 90	Metabolism	15513
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	AADILVNFFEK	Uniref 90	Metabolism	20592
mixed	2	9	Sucrose synthase 1 (*O. sativa*)	P30298	1004.02	LGVTQCTIAHALEK	Uniref 90	Metabolism	27923
mixed	1	9	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	177.55	EQFPGANDFGSEVIPGATSTGMR	Uniref 90	Metabolism	5909

mixed	1	9	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	177.55	VLDADVTDSVIGEGCVIK	Uniref 90	Metabolism	6561
mixed	1	9	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	177.55	AYGSNIGGYK	Uniref 90	Metabolism	8442
mixed	1	9	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	135.02	NEGFVEVLAAQQSPDNPDWFQGTADAVR	Uniref 90	Metabolism	28345
mixed	1	10	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	186.4	LIDIPVSNCLNSNISK	Uniref 90	Metabolism	2030
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	MDVPLASK	Uniref 90	Metabolism	9999
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	DALLPSGTVI	Uniref 90	Metabolism	10003
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	AKEMPYIASMGIYVISK	Uniref 90	Metabolism	11313
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	MDVPLASKTFPSPSPSK	Uniref 90	Metabolism	14628
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	MDYEKFIQAHR	Uniref 90	Metabolism	15688
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	ETDADITVAALP	Uniref 90	Metabolism	21164
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	EQFPGANDFGSEVIPGATSTGMR	Uniref 90	Metabolism	21338
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	AYGSNIGGYK	Uniref 90	Metabolism	21674
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	SCISEGAIIEDTLLMGADYYETEADKK	Uniref 90	Metabolism	21874
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	AMMVDTTILGLDDAR	Uniref 90	Metabolism	22681
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	IYVRTQFNSASLNR	Uniref 90	Metabolism	25675
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	KPIPDFSFYDR	Uniref 90	Metabolism	28218
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	IIEFAEKPK	Uniref 90	Metabolism	29931
mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	PAVPLGANYR	Uniref 90	Metabolism	30722

mixed	2	1	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	576.01	NEGFVEVLAAQQSPDNPDWFQGTADAVR	Uniref 90	Metabolism	32693
mixed	2	2	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	162.53	IYVRTQFNSASLNR	Uniref 90	Metabolism	4634
mixed	2	2	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	162.53	ETDADITVAALPMDEERATAFGLMK	Uniref 90	Metabolism	6177
mixed	2	2	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	162.53	IGDNVMIINVDNVQEAAR	Uniref 90	Metabolism	16828
mixed	2	9	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	289.03	ETDADITVAALPMDEER	Uniref 90	Metabolism	3350
mixed	2	9	Glucose 1 phosphate adenylyltransferase small subunit (*T. aestivum*)	P30523	289.03	EQFPGANDFGSEVIPGATSTGMR	Uniref 90	Metabolism	11905
mixed	1	2	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	LIDIPMSNCFNSGINK	Uniref 90	Metabolism	421
mixed	1	2	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	MCNGGARGPAATGAQCVLTSDASPADTLVLR	Uniref 90	Metabolism	606
mixed	1	2	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	VDTSFLNFAIDDPAK	Uniref 90	Metabolism	3707
mixed	1	6	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	LIDIPMSNCFNSGINKIFVMTQFNSASLNR	Uniref 90	Metabolism	132
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	ATPAVPIGGCYR	Uniref 90	Metabolism	1221
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	TPFFTSPR	Uniref 90	Metabolism	2043
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.23	LIDIPMSNCFNSGINK	Uniref 90	Metabolism	4308
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.23	ISNCIIDMNAR	Uniref 90	Metabolism	5136
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.23	VDTSFLNFAIDDPAK	Uniref 90	Metabolism	5360
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	305.87	PAVPIGGCYR	Uniref 90	Metabolism	5754
mixed	1	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	305.87	PIGGCYR	Uniref 90	Metabolism	6800
mixed	1	10	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	234.26	VPIGVGENTK	Uniref 90	Metabolism	1537

mixed	1	10	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.23	EGVQEADRPEEGYYIR	Uniref 90	Metabolism	5441
mixed	1	10	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.23	GPAATGAQCVLTSDASPADTLVLR	Uniref 90	Metabolism	7288
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	YPYIASMGVYVFK	Uniref 90	Metabolism	2781
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	VPIGVGENTK	Uniref 90	Metabolism	4950
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	VDTSFLNFAIDDPAK	Uniref 90	Metabolism	6043
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	ISNCIIDMNAR	Uniref 90	Metabolism	7209
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	EGVQEADRPEEGYYIR	Uniref 90	Metabolism	10132
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	IASMGVYVFK	Uniref 90	Metabolism	10883
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	YPYIASMGVYVFK	Uniref 90	Metabolism	10963
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	ASEYGLVK	Uniref 90	Metabolism	15309
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	YAELHDFGSEILPR	Uniref 90	Metabolism	15827
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	DVLLNLLK	Uniref 90	Metabolism	21794
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	HVDDNADITLSCAPVGESR	Uniref 90	Metabolism	28245
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	NYADPNEVAAVILGGGTGTQLFPLTSTR	Uniref 90	Metabolism	28295
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	SFFDANMALCEQPPK	Uniref 90	Metabolism	29085
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	SSMQFSSVLPLEGKACVSPVR	Uniref 90	Metabolism	30427
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	FIWVLEDYYK	Uniref 90	Metabolism	31382
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	770.2	IEHSIIGVR	Uniref 90	Metabolism	37256

mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	ECKIEHSIIGVR	Uniref 90	Metabolism	43280
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	VIQFSEKPK	Uniref 90	Metabolism	44366
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	GPAATGAQCVLTSDASPADTLVLR	Uniref 90	Metabolism	50839
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	HVDDNADITLSCAPVGESR	Uniref 90	Metabolism	52054
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	EAIISHGCFLR	Uniref 90	Metabolism	54850
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	IGDSSSIRHER	Uniref 90	Metabolism	68962
mixed	2	1	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	220.52	SHGCFLR	Uniref 90	Metabolism	71616
mixed	2	2	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.91	SGIVVIQK	Uniref 90	Metabolism	2020
mixed	2	2	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	204.91	ATPAVPIGGCYR	Uniref 90	Metabolism	2968
mixed	2	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	113.99	IGDSSSIR	Uniref 90	Metabolism	368
mixed	2	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	113.99	EGVQEADRPEEGYYIR	Uniref 90	Metabolism	4703
mixed	2	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	113.99	SSMQFSSVLPLEGK	Uniref 90	Metabolism	10611
mixed	2	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	113.99	GPAATGAQCVLTSDASPADTLVLR	Uniref 90	Metabolism	10709
mixed	2	9	Glucose 1 phosphate adenylyltransferase large subunit 1 (*H. vulgare*)	P30524	113.99	YAELHDFGSEILPR	Uniref 90	Metabolism	27853
mixed	1	9	Sucrose synthase 2 (*H. vulgare*)	P31923	228.56	LMTLSGVYGFWK	Uniref 90	Metabolism	2241
mixed	1	9	Sucrose synthase 2 (*H. vulgare*)	P31923	330.43	NTPFEDLLR	Uniref 90	Metabolism	5783
mixed	1	9	Sucrose synthase 2 (*H. vulgare*)	P31923	330.43	SIGNGVQFLNR	Uniref 90	Metabolism	6382
mixed	1	9	Sucrose synthase 2 (*H. vulgare*)	P31923	330.43	SLGTLQGALR	Uniref 90	Metabolism	7620
mixed	1	9	Sucrose synthase 2 (*H. vulgare*)	P31923	254.27	VVHGIDVFDPK	Uniref 90	Metabolism	15458
mixed	1	10	Sucrose synthase 2 (*H. vulgare*)	P31923	330.43	PFEDLLR	Uniref 90	Metabolism	5460
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	YVSNLDR	Uniref 90	Metabolism	6338
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	NTPFEDLLR	Uniref 90	Metabolism	11162
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	ADMSIYFPYTEQQK	Uniref 90	Metabolism	11580

mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	VSKDKEEQVEFK	Uniref 90	Metabolism	13520
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	FNIVSPGADMSIYFPYTEQQK	Uniref 90	Metabolism	16210
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	GMTMMLNDR	Uniref 90	Metabolism	18882
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	LMTLSGVYGFWK	Uniref 90	Metabolism	25395
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	NMTGLVEMYGR	Uniref 90	Metabolism	28561
mixed	2	1	Sucrose synthase 2 (*H. vulgare*)	P31923	445.03	KKPIIFSMAR	Uniref 90	Metabolism	29573
mixed	2	9	Sucrose synthase 2 (*H. vulgare*)	P31923	907.6	MLPDAHGTTCGQR	Uniref 90	Metabolism	3216
mixed	2	9	Sucrose synthase 2 (*H. vulgare*)	P31923	907.6	SLGTLQGALR	Uniref 90	Metabolism	8695
mixed	2	9	Sucrose synthase 2 (*H. vulgare*)	P31923	907.6	NMTGLVEMYGR	Uniref 90	Metabolism	10785
mixed	2	9	Sucrose synthase 2 (*H. vulgare*)	P31923	907.6	GMLQPHQITAEYNAAIPEAER	Uniref 90	Metabolism	15796
mixed	2	9	Sucrose synthase 2 (*H. vulgare*)	P31923	907.6	FNIVSPGADMSIYFPYTEQQK	Uniref 90	Metabolism	20080
mixed	1	10	Aspartate aminotransferase (*O. sativa*)	P37833	412.89	LIFGADSPAIQENR	Uniref 90	Metabolism	2142
mixed	1	10	Aspartate aminotransferase (*O. sativa*)	P37833	412.89	EYLPITGLADFNK	Uniref 90	Metabolism	2790
mixed	1	10	Aspartate aminotransferase (*O. sativa*)	P37833	167.82	VATVQCLSGTGSLR	Uniref 90	Metabolism	7290
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	VGGEFLAR	Uniref 90	Metabolism	3409
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	NMGLYGER	Uniref 90	Metabolism	4748
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	VATVQCLSGTGSLR	Uniref 90	Metabolism	8274
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	VNLGVGAYR	Uniref 90	Metabolism	14075
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	VFTLAGLTVR	Uniref 90	Metabolism	14661
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	VFTLAGLTVR	Uniref 90	Metabolism	14724
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	TVQCLSGTGSLR	Uniref 90	Metabolism	16172
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	QQLFDALK	Uniref 90	Metabolism	18445
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	ISMAGLSGRTIPHLADAIHAAVTK	Uniref 90	Metabolism	21364
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	QIGMFTFTGLNSDQVAFMR	Uniref 90	Metabolism	21481
mixed	2	1	Aspartate aminotransferase (*O. sativa*)	P37833	479.23	QIGMFTFTGLNSDQVAFMR	Uniref 90	Metabolism	34643
mixed	2	9	Aspartate aminotransferase (*O. sativa*)	P37833	298	LIFGADSPAIQENR	Uniref 90	Metabolism	458
mixed	2	9	Aspartate aminotransferase (*O. sativa*)	P37833	298	EYLPITGLADFNK	Uniref 90	Metabolism	10790
mixed	2	9	Aspartate aminotransferase (*O. sativa*)	P37833	298	TEEGKPLVLNVVR	Uniref 90	Metabolism	12071
mixed	2	9	Aspartate aminotransferase (*O. sativa*)	P37833	298	TIYIPQPTWGNHPK	Uniref 90	Metabolism	28091
mixed	1	2	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	APLILIQDGDSKK	Harvest Hv	Disease/Defence	555
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	TADEIVDYIR	Harvest Hv	Disease/Defence	68
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	VDQAPLILIQDGDSK	Harvest Hv	Disease/Defence	127
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	VVVADNVHDVVFK	Harvest Hv	Disease/Defence	828
mixed	1	4	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	VDQAPLILIQDGDSKK	Harvest Hv	Disease/Defence	226
mixed	1	4	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	121.47	MDATENDVPGEFDVQGYPTLYFVTPSGK	Harvest Hv	Disease/Defence	3094
mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	GDAAVERPVVR	Harvest Hv	Disease/Defence	78
mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	VVADNVHDVVFK	Harvest Hv	Disease/Defence	327

mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	DQAPLILIQDGDSKK	Harvest Hv	Disease/Defence	964
mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	ADNVHDVVFK	Harvest Hv	Disease/Defence	1114
mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	FFQSNAPK	Harvest Hv	Disease/Defence	1595
mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	121.47	VVIFDKNPDNHPYLLK	Harvest Hv	Disease/Defence	12424
mixed	1	6	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	QAPLILIQDGDSKK	Harvest Hv	Disease/Defence	671
mixed	1	6	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	2047.72	MDATENDVPGEFDVQGYPTLYFVTPSGK	Harvest Hv	Disease/Defence	864
mixed	1	6	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	146.35	NPDNHPYLLK	Harvest Hv	Disease/Defence	2697
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	1024.26	TADEIVDYIR	Harvest Hv	Disease/Defence	256
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	1024.26	AAEPAATEPLKDEL	Harvest Hv	Disease/Defence	751
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	1024.26	FFQSNAPK	Harvest Hv	Disease/Defence	839
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	1024.26	VVVADNVHDVVFK	Harvest Hv	Disease/Defence	14884
mixed	2	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	133.27	TADEIVDYIR	Harvest Hv	Disease/Defence	1174
mixed	2	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	133.27	VDQAPLILIQDGDSKK	Harvest Hv	Disease/Defence	1361
mixed	2	5	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	133.27	SDYDFGHTVHANHLPR	Harvest Hv	Disease/Defence	49810
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	SEPIPEANNEPVK	Harvest Hv	Disease/Defence	4692
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	VVIFDK	Harvest Hv	Disease/Defence	7174
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	ETAGQAAAATEK	Harvest Hv	Disease/Defence	7723
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	AAQLLSK	Harvest Hv	Disease/Defence	8920
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	AAEPAATEPLK	Harvest Hv	Disease/Defence	9098
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	AAEPAATEPLKDEL	Harvest Hv	Disease/Defence	19716
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	VSYEGGRTADEIVDYIR	Harvest Hv	Disease/Defence	25641
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	FFQSNAPK	Harvest Hv	Disease/Defence	31464
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	SIQEYK	Harvest Hv	Disease/Defence	31923
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	DYFDGKLTPFR	Harvest Hv	Disease/Defence	33862
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	NPDNHPYLLK	Harvest Hv	Disease/Defence	34247
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	SAYYGAVEEFSGKDVK	Harvest Hv	Disease/Defence	35006
mixed	2	1	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	299.36	SEPIPEANNEP	Harvest Hv	Disease/Defence	36374
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	486.39	FFQSNAPK	Harvest Hv	Disease/Defence	8665
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	486.39	FLIGDIESSQGAFQYFGLK	Harvest Hv	Disease/Defence	12205
mixed	2	9	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	750.31	AAVERPVVR	Harvest Hv	Disease/Defence	1806
mixed	2	9	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	750.31	GDAAVERPVVR	Harvest Hv	Disease/Defence	2712
mixed	2	9	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	750.31	VDQAPLILIQDGDSKK	Harvest Hv	Disease/Defence	20276
mixed	2	9	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	750.31	MDATENDVPGEFDVQGYPTLYFVTPSGK	Harvest Hv	Disease/Defence	49717
mixed	2	8	Protein disulfide isomerase precursor (*T. aestivum*)	35_14571	367.49	VVVADNVHDVVFK	Harvest Hv	Disease/Defence	2251
mixed	1	1	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	315.17	SEPIPEANNEPVK	Uniref 90	Disease/Defence	29361
mixed	1	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	NKETAGQAAAAATEK	Uniref 90	Disease/Defence	1320
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	APEDATYLEDGK	Uniref 90	Disease/Defence	43

mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	YEVQGFPTLK	Uniref 90	Disease/Defence	56
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	HDPAIVLAK	Uniref 90	Disease/Defence	107
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	697.3	SEPIPEANNEPVK	Uniref 90	Disease/Defence	118
mixed	1	3	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	SAYYGAVEEFSGK	Uniref 90	Disease/Defence	8771
mixed	1	4	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	SEPIPEANNEPVK	Uniref 90	Disease/Defence	246
mixed	1	5	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	FIDASSTPK	Uniref 90	Disease/Defence	700
mixed	1	6	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	118.49	ETAGQAAAAATEK	Uniref 90	Disease/Defence	1758
mixed	1	6	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	118.49	NPDNHPYLLK	Uniref 90	Disease/Defence	2697
mixed	1	8	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	ETAGQAAAAATEK	Uniref 90	Disease/Defence	504
mixed	1	9	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	SEPIPEANNEPVK	Uniref 90	Disease/Defence	7341
mixed	1	9	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	195.07	ETAGQAAAAATEK	Uniref 90	Disease/Defence	8169
mixed	1	9	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	315.17	NPDNHPYLLK	Uniref 90	Disease/Defence	46066
mixed	1	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	EAEGIVEYLK	Uniref 90	Disease/Defence	2314
mixed	1	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	315.17	SAYYGAVEEFSGK	Uniref 90	Disease/Defence	45082
mixed	1	7	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1323.87	AAEPAATEPLKDEL	Uniref 90	Disease/Defence	38
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	YEVQGFPTLK	Uniref 90	Disease/Defence	273
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	APEDATYLEDGK	Uniref 90	Disease/Defence	285
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	SAYYGAVEEFSGK	Uniref 90	Disease/Defence	376
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	SEPIPEANNEPVK	Uniref 90	Disease/Defence	421
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	HDPAIVLAK	Uniref 90	Disease/Defence	1675
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	ETAGQAAAAATEK	Uniref 90	Disease/Defence	1682
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	SLAPEYEK	Uniref 90	Disease/Defence	1771
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	DFDVSALEK	Uniref 90	Disease/Defence	2159
mixed	2	10	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	1878.02	LAPILDEAAATLQSEEDVVIAK	Uniref 90	Disease/Defence	14866
mixed	2	6	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	132.79	HDPAIVLAK	Uniref 90	Disease/Defence	19920
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	KSEPIPEANNEPVK	Uniref 90	Disease/Defence	1327
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	AMLFLNFSTGPFESFK	Uniref 90	Disease/Defence	2733
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	SLAPEYEK	Uniref 90	Disease/Defence	2783
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	APEDATYLEDGK	Uniref 90	Disease/Defence	4585
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	NKETAGQAAAAATEK	Uniref 90	Disease/Defence	7771
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	FIDASSTPK	Uniref 90	Disease/Defence	9443
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	EAEGIVEYLK	Uniref 90	Disease/Defence	28554
mixed	2	2	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	417.61	LAPILDEAAATLQSEEDVVIAK	Uniref 90	Disease/Defence	28717
mixed	2	9	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	299.37	KSEPIPEANNEPVK	Uniref 90	Disease/Defence	1131
mixed	2	9	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	299.37	AAEPAATEPLKDEL	Uniref 90	Disease/Defence	14979
mixed	2	8	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	450.96	LAPILDEAAATLQSEEDVVIAK	Uniref 90	Disease/Defence	2832
mixed	2	8	Protein disulfide isomerase precursor (*T. aestivum*)	P52589	450.96	LFKPFDELVVDSK	Uniref 90	Disease/Defence	13082

mixed	1	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	GVTCQLISSTNV	Uniref 90	Metabolism	4970
mixed	1	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	YDVYNDLGDSR	Uniref 90	Metabolism	5357
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	Q42847	177.32	LEGIEK	Uniref 90	Metabolism	163
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	Q42847	177.32	YDVYNDLGDSR	Uniref 90	Metabolism	649
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	QVVAMNSDPQLK	Uniref 90	Metabolism	1096
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	GVTCQLISSTNVDHNNGGR	Uniref 90	Metabolism	1878
mixed	1	6	Lipoxygenase 2 (*H. vulgare*)	Q42847	177.32	STLDPSK	Uniref 90	Metabolism	3260
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	TITLDNVPGR	Uniref 90	Metabolism	598
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	LGVPGAIIVK	Uniref 90	Metabolism	851
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	LPNIPALEEVR	Uniref 90	Metabolism	1067
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	GDDQQGPYLDHDR	Uniref 90	Metabolism	2267
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	GMAVEDASSPHK	Uniref 90	Metabolism	3209
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	QLSVTHPVYK	Uniref 90	Metabolism	4240
mixed	1	9	Lipoxygenase 2 (*H. vulgare*)	Q42847	406.29	GVTCQLISSTNVDHNNGGR	Uniref 90	Metabolism	19261
mixed	1	10	Lipoxygenase 2 (*H. vulgare*)	Q42847	637.05	SLEGLTVQQALAGNR	Uniref 90	Metabolism	153
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	FAVTFDWSVDK	Uniref 90	Metabolism	6428
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	DTMNINAR	Uniref 90	Metabolism	9359
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	EVGHGDLKDAAWWPK	Uniref 90	Metabolism	13215
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	RGMAVEDASSPHK	Uniref 90	Metabolism	13473
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	EMLAGVNPMMIK	Uniref 90	Metabolism	14392
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	YDVYNDLGDSR	Uniref 90	Metabolism	15506
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	SLEGLTVQQALAGNR	Uniref 90	Metabolism	18715
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	RPMPVQGSEEYAELER	Uniref 90	Metabolism	23436
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	HSSDEVYLGQHDTPAWTSDAK	Uniref 90	Metabolism	26061
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	DAAWWPK	Uniref 90	Metabolism	26922
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	FPYMLLYPNTSDHTGQAEGLTAR	Uniref 90	Metabolism	29541
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	TYVDLSPGEFDSFADILK	Uniref 90	Metabolism	29845
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	GMAVEDASSPHK	Uniref 90	Metabolism	32541
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	NALDFNDFGAHVMDGVTELLGRGVTCQLISSTNVDHNNGGR	Uniref 90	Metabolism	32709
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	RPMPVQGSEEYAELERDPEK	Uniref 90	Metabolism	33214
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	HWNFTEQALPADLIK	Uniref 90	Metabolism	35209
mixed	2	1	Lipoxygenase 2 (*H. vulgare*)	Q42847	472.31	VQGSEEYAELER	Uniref 90	Metabolism	37408
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	QVVAMNSDPQLK	Uniref 90	Metabolism	195
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	LGVPGAIIVK	Uniref 90	Metabolism	455
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	TITLDNVPGR	Uniref 90	Metabolism	1342
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	TYVDLSPGEFDSFADILK	Uniref 90	Metabolism	1624

mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	VGAEANLEQWLLPTNLPFITTGENK	Uniref 90	Metabolism	1857
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	AWMTDEEFAR	Uniref 90	Metabolism	2347
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	GMAVEDASSPHK	Uniref 90	Metabolism	3238
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	LGVGGIVSDLTGGIR	Uniref 90	Metabolism	3245
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	GVTCQLISSTNVDHNNGGR	Uniref 90	Metabolism	3515
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	YDVYNDLGDSR	Uniref 90	Metabolism	3761
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	GDDQQGPYLDHDR	Uniref 90	Metabolism	4249
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	DTMNINAR	Uniref 90	Metabolism	5458
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	GDGTLAPVAIELSSPLIQGELTTAK	Uniref 90	Metabolism	5761
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	YNRVFFANDTYLPHQMPAALKPYR	Uniref 90	Metabolism	18562
mixed	2	2	Lipoxygenase 2 (*H. vulgare*)	Q42847	627.75	HSSDEVYLGQHDTPAWTSDAK	Uniref 90	Metabolism	22298
mixed	1	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	260.89	YLSGEAEQIEWSK	Uniref 90	Metabolism	1646
mixed	1	6	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	260.89	IVTEDFLPLPSK	Uniref 90	Metabolism	101
mixed	1	6	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	260.89	LEIPDGAVLENK	Uniref 90	Metabolism	988
mixed	1	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	260.89	SIPSIVELDSLK	Uniref 90	Metabolism	338
mixed	1	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	260.89	PSIVELDSLK	Uniref 90	Metabolism	465
mixed	1	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	213.86	IQTPTDEVVVPYDTLAPPPEDLDAMK	Uniref 90	Metabolism	1448
mixed	1	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	213.86	LNGGLGTTMGCTGPK	Uniref 90	Metabolism	6456
mixed	1	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	213.86	LEIPDGAVLENK	Uniref 90	Metabolism	7715
mixed	1	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	213.86	DGWYPPGHGDVFPSLNNSGK	Uniref 90	Metabolism	24946
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	LVDAEALK	Uniref 90	Metabolism	1211
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	LNGGLGTTMGCTGPK	Uniref 90	Metabolism	2043
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	LDTLLSQGK	Uniref 90	Metabolism	2893
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	GGTLISYEGR	Uniref 90	Metabolism	10200
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	VKPSNPSIELGPEFK	Uniref 90	Metabolism	17041
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	IFNTNNLWVNLK	Uniref 90	Metabolism	22249
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	YGCSVPLLLMNSFNTHDDTQK	Uniref 90	Metabolism	26030
mixed	2	1	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	401.61	ILNHLIHNQNEYCMEVTPKTLADVK	Uniref 90	Metabolism	32111
mixed	2	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	240.45	IQTPTDEVVVPYDTLAPPPEDLDAMK	Uniref 90	Metabolism	693
mixed	2	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	240.45	IVTEDFLPLPSK	Uniref 90	Metabolism	1012
mixed	2	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	240.45	SIPSIVELDSLK	Uniref 90	Metabolism	1160
mixed	2	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	240.45	LEIPDGAVLENK	Uniref 90	Metabolism	1917
mixed	2	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	240.45	IVTEDFLPLPS	Uniref 90	Metabolism	3646
mixed	2	2	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	240.45	VSGDVSFGSGVVLK	Uniref 90	Metabolism	9155
mixed	2	9	UTP glucose 1 phosphate uridylyltransferase (*H. vulgare*)	Q43772	108.43	VKPSNPSIELGPEFK	Uniref 90	Metabolism	10824

Table A 4: Proteins, which were detected in the profiling of nucellar projection of a developing barley grain (8 DAF) using nanoLC-based separation coupled to label-free MS detection. Each protein is associated with ist accession number, theoretical isoelectric point and molecular mass, function, and PLGS score, number of peptides, and sequence coverage for each of the three experiments. Proteins, which were also detected in the profiling of endosperm transfer cells, are marked (*).

No.	Protein	Accession number	Score 1/2/3	Peptides 1/2/3	Sequence coverage in % 1/2/3	Theor. molecular mass in Da	Theor. isoelectric point	Function
1	BP 2B (*H. vulgare*)	35_13648	139/240/273	4/4/4	17/17/16	27127	8.1	Disease/Defence
2	Heat shock protein 90 (*T. aestivum*)*	35_14129	212/297/281	4/6/4	6/9//6	83504	4.8	Disease/Defence
3	Thaumatin like protein TLP3 (*H. vulgare*)*	35_16712	93/220/156	3/4/2	22/25/20	18833	5.6	Disease/Defence
4	BP 2B (*H. vulgare*)	35_36536	126/161/114	2/2/2	25/18/20	11014	7.7	Disease/Defence
5	Heat shock cognate 70 kDa protein 2 (*S. lycopersicum*)*	35_432	202/326/236	6/7/5	12/13/11	72264	5.0	Disease/Defence
6	Heat shock cognate 70 kDa protein (*A.thaliana*)	P22954	147/253/152	4/5/5	8/10/10	71387	5.0	Disease/Defence
7	BP 2B (*H. vulgare*)	Q42854	209/252/417	5/5/6	17/19/18	39114	5.9	Disease/Defence
8	Histone H4 (*A.thaliana*)*	P59259	348/387/414	6/5/6	53/43/43	11409	11.5	DNA binding
9	Probable histone H2AXb (*O. sativa*)	Q2QPG9	123/127/134	1/1/1	7/7/7	14340	10.20	DNA binding
10	Fructose bisphosphate aldolase (*O. sativa*)*	35_14100	151/294/260	4/4/5	11/14/16	41335	8.1	Energy metabolism
11	Malate dehydrogenase (*O. sativa*)*	35_14420	132/236/149	3/4/3	10/18/15	37174	5.7	Energy metabolism
12	Triosephosphate isomerase (*H.vulgare*)*	35_14505	138/257/161	3/4/2	14/21/9	30534	7.7	Energy metabolism
13	Phosphoglycerate kinase (*T. aestivum*)*	35_384	153/283/176	5/6/5	18/18/17	46643	7.6	Energy metabolism
14	Glyceraldehyde 3 phosphate dehydrogenase (*Z. mays*)*	35_49	248/406/450	5/6/7	18/25/21	40464	6.7	Energy metabolism
15	Lactoylglutathione lyase (*O. sativa*)*	35_118	94/135/96	3/3/2	8/9/7	37195	6.3	Metabolism
16	Chromosome undetermined SCAF14565 (*T. nigroviridis*)*	35_13647	504/559/504	6/6/6	43/40/44	13409	12.1	Metabolism
17	Adenosylhomocysteinase 1 (*A. thaliana*)*	35_14558	91/183/141	3/4/3	6/9/8	55144	5.7	Metabolism
18	Alpha galactosidase precursor (*O. sativa*)*	35_15726	150/244/253	5/4/5	14/10/13	46310	7.8	Metabolism
19	Luminal binding protein 3 precursor (*Z. mays*)*	35_14470	189/287/356	6/6/8	9/10/13	77498	5.5	Protein destination
20	Protein disulfide isomerase precursor (*T. aestivum*)*	35_14571	474/710/734	9/12/11	20/24/25	57460	4.9	Protein destination
21	Alpha amylase subtilisin inhibitor precursor (*O. sativa*)*	35_1577	335/460/240	6/5/3	27/21/16	26631	7.1	Protein destination
22	Putative leucine rich repeat protein (*T. aestivum*)	35_17524	78/99/98	3/2/2	20/20/15	20586	8.8	Protein destination
23	Nucellin (*H. vulgare*)*	35_1774	371/606/676	6/6/6	22/20/24	46581	7.2	Protein destination
24	LGC1 (*O. sativa*)	35_2002	135/181/171	2/2/2	14/17/14	14289	4.8	Protein destination
25	Eukaryotic aspartyl protease family protein (*O. sativa*)*	35_3990	287/367/296	5/5/4	32/32/30	20111	8.3	Protein destination
26	Predicted protein (*O. sativa*)	B9GIR0	179/234/200	3/4/4	6/7/6	80862	4.9	Protein destination
27	EEA1 (*H. vulgare*)*	O22491	259/399/340	5/5/5	17/17/19	45027	7.1	Protein destination
28	Putative chemocyanin (*O. sativa*)*	35_1567	163/149/181	3/2/3	21/19/21	16037	9.5	Transport
29	7 kDa lipid transfer protein (*H. vulgare*)*	O81135	151/181/208	1/1/1	13/13/13	9468	9.0	Transport
30	5a2 protein (*T. aestivum*)*	35_14583	445/574/541	3/3/3	27/27/27	13704	7.4	Unclassified

31	5a2 protein (*T. aestivum*)*	35_14585	426/547/541	3/4/3	28/33/29	13621	8.3	Unclassified
32	5a2 protein (*T. aestivum*)*	35_14586	365/515/530	3/3/3	27/27/27	13610	8.1	Unclassified
33	Hypothetical protein (*O. sativa*)	35_1552	144/131/111	2/2/3	8/9/12	26089	7.0	Unclassified
34	Pectinesterase inhibitor domain containing protein (*O. sativa*)*	35_15670	486/561/577	4/5/4	17/22/25	24092	6.3	Unclassified
35	Hypothetical protein (*H. vulgare*) *	35_15733	529/707/627	5/5/5	29/32/31	22923	5.4	Unclassified
36	Hypothetical protein P0473D02 34 (*O. sativa*)*	35_17703	489/515/516	5/5/5	31/27/29	21224	8.2	Unclassified
37	Putative ZmEBE 1 (*O. sativa*)*	35_22061	114/184/117	2/2/2	8/8/7	35176	8.7	Unclassified
38	Hypothetical protein (*H. vulgare*)*	35_2643	178/239/208	3/4/3	15/15/15	25401	5.4	Unclassified
39	Hypothetical protein (*H. vulgare*)	35_29554	137/275/143	3/3/3	42/35/35	8963	9.2	Unclassified
40	Hypothetical protein P0473D02 34 (*O. sativa*)*	35_3216	271/343/325	4/4/5	22/21/25	21304	6.9	Unclassified
41	Hypothetical protein (*H. vulgare*)	35_3681	132/268/245	4/5/4	22/27/26	25809	7.9	Unclassified
42	Putative uncharacterized protein (*O. sativa*)	A3AV14	136/287/311	4/4/4	12/11/11	42052	6.4	Unclassified
43	Putative uncharacterized protein (*O. sativa*)	B8AWF8	106/171/129	3/3/2	7/8/4	57555	7.7	Unclassified
44	Os03g0369100 (*O. sativa*)*	Q10KV4	182/238/247	1/1/1	11/12/11	12752	8.1	Unclassified

Table A 5: Proteins, which were detected in the profiling of endosperm transfer cells of a developing barley grain (8 DAF) using nanoLC-based separation coupled to label-free MS detection. Each protein is associated with ist accession number, theoretical isoelectric point and molecular mass, function, and PLGS score, number of peptides, and sequence coverage for each of the three experiments. Proteins, which were also detected in the profiling of nucellar projection, are marked (*).

No.	**Protein**	**Accession number**	**Score 1/2/3**	**Peptides 1/2/3**	**Sequence coverage in % 1/2/3**	**Theor. molecular mass in Da**	**Theor. isoelectric point**	**Function**
1	Putative reversibly glycosylated polypeptide (*O. sativa*)	35_85	241/230/295	3/4/4	9/11/13	42247	6.6	Cell wall synthesis
2	Alpha-1,4-glucan-protein synthase (*Z. mays*)	35_272	355/317/327	6/5/6	18/12/15	45926	5.5	Cell wall synthesis
3	Actin 5C (*D. melanogaster*)	35_14175	221/193/277	4/4/5	14/14/20	41918	5.3	Cell wall synthesis
4	Actin 5C (*D. melanogaster*)	35_14173	210/184/254	3/3/5	12/12/15	46756	5.6	Cell wall synthesis
5	RGP1 protein (*O. sativa*)	O82705	170/170/200	4/4/4	11/11/14	39451	7.9	Cell wall synthesis
6	Tubulin alpha 2 alpha 4 chain (*A. thaliana*)	P29510	406/409/440	5/4/6	13/10/15	49509	4.7	Cell wall synthesis
7	Cytosolic aldehyde dehydrogenase (*O. sativa*)	35_2787	102/148/114	3/3/2	9/7/6	56221	6.0	Disease/Defence
8	Thaumatin like protein TLP3 (*H. vulgare*)*	35_16712	101/170/105	2/2/2	19/20/17	18833	5.6	Disease/Defence
9	Formate dehydrogenase (*H. vulgare*)	35_14430	179/141/146	3/2/2	8/6/7	43072	6.5	Disease/Defence
10	14 3 3 like protein A (*H. vulgare*)	35_14382	672/625/583	7/7/7	30/32/30	29717	4.7	Disease/Defence
11	Heat shock cognate 70 kDa protein (*S. lycopersicum*)	P24629	526/515/647	6/7/8	14/15/16	71242	5.0	Disease/Defence
12	14 3 3 like protein B (*H. vulgare*)	Q43470	296/351/343	5/7/5	22/28/21	29672	4.5	Disease/Defence
13	Histone H2B 4 (*T. aestivum*)	35_13981	253/124/119	2/1/1	19/10/6	17269	10.7	DNA binding

14	Chromosome undetermined SCAF14565 (*T. nigroviridis*)*	35_13647	789/857/718	6/6/5	41/41/38	13409	12.1	DNA binding
15	Histone H4 (*A. thaliana*)*	P59259	777/829/772	5/6/7	44/49/48	11402	11.9	DNA binding
16	Nucleoside diphosphate kinase (*L. perenne*)	35_610	306/272/303	3/4/4	22/27/25	17194	9.1	Energy metabolism
17	Glyceraldehyde 3 phosphate dehydrogenase (*Z. mays*)*	35_49	1146/1216/1076	10/10/11	38/37/36	40464	6.7	Energy metabolism
18	Fructose bisphosphate aldolase (*O. sativa*)	35_48114	137/150/191	3/2/3	36/20/24	12304	6.3	Energy metabolism
19	Fructose-bisphosphate aldolase (*O. sativa*)	35_38591	427/410/450	3/2/3	36/19/28	18505	5.6	Energy metabolism
20	Phosphoglycerate kinase (*T. aestivum*)*	35_384	817/765/856	10/8/10	34/25/33	46643	7.6	Energy metabolism
21	Glyceraldehyde-3-phosphate dehydrogenase (*Z. mays*)	35_286	578/622/636	5/6/7	18/22/25	40275	7.0	Energy metabolism
22	Putative pyrophosphate-dependent phosphofructokinase alpha subunit (*O. sativa*)	35_15973	196/188/172	4/3/3	7/7/9	71583	7.6	Energy metabolism
23	Putative NAD malate dehydrogenase (*O. sativa*)	35_15554	119/158/137	3/3/3	10/9/9	43183	6.3	Energy metabolism
24	H0402C08 9 protein (*O. sativa*)	35_15328	310/311/264	7/6/6	19/14/14	63394	8.5	Energy metabolism
25	Pyruvate kinase (*O. sativa*)	35_15127	424/404/491	9/7/8	22/19/21	58054	6.5	Energy metabolism
26	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (*R. communis*)	35_15071	248/273/401	8/5/8	19/15/23	64658	6.8	Energy metabolism
27	Triosephosphate isomerase (*H. vulgare*)*	35_14505	478/557/561	5/6/7	22/25/32	30534	7.7	Energy metabolism
28	Enolase 2 (*Z. mays*)	35_14451	1012/758/699	14/10/9	48/36/33	50919	5.6	Energy metabolism
29	Enolase 2 (*Z. mays*)	35_14444	1225/1009/741	13/10/8	45/36/30	51437	5.6	Energy metabolism
30	Malate dehydrogenase (*O. sativa*)*	35_14420	1068/805/822	8/7/8	31/26/33	37174	5.7	Energy metabolism
31	Fructose-bisphosphate aldolase (*O. sativa*)*	35_14100	1001/1067/1201	8/7/8	28/25/27	41335	8.1	Energy metabolism
32	Fructose-bisphosphate aldolase (*O. sativa*)	35_14090	604/652/743	3/3/3	22/22/22	21464	10.6	Energy metabolism
33	Malate dehydrogenase (*O. sativa*)	A2WT84	149/166/159	2/3/2	9/10/10	35438	8.8	Energy metabolism
34	Malate dehydrogenase (*O. sativa*)	A2Z8J9	654/674/710	5/5/5	20/22/23	34327	5.7	Energy metabolism
35	Glyceraldehyde 3 phosphate dehydrogenase (*H. vulgare*)	P08477	1183/1087/1064	11/9/9	41/34/35	33214	6.2	Energy metabolism
36	Malate dehydrogenase (*A. thaliana*)	P57106	617/630/717	6/6/5	22/24/19	35652	6.3	Energy metabolism
37	Malate dehydrogenase (*O. sativa*)	Q0J5H3	189/138/166	3/3/3	12/9/13	37412	6.3	Energy metabolism
39	UTP-glucose-1-phosphate uridylyltransferase (*H. vulgare*)	35_751	690/652/751	11/11/12	26/27/29	53929	5.1	Metabolism
40	Ketol-acid reductoisomerase (*O. sativa*)	35_730	150/139/129	3/3/3	8/7/6	65784	6.3	Metabolism
41	Alanine aminotransferase 2 (*H. vulgare*)	35_27721	120/134/151	2/2/2	33/33/33	8331	4.7	Metabolism
42	Alpha galactosidase precursor (*O. sativa*)*	35_15726	360/346/293	4/5/5	12/14/14	46310	7.8	Metabolism
43	Phosphoglucomutase (*B. inermis*)	35_15040	388/388/464	10/8/10	20/17/20	70941	6.6	Metabolism
44	UDP-D-glucuronate decarboxylase (*H. vulgare*)	35_14654	294/196/246	5/4/4	18/13/12	40167	7.4	Metabolism
45	Aspartate aminotransferase (*O. sativa*)	35_14619	956/876/942	10/11/15	24/25/28	53186	9.6	Metabolism
46	Adenosylhomocysteinase 1 (*A. thaliana*)*	35_14558	275/264/290	5/5/6	10/10/12	55144	5.7	Metabolism
47	Sucrose synthase 1 (*O. sativa*)	35_14484	264/295/394	5/5/6	12/14/16	51268	5.7	Metabolism
48	Sucrose synthase 2 (*H. vulgare*)	35_14483	394/614/571	9/10/10	13/14/14	94485	6.3	Metabolism
49	Sucrose synthase 1 (*O. sativa*)	35_14479	375/479/597	8/10/10	14/18/19	68172	5.6	Metabolism

50	Alpha galactosidase (*H. vulgare*)	O04944	192/174/215	4/3/3	18/16/15	22038	6.5	Metabolism
51	Sucrose synthase 2 (*O. sativa*)	P31924	307/305/263	6/5/5	8/7/7	92849	5.9	Metabolism
52	Adenosylhomocysteinase (*O. sativa*)	Q0ISV7	267/269/280	5/5/5	12/13/11	51424	6.2	Metabolism
53	Sucrose synthase type 2 (*O. sativa*)	Q7DMV5	144/174/111	2/3/2	9/13/11	27090	8.7	Metabolism
54	Cytosolic glyceraldehyde 3 phosphate dehydrogenase (*T. aestivum*)	Q9M4V4	951/904/867	8/7/8	46/39/41	25276	8.0	Metabolism
55	Heat shock cognate 70 kDa protein 2 (*S. lycopersicum*)*	35_432	894/737/699	10/10/10	20/20/19	72264	5.0	Protein destination
56	Putative ribophorin II (*O. sativa*)	35_4053	83/156/90	3/4/3	8/8/7	56907	5.9	Protein destination
57	Eukaryotic aspartyl protease family protein (*O. sativa*)*	35_3990	461/493/531	6/5/7	35/32/44	20111	8.3	Protein destination
58	Nucellin (*H. vulgare*)*	35_1774	226/197/126	4/5/2	15/16/6	46581	7.2	Protein destination
59	Alpha-amylase/subtilisin inhibitor (*O. sativa*)*	35_1577	1130/100/1062	8/8/8	41/42/38	26631	7.1	Protein destination
60	Calreticulin like protein (*T. aestivum*)	35_14693	510/416/306	7/6/6	22/21/21	51112	4.3	Protein destination
61	Protein disulfide-isomerase (*T. aestivum*)*	35_14571	2304/2275/2314	16/15/16	33/31/33	57460	4.9	Protein destination
62	Luminal-binding protein 3 (*Z. mays*)*	35_14470	1332/1191/1079	15/14/13	29/27/24	77498	5.5	Protein destination
63	Heat shock protein 90 (*T. aestivum*)*	35_14129	382/400/253	8/5/5	14/9/9	83504	4.8	Protein destination
64	Heat shock protein 81 (*A. thaliana*)	35_14120	221/356/195	5/5/4	8/9/7	85577	4.9	Protein destination
65	Endoplasmin homolog precursor (*H. vulgare*)	35_14098	874/736/743	13/11/11	20/17/16	95312	4.7	Protein destination
66	Putative immunophilin (*H. vulgare*)	35_13944	212/140/130	3/3/3	25/25/25	17642	5.3	Protein destination
67	Heat shock cognate 70 kDa protein 2 (*S. lycopersicum*)	35_137	355/315/318	5/5/6	15/15/17	46756	4.9	Protein destination
68	EEA1 (*H. vulgare*)*	O22491	130/169/204	3/4/3	8/12/13	44998	7.1	Protein destination
69	Luminal binding protein 2 (*Z. mays*)	P24067	789/860/931	8/8/10	16/15/19	73039	4.9	Protein destination
70	Endoplasmin homolog (*H. vulgare*)	P36183	749/783/853	11/13/14	17/21/23	92858	4.7	Protein destination
71	Os06g0250300 protein (*O. sativa*)	Q0DD67	145/146/149	1/1/1	4/4/4	22473	12.1	Protein destination
72	Peptidyl prolyl cis trans isomerase (*O. sativa*)	Q1KL27	164/143/201	1/1/1	8/8/8	18349	8.4	Protein destination
73	Protein disulfide isomerase (*O. sativa*)	Q52PJ0	290/251/236	2/3/3	3/4/10	56820	4.8	Protein destination
74	DnaK protein (*O. sativa*)	Q53RJ5	125/150/173	1/1/1	3/2/2	73328	5.2	Protein destination
75	40S ribosomal protein S3a (*O. sativa*)	35_685	186/268/193	4/4/4	14/19/14	32896	10.4	Protein synthesis
76	Eukaryotic initiation factor 4A 2 (*A. thaliana*)	35_665	363/367/210	7/6/4	20/15/12	52244	5.3	Protein synthesis
77	OSIGBa0140J09 10 protein (*O. sativa*)	35_650	104/150/128	2/2/2	13/12/14	17387	10.6	Protein synthesis
78	Elongation factor 1 gamma 3 (*O. sativa*)	35_593	393/541/373	7/6/6	22/20/19	51016	7.7	Protein synthesis
79	40S ribosomal protein S5 (*O. sativa*)	35_555	366/243/277	3/3/2	17/17/12	24647	10.2	Protein synthesis
80	Elongation factor 1 beta (*T. aestivum*)	35_41584	322/317/361	5/4/4	28/21/24	23966	4.2	Protein synthesis
81	40S ribosomal protein S15a-4 (*A. thaliana*)	35_15083	144/121/217	2/2/3	10/13/19	18703	11.6	Protein synthesis
82	Putative 60S ribosomal protein L1 (*O. sativa*)	35_14967	703/619/641	8/8/9	27/28/31	46087	11.1	Protein synthesis
83	40S ribosomal protein S19 (*O. sativa*)	35_14825	146/122/188	3/4/4	19/21/23	18532	10.8	Protein synthesis
84	60S acidic ribosomal protein P0 (*O. sativa*)	35_14696	523/389/344	7/6/7	29/28/29	35914	5.5	Protein synthesis
85	40S ribosomal protein S20 (*O. sativa*)	35_14677	192/245/214	2/2/2	16/15/16	18400	10.7	Protein synthesis

86	40S ribosomal protein S9 (*O. sativa*)	35_14662	212/207/124	3/4/3	18/18/16	25138	11.2	Protein synthesis
87	Ribosomal protein L11 (*T. aestivum*)	35_14637	305/230/274	4/3/3	17/11/16	23660	10.5	Protein synthesis
88	Putative 40S ribosomal protein (*O. sativa*)	35_14622	233/233/246	2/3/4	30/11/16	29996	9.7	Protein synthesis
89	Acidic ribosomal protein P2 (*T. aestivum*)	35_14590	193/97/82	3/2/2	31/28/31	14499	4.4	Protein synthesis
90	OSJNBa0038P21 4 protein (*O. sativa*)	35_14504	279/318/235	4/5/3	21/24/17	26663	10.9	Protein synthesis
91	40S ribosomal protein S4 (*Z. mays*)	35_14431	321/322/318	5/6/4	19/26/21	30442	10.5	Protein synthesis
92	60S ribosomal protein L3 (*O. sativa*)	35_14391	177/87/128	4/2/3	10/10/8	47794	10.6	Protein synthesis
93	60S ribosomal protein L8 (*S. lycopersicum*)	35_14319	155/159/186	3/2/3	14/11/15	30163	11.6	Protein synthesis
94	Putative elongation factor 1 beta (*H. vulgare*)	35_14285	129/125/146	4/3/4	19/16/19	24730	4.4	Protein synthesis
95	Os07g0173500 protein (*O. sativa*)	35_14252	283/315/281	3/4/4	17/19/19	21679	11.0	Protein synthesis
96	Ubiquitin/ribosomal protein S27 fusion protein (*P. gouldii*)	35_13872	238/283/206	4/4/3	23/22/17	21327	10.8	Protein synthesis
97	60S acidic ribosomal protein P2B (*Z. mays*)	35_1145	202/165/165	2/2/2	38/34/34	12106	4.3	Protein synthesis
98	60S ribosomal protein L5 (*O. sativa*)	A2WXX3	119/145/128	2/3/2	9/11/9	34733	9.4	Protein synthesis
99	60S ribosomal protein L6 (*O. sativa*)	A3A8J3	241/225/224	4/3/2	7/4/5	92302	8.9	Protein synthesis
100	60S ribosomal protein L12 (*P. Armeniaca*)	O50003	229/314/291	3/3/4	22/22/28	17871	9.4	Protein synthesis
101	Elongation factor 1 alpha (*A. thaliana*)	P13905	624/552/576	6/5/5	14/11/10	49470	9.5	Protein synthesis
102	Cytoplasmatic ribosomal protein S13 (*T. aestivum*)	Q5XUU9	125/101/144	2/3/3	18/19/24	17054	11.0	Protein synthesis
103	QM (*T. aestivum*)	Q7X9L9	181/239/215	2/2/2	16/13/14	20070	10.9	Protein synthesis
104	ADP-ribosylation factor-like protein (*A. thaliana*)	35_13917	329/223/270	5/4/4	29/21/22	25984	9.5	Signal transduction
105	ATP synthase subunit alpha (*T. aestivum*)	35_36498	262/333/336	3/4/4	28/33/30	14397	4.7	Transport
106	ATP synthase subunit beta (*Z. mays*)	35_14758	746/641/590	11/10/9	28/26/23	60013	5.9	Transport
107	ADP,ATP carrier protein 1 (*Z. mays*)	35_14437	296/246/246	3/4/4	9/10/10	46971	10.1	Transport
108	7 kDa lipid transfer protein (*H. vulgare*)*	O81135	212/211/217	2/1/1	18/13/13	9564	8.5	Transport
109	RNA binding protein Rp120 (*O. sativa*)	Q6H547	249/224/205	4/5/3	5/5/4	108115	6.5	Transcription
110	RNA binding protein Rp120 (*O. sativa*)	35_617	489/427/387	8/8/7	9/9/7	114040	8.1	Unclassified
111	Hypothetical protein P0473D02 34 (*O. sativa*)*	35_3216	331/344/249	4/4/4	24/22/26	21304	6.9	Unclassified
112	Osr40g2 protein (*O. sativa*)	35_268	379/292/283	4/3/3	21/14/13	30280	11.1	Unclassified
113	Ribosomal protein L10E (*M. truncatula*)	35_264	210/240/181	2/2/2	11/9/11	27654	11.6	Unclassified
114	Putative ZmEBE 1 protein (*O. sativa*)*	35_22061	285/223/250	4/4/3	16/16/13	35176	8.6613	Unclassified
115	Hypothetical protein P0473D02 34 (*O. sativa*)*	35_17703	558/456/320	5/4/4	36/28/26	21224	8.2	Unclassified
116	Pectinesterase inhibitor domain containing protein (*O. sativa*)*	35_15670	640/589/363	4/4/3	19/19/14	24092	6.3	Unclassified
117	Putative chemocyanin (*O. sativa*)*	35_1567	394/348/394	3/3/3	25/22/25	16037	9.5	Unclassified
118	Putative chemocyanin (*O. sativa*)	35_1566	377/315/351	4/4/4	36/36/36	16163	9.8	Unclassified
119	5a2 protein (*T. aestivum*)*	35_14586	544/555/566	3/3/3	45/49/35	13610	8.1	Unclassified
120	5a2 protein (*T. aestivum*)*	35_14585	644/642/638	4/4/4	30/33/32	13621	8.3	Unclassified
121	5a2 protein (*T. aestivum*)*	35_14584	554/553/548	3/3/3	27/27/27	13627	8.4	Unclassified

122	5a2 protein (*T. aestivum*)*	35_14583	624/626/610	3/3/3	27/27/27	13704	7.4	Unclassified
123	Translationally-controlled tumor protein homolog (*H. vulgare*)	35_14522	227/189/186	3/3/3	19/16/16	22587	4.6	Unclassified
124	Lactoylglutathione lyase (*O. sativa*)	35_118*	158/167/185	3/4/3	10/14/8	37195	6.3	Unclassified
125	111P0402A09 25 protein (*O. sativa*)	35_1149	263/213/181	4/3/3	25/15/19	22647	10.1	Unclassified
126	Putative uncharacterized protein (*O. sativa*)	A2X1E7	123/123/118	2/2/2	4/7/5	54818	9.7	Unclassified
127	Putative uncharacterized protein (*O. sativa*)	A2XMW9	250/184/328	3/3/4	5/6/6	90206	10.3	Unclassified
128	Putative uncharacterized protein (*O. sativa*)	A2XUU7	691/764/720	6/6/6	16/18/17	42025	6.4	Unclassified
129	Putative uncharacterized protein (*O. sativa*)	A2YB91	175/150/255	3/3/6	8/7/14	61223	6.0	Unclassified
130	Putative uncharacterized protein (*O. sativa*)	A2YIS2	236/192/242	4/3/4	15/10/12	44682	11.0	Unclassified
131	Putative uncharacterized protein (*O. sativa*)	A2Z2G4	217/304/271	4/3/4	8/7/10	65303	4.8	Unclassified
132	Putative uncharacterized protein (*O. sativa*)	A2ZN74	222/181/205	4/3/3	14/13/14	42961	5.0	Unclassified
133	Putative uncharacterized protein (*O. sativa*)	A2ZPX3	185/170/185	2/2/2	20/20/20	12359	5.6	Unclassified
134	Putative uncharacterized protein (*O. sativa*)	A3A343	282/360/383	5/5/6	5/4/7	161253	5.4	Unclassified
135	Putative uncharacterized protein (*O. sativa*)	A3BDB6	118/161/177	3/3/3	5/5/10	71879	8.2	Unclassified
136	Os04g0628100 protein (*O. sativa*)	Q0J9W6	167/211/190	3/3/3	7/9/9	43957	7.5	Unclassified
137	Expressed protein (*O. sativa*)*	Q10KV4	251/253/265	1/1/1	11/11/11	12743	7.8	Unclassified