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The analysis of *Lupinus albus* root proteome revealed cytoskeleton altered features due to long-term boron deficiency

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ABSTRACT

Boron (B) deficiency greatly limits plants' growth and development. Since the root is the organ that first senses the deficiency, we have analyzed the adaptive responses of *Lupinus albus* roots to long-term B deficiency. Large morphological differences were observed between plants grown with or without B, and 265 polypeptides were found to be responsive to B deficiency out of a total of 406 polypeptides detected by two-dimensional electrophoresis in the *L. albus* root proteome. By using mass spectrometry techniques we were able to securely identify 128 of the responsive polypeptides that are related to cell wall metabolism, cell structure, defense, energy pathways and protein metabolism. The detection of multiple peptide isoforms is striking, suggesting that protein modification may have an important contribution during the plant response to long-term B deficiency. Furthermore, detected changes in cytoskeletal associated proteins indicate altered cytoskeletal biosynthesis and suggest that B may have an important contribution in this process.

1. Introduction

Boron (B) has for long been known as an essential micronutrient for higher plants [1]. Since the B sufficiency range for plant growth and development is narrow, problems of both deficiency and toxicity can easily arise, as it has been observed in farmlands. B toxicity is characteristic of alkaline and saline soils, often associated with low rainfall and very scarce leaching, or it can be a consequence of over-fertilization and/or irrigation with water of high B levels [2]. However, B-deficient soils are more prevalent and widespread worldwide [3] than B-rich soils and so the deficiency is an important agriculture problem. It causes large yield losses, annually, which were reported for at least 132 crops in more than 80 countries [3]. In Portugal it was detected in woody crops (grapevine, olive, apple and pear trees) [3], as well as in herbaceous species, like the legume pastures [4].

The functioning of B in plant development has been associated with diverse physiological processes of both vegetative and reproductive growth [5,6], that involve, for instance, the metabolism of carbohydrates and RNA, respiration, lignification, cell wall synthesis and structure, and membrane transport. However, to date, the precise B roles in central plant biological processes remain elusive. So far, B is known to have a structural participation in the cell wall, through the borate cross-linking of rhamnogalacturonan-II chains [7–9], but the plethora of biochemical, physiological and anatomical effects due to B suppression [6] cannot be well explained by this role alone. This conclusion is strengthened by the recent indications that B might be also essential for development of animal cells [10,11], devoid of cell wall.

Due to the economic implications of B imbalance in plants and the elusive nature of the B role, studies involving this

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element in plant metabolism continue to be an important subject. More recently, molecular techniques, namely of transcriptomic [12–15] and proteomic nature [16–18], are being applied to such studies.

We have been studying B deficiency in the white lupin (*Lupinus albus*) [19,20], a winter grain legume crop valuable for its edible seed [21], that is nitrogen-fixing with reduced need for fertilizers, grows in infertile soils and can withstand adverse conditions. It is a species sensitive to B deficiency, a condition that is exacerbated by the environments under which *L. albus* grows, such as high light intensity, low temperature, drought and freely-draining sandy or gravelly soils [3].

In order to mimic low B field conditions, we have evaluated long-term B deficiency responses. Since nutrient imbalance is primarily sensed by the root system and because this organ is responsible for sending signals to the shoots for growth and developmental modulation [22], we have analyzed the *L. albus* root adaptive responses to long-term B deficiency. For this purpose, the root proteome of plants grown with and without B were analyzed by two-dimensional electrophoresis (2-DE) and mass spectrometry (MS) techniques.

2. Material and methods

2.1. Plant material

Lupin seeds (*Lupinus albus* cv. Rio Maior) were pre-germinated in distilled water for 48 h, sown in white sand and grown under controlled conditions of temperature (19/25 °C, night/day), photoperiod (12 h) and light intensity (250 μmol m^{-2} s^{-1}, PAR). The plants were watered every other day with a nutritive solution [23] containing either 0 or 23.1 μM B [19]. For biomass analysis, roots and shoots were harvested 2, 3 and 4 weeks from sowing.

2.2. Protein extraction and solubilisation

Roots from four week-old plants were ground to a fine powder in liquid nitrogen, resuspended in a cold acetone solution containing 0.06 M DTT and 10% (w/v) TCA (12.5 mL/g) and kept at −20 °C for 1 h. After a 15 min centrifugation at 27,200 *g* and 4 °C, the pellet was resuspended in cold acetone with 0.06 M DTT (25 mL/g) and kept at −20 °C for 1 h. After centrifugation, the pellet was dried under vacuum and resuspended (0.05 g/mL) in a solubilization buffer containing 2 M thiourea, 7 M urea, 4% (w/v) CHAPS, 0.4% (v/v) Triton X-100, 0.06 M DTT and 1% (v/v) IPG buffer 3–10 NL (GE, Uppsala, Sweden). After 2 h dissolution at room temperature, the protein extracts were centrifuged at 15,000 *g* for 10 min and the supernatant collected and stored at −80 °C until further use. The protein concentration was determined according to the Bradford method as modified by Ramagli [24].

2.3. Two-dimensional gel electrophoresis

For isoelectric focusing (IEF) electrophoresis, the IPGphor system was used (Amersham Biosciences, Uppsala, Sweden) with a non-linear pH gradient gel of 3–10 (IPGstrips, GE) loaded with 200 μg of protein resolubilized in 8 M urea, 4% (w/v) CHAPS, 0.06 M DTT and 0.5% (v/v) IPG buffer 3–10 NL (GE, Uppsala, Sweden). The IEF was carried out at 30 V for 12 h, followed by 200 V for 1 h, 500 V for 1.5 h, 1000 V for 1.5 h, and 8000 V for 6.5 h, at 20 °C. Prior to SDS-PAGE the IPGstrips were equilibrated for 2 × 15 min in a buffer solution containing 0.05 M Tris–HCl pH 8.8, 6 M urea, 30% (v/v) glycerol and 2% (w/v) SDS. 0.06 M DTT was added to the first equilibration step and 0.135 M iodoacetamide to the second one. The SDS-PAGE was performed on slab gels [25] and run at constant temperature of 15 °C. The 2-DE gels were stained with colloidal Coomassie Blue [26] and scanned using the ImageScanner (Amersham Biosciences, Uppsala, Sweden).

2.4. Two-dimensional gel analysis

Gels from independent biological triplicates were analyzed in ImageMaster 2D Platinum software v5.0 (GE, Uppsala, Sweden) for spot detection, measurement and matching. In order to correct for variation in gel staining that could affect protein spot intensities, the total spot volume of each gel was normalized to 100, and a volume % per spot calculated. A protein spot was kept for further analysis and declared reliable if at least $n-1$ volume values were available in each condition.

The protein spots found to be commonly expressed in the control and B deficiency 2-DE gels were statistically evaluated by two distinct methods. For the Kolmogorov–Smirnov test ($p < 0.05$) the raw data were used whereas for the Student's *t*-test ($p < 0.05$) a complete data matrix of volume % was generated by replacing the missing values in a condition by the mean of the existing values for that protein spot [27]. To eliminate the small between-condition bias observed in the two data sets the data were normalized and transformed according to Meunier et al. 2005 [28]. Only the spots having statistically significance in both statistical tests were considered as differentially expressed due to the deficiency.

2.5. In-gel digestion

The protein spots were rinsed with a washing solution of 50% (v/v) acetonitrile and 0.1 M ammonium bicarbonate for 4 h. Prior to digestion the dried spots were reduced with 0.01 M DTT for 2 h at 37 °C, then alkylated with 0.05 M iodoacetamide for 15 min at room temperature, in the dark. The gel spots were again rinsed with the washing solution for 2 h. The digestion was made overnight, with 125 ng of trypsin (Promega, Madison, WI) in 0.05 M ammonium bicarbonate at 37 °C. The peptides in the supernatant were collected and the gel pieces were extracted with a solution of 0.1% (v/v) acetic acid and 50% (v/v) acetonitrile. The extract was pooled with the tryptic peptides and dried in a speed vac. The pellet was redissolved in 0.1% (v/v) acetic acid and 2% (v/v) acetonitrile solution was used for mass spectrometric analysis.

2.6. MS/MS analysis

The trypsin digested proteins were analyzed by capillary liquid chromatography tandem MS (LC/MS/MS) using a set up of a trapping 300SB C-18 column (0.3 × 50 mm) (Agilent Technologies, Basel, Switzerland) and a separating column (0.1 mm × 10 cm) that had been packed with Magic 300 Å C18 reverse-phase material (5 μm particle size, Michrom Bioresources, Auburn, CA, USA). The columns were connected on line to an Orbitrap FT hybrid instrument (Thermo Finnigan, San Jose, CA, USA). A linear gradient from 2 to 80% of solvent B [0.1% (v/v) acetic acid and 80% (v/v) acetonitrile] in solvent A [0.1% (v/v) acetic acid and 2% (v/v) acetonitrile] was delivered with a Rheos 2200 pump (Flux Instruments, Basel, Switzerland) for 85 min at a flow rate of 100 μL/min. A pre-column split was used to reduce the flow to approximately 100 nL/min. The injection of 10 μL of peptide digest was made by an auto-sampler thermostated to 4 °C and the eluting peptides ionized at 1.7 kV. Precursor ions were scanned between m/z range of 400–1600 in profile mode at a resolution of 60,000. MS/MS scans were triggered at 1000 ion counts and the fragmentation energy was set to 35% normalized collision energy. The mass spectrometer was operated in a data-dependent fashion. The precursor scan was done in the Orbitrap, while the fragment ions were mass analyzed in the LTQ instrument. The five most intense signals of each precursor scan were selected for fragmentation. The MS/MS spectra were then searched against the NCBI non-redundant database, version August 15th 2008, using TurboSequest software [29]. The databank was searched with Bioworks version 3.3.1. SP1 by setting the precursor ion tolerance to 10 ppm, while the fragment ion tolerance was set to 0.5 Da. Cleavage rules were set to Fully enzymatic-cleaves at both ends, allowing 2 missed cleavages. In the databank search, carbamidomethylation of cysteine was set to fixed, while oxidation of methionine was set to variable modification. The SEQUEST search results were filtered to only show variable peptides; the ΔCN was set to 0.1; peptide and protein probability was set to 0.5 and 0.01, respectively. The Xcorr for singly, doubly, triply, and quadruply charged peptides was set to 1.50, 2.00, 2.50, and 3.00, respectively.

Protein coverage and unique peptide number were calculated by using Protein Coverage Summarizer software from the Pacific Northwest National Laboratory (Richland, WA, USA).

2.7. *Statistical analysis*

For the statistical analysis, the following software programs were used: in house software for the Kolmogorov–Smirnov test, the SigmaStat v3.10 software (Systat Software Inc, Erkrath, Germany) for the Student's *t*-test and the R program with the ade4 package [30] for a multivariate analysis (principal component analysis, PCA).

3. Results and discussion

3.1. *Morphological effects of B deficiency*

As a dicot plant, *Lupinus albus* is quite sensitive to B deficiency. Morphological alterations were already evident in two weeks deficient plants (Fig. 1). Despite no detectable effect in biomass at this time the roots were shorter, darker and lacked ramifications and proteoid formations. The morphological differences observed in the roots indicate that, at this early stage of development, the B present in the lupin seed was already insufficient to ensure adequate plant development. Three weeks from sowing, morphological alterations in the roots become more evident, and significant differences in biomass were found. In shoots, morphological differences due to B deficiency (darker and deformed leaves) become also visible, but no significant biomass differences were detected. After 4 weeks the morphological differences were much more marked, with significant reduced biomass in both shoots and roots (Figs. 1 and 2).

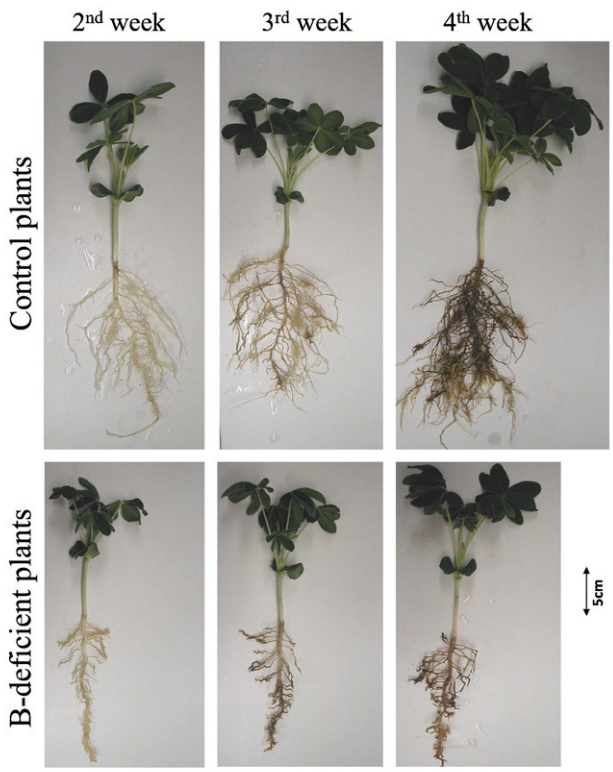

Fig. 1 – Morphological differences of *Lupinus albus* plants grown under B deficiency. The development of the plants grown with (C) or without B (BD) in the nutrient solution was monitored 2, 3 and 4 weeks after germination.

3.2. *Quantitative variations of the root proteome*

As we considered that the lupin root system is very important for the plant ability to cope with long-term B deficiency, we analyzed by 2-DE the root proteomes of plants grown for 4 weeks with or without B (Fig. 3; Supplementary Fig. 1). 2-DE coupled to MS techniques and adequate statistical analysis, is a powerful tool to investigate the proteins whose expression is affected by the long-term B deficiency.

From a total of 406 reproducibly detected spots in the root proteome, 265 spots (65%) were responsive to B deficiency (Table 1). These include the specifically responsive spots, either suppressed (51%) or expressed *de novo* (10%) and those differentially expressed (4%). A PCA analysis was performed with all the reproducible protein spots (406) detected by 2-DE. This analysis shows that it is possible to distinguish the plants grown with or without B considering the first principal component (Fig. 4a), which explains 49% of the total variance (Table 2). In order to pinpoint the protein spots associated to this discrimination we performed two additional analyses. One involving the sub-set of spots common to both control and B deficiency treatments, *i.e.* non-responsive and differentially expressed spots (Fig. 4b), and the other analysis, the sub-set of

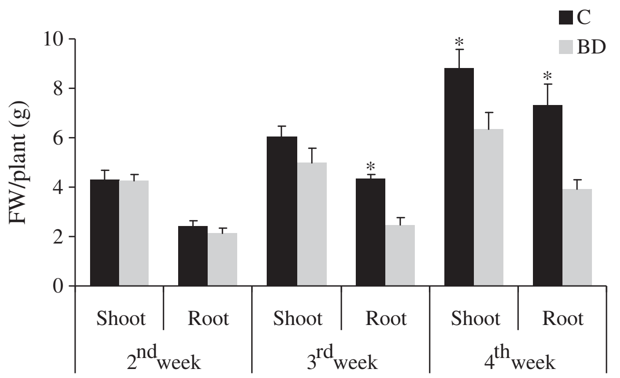

Fig. 2 – Shoots and roots fresh weight of *Lupinus albus* grown with (C) or without B (BD) for 2, 3 and 4 weeks after germination. Bars indicate standard errors. Significant changes were evaluated by the Student's *t*-test (*$p<0.05$).

spots specifically responsive to B deficiency (Fig. 4c). These analyses revealed that the common protein spots do not discriminate the treatments, whereas the spots specifically responsive to B deficiency gave a marked separation of the treatments (Table 2). The 265 spots reproducibly detected as responsive to B deficiency were analyzed by MS/MS techniques, and 213 were identified. In general, the analysis by LC–MS/MS techniques of the 2-DE gel spots reveals some spots containing multiple proteins [31], what we have found for 85 spots (40%) (Supplementary Table 1). Thus, only the remainder 128 spots were considered for secure quantification (Table 3; Supplementary Table 2).

3.3. *Metabolic changes associated with B deficiency*

In an attempt to identify the metabolic events associated with the plant root response to a long-term B deficiency, the identified proteins were grouped according to the biological functions annotated in the UniProt database (http://www.uniprot.org; Fig. 5).

The majority of the suppressed proteins are from classes related with plant growth and developmental processes. This observation is an indication of an adjusted biosynthetic flux that may be directly related with the reduced growth rates observed due to B deficiency. The fact that the up regulated or expressed *de novo* proteins belong to some of the same classes of the suppressed or down regulated proteins (energy pathways, protein metabolism, defense and cytoskeleton biosynthesis) can be an indication that the plant metabolism was not just impaired as a whole, but instead, was modified in a controlled manner.

The identified proteins showed in Table 3, were grouped according to the biological processes considered to be more relevant in relation to B deficiency.

3.3.1. *Energy metabolism*

Changes in several proteins that are related to cellular energy metabolism were observed in B deficient roots. Key enzymes of respiration, such as glucose-6-phospate-1-dehydrogenase (spot 700) from the pentose phosphate pathway, and the glycerladeyde-3-phosphate dehydrogenase (spot 146) from the glycolysis pathways were suppressed. Also suppressed were several kinases, namely frutokinase (spot 421) and phosphoglycerate kinase (spots 493, 499 and 511), while the UDP-glucose pyrophosphorylase (spot 216) was expressed *de novo*. This enzyme is part of an alternative biochemical pathway for sucrose degradation that requires inorganic pyrophosphate, whereas the breakdown involving kinases requires two molecules of ATP [32]. The activation of bypass pathways allows the carbon flow to continue under stressful conditions by using alternative energy sources and thereby reducing ATP demand. Indeed, ATP availability could be compromised, since several ATPases were affected by B deficiency. A subunit B2 isoform from the V-type proton ATPase (spot 626) was suppressed as well as some other ATPase synthases subunit isoforms (spots 636, 640 and 646). A possible membrane damage caused by B deficiency, previously hypothesized to cause the reduced activity of proton-pumping ATPase observed in sunflower cells [33], could also be responsible for the release of membrane-bound proteins, as observed by the *de novo* expression of a V-type proton ATPase subunit A (spot 739) and B2 (spot 264). The *de novo* expression of pyruvate dehydrogenase E1 beta subunit component (spot 251) is also relevant since E1 protein levels correlate with the mitochondrial pyruvate dehydrogenase complex activity [34], and the higher expression of this enzyme correlates with metabolic and structural changes that accompany membrane remodeling [35].

Therefore, these results indicate an effect of B deficiency on membranes, and it should be referred that a physiological role for B in membranes has been proposed by a wealth of information in which B deficiency has been shown to disrupt membrane-associated processes, including membrane potential and electron transport [6].

Several aconitate hydratase isoforms were suppressed (spots 780, 783, 784, 785, 786 and 788) or down regulated (spot 790) due to B deficiency and another form (spot 232) was *de novo* expressed. Since this protein spot has a considerable lower molecular mass than that annotated in the database, it may have been targeted for degradation during B deficiency. Considering that the aconitase cluster is lost under oxidative stress [36] and that oxidative damage is the major cause of cell death induced by B-deprivation in tobacco cells [14], the aconitase suppression or degradation could result from the oxidative damage caused by B deficiency.

3.3.2. *Protein metabolism*

The Rubisco large subunit-binding protein subunit β (spot 710) belongs to the heat shock protein 60 (Hsp60) family. Both this Hsp60 and a Hsp70 (spot 749) were *de novo* expressed under B deficiency and are molecular chaperones responsible for preventing irreversible aggregation of non-native proteins under both normal and stressful conditions [37]. Another protein involved in the protein folding processes, that was also *de novo* expressed under B deficiency, is a peptidylprolyl *cis–trans* isomerase (spot 291), that can additionally play important roles in protein degradation, signal transduction and mRNA processing [38].

The nascent polypeptide-associated complex (NAC) is a heterodimeric complex of α- and β-chains that is postulated to be involved in protein transport for an appropriate targeting of ribosome–nascent polypeptide complexes [39]. The *de novo*

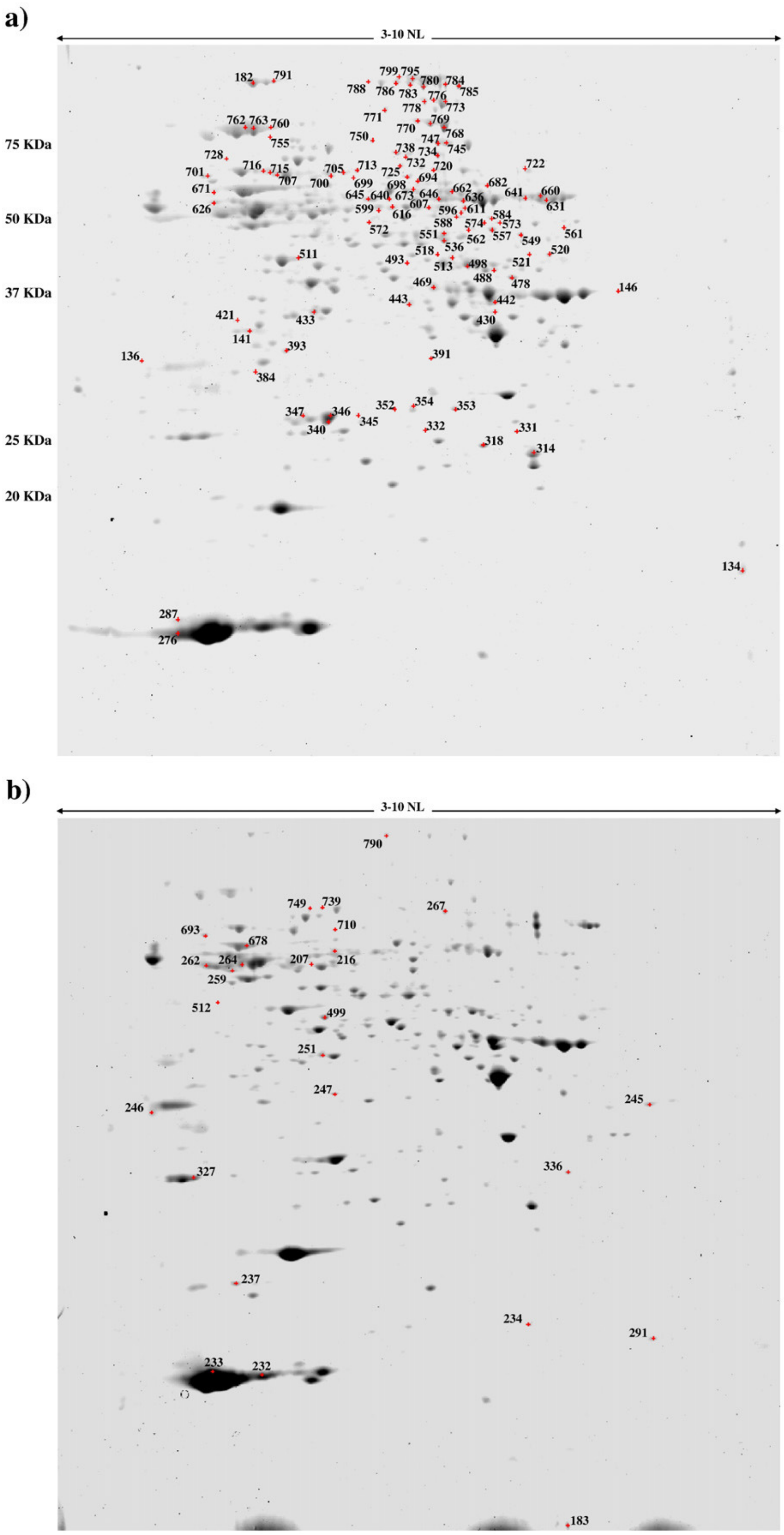

Fig. 3 – Representative 2-DE gels of *Lupinus albus* roots grown with (a) or without B (b) for 4 weeks. The gels were Coomassie Blue stained. Numbered proteins were identified by MS/MS (see Table 3). Labeled proteins in gel a) are those suppressed due to B deficiency, while those labeled in gel b) are differentially expressed or *de novo* expressed due to B deficiency.

Table 1 – Number of protein spots that have quantitative or qualitative variation due to B deficiency.

Protein spot expression	No. of protein spots
de novo expressed	42
Suppressed	209
Differentially expressed	
According to K–S test	33
According to Student's *t*-test	16
With both statistical tests	14
Total B responsive protein spots	265

expression of a NAC subunit α-like protein 2 (spot 247), might suggest altered protein translation and targeting, important for adaptive stress responses.

The CND41 (spot 259), that was *de novo* expressed, and the predicted protein A9PEP6 (spot 512), that was down regulated under B deficiency, have aspartic-type endopeptidase activity. This activity is apparently related with proteolitic processes implicated in post-mortem proteolysis of the 7S globular storage protein and in the degradation of extracellular pathogenesis-related (PR) proteins [40]. Indeed, a 7S seed storage protein, the globulin-1S allele (spot 682) and two pathogenesis-related (PR)-10 proteins (spots 276 and 287) were suppressed due to B deficiency.

Protein degradation is an ATP-demanding process, so its repression will decrease protein synthesis and turnover, thereby reducing ATP demand [41]. The fact that suppressed and *de novo* expressed proteins belong to the same metabolic class, points out for a shift in protein folding and proteolysis processes, that may lead to a redirected protein metabolism towards plant survival under stressful conditions.

3.3.3. *Amino acid metabolism*

Some proteins related with amino acid metabolism were suppressed by B deficiency. The majority of these proteins (Adenosylhomocysteinase, spot 616; Cysteine synthase, spot 393 and 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, spots 773, 776 and 778) are related with the metabolism of sulfur containing amino acids. Such effect was not previously reported, although a relation of B deficiency with sulfur metabolism was reported through the reduction of the SH-containing compound, glutathione, higher glutathione reductase activity and glutathione S-transferase expression [5,18,42]. In our study, however, glutathione-S-transferase (spot 318) was suppressed due to the long-term B deficiency, whereas an increase in glutathione S-transferase proteins and genes has been reported in short-term B deficiency studies [18,43].

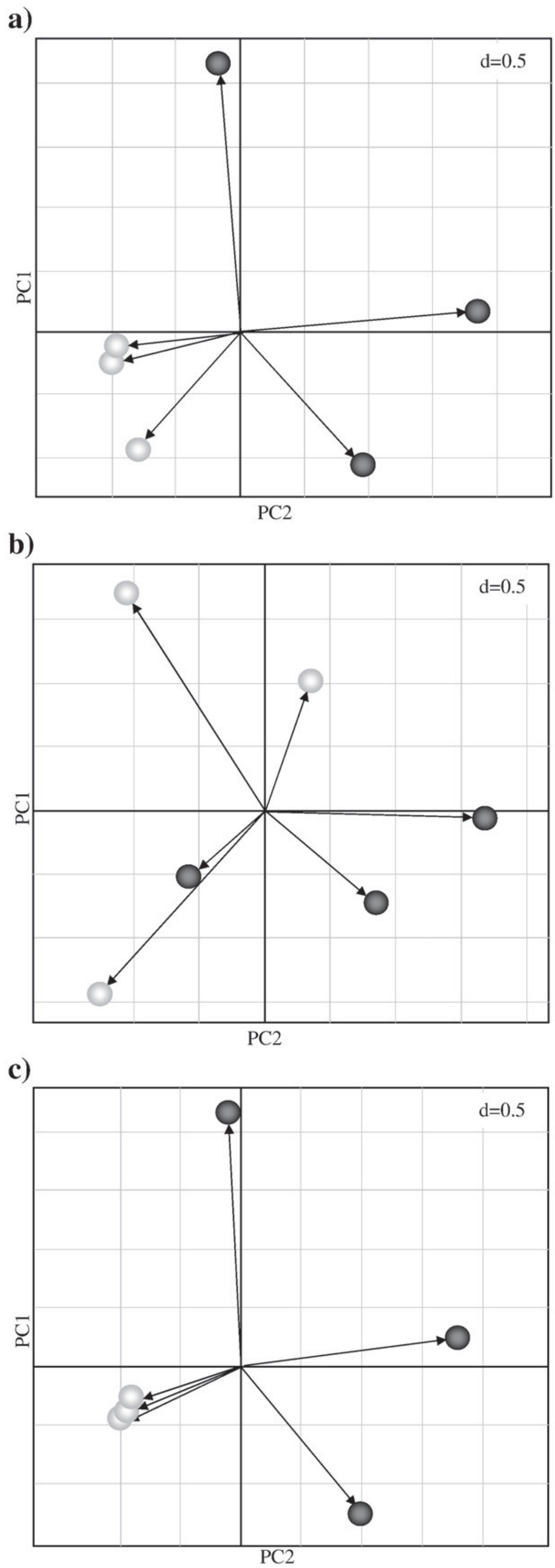

Fig. 4 – Principal component analysis of *Lupinus albus* root 2-DE protein profiles from plants grown with or without B. Each point summarizes either the complete protein profile (a), or the sub-set profile of commonly expressed proteins (b), or the sub-set profile of specifically B-responsive proteins (c). Black circles represent the control samples and the gray circles represent the B-deficient samples.

3.3.4. *Cell wall metabolism*

Altered cell wall metabolism can be envisaged considering the described participation of B in the cell wall structure. Two enzymes, UDP-glucose 6-dehydrogenase (spot 673) and GDP-

Table 2 – Principal components (PCs) calculated from the different protein spots sets.

Component	Eigenvalues					
	Whole dataset		Common spots		Specifically responsive spots	
	Total spots no.	% Variance	Total spots no.	% Variance	Total spots no.	% Variance
PC1	199	49	53	34	152	61
PC2	69	17	31	20	43	17
PC3	57	14	28	18	33	13
PC4	43	10	22	14	14	6
PC5	38	9	21	14	8	3
SUM	406	99	155	100	251	100

Table 3 – Protein identification of the 2-DE gel spots selected as responsive to B deficiency. Proteins were grouped according to the most relevant biological process where they are involved. In the column FC are indicated the fold change of the differentially expressed proteins, the *de novo* expressed proteins (+) and the suppressed proteins (–).

ID [a]		Protein identification [b]	Species	FC	pI/MW (kDa)	
					Predicted [c]	Exp
Energy pathways						
146	P08477	Glyceraldehyde-3-phosphate dehydrogenase	*Hordeum vulgare*	–	–	8.2/38
216	Q8W557	UDP-glucose pyrophosphorylase	*Amorpha fruticosa*	+	6.07/51.6	5.6/54
232	P49608	Aconitate hydratase	*Cucurbita maxima*	+	5.74/98.0	5.1/15
245	Q41712	Ascorbate peroxidase	*Vigna unguiculata*	+	5.64/27.0	8.6/31
251	Q38799	Pyruvate dehydrogenase E1 component subunit	*Arabidopsis thaliana*	+	5.11/35.9	5.5/36
264	Q40079	V-type proton ATPase subunit B2	*Hordeum vulgare*	+	5.12/53.7	5.0/53
340	Q41712	Ascorbate peroxidase	*Vigna unguiculata*	–	5.64/27.0	6.3/26
346	Q43758	Ascorbate peroxidase	*Glycine max*	–	5.51/27.1	6.4/27
347	Q8H1K7	Ascorbate peroxidase	*Retama raetam*	–	5.88/23.6	5.7/27
421	Q0JGZ6	Fructokinase-1	*Oryza sativa*	–	5.07/34.7	5.1/35
442	Q8GZN3	Malate dehydrogenase	*Lupinus albus*	–	6.10/35.6	6.4/37
443	Q8GZN3	Malate dehydrogenase	*Lupinus albus*	–	6.10/35.6	5.9/36
469	Q40676	Fructose-bisphosphate aldolase	*Oryza sativa*	–	6.55/38.7	6.0/38
478	Q9SXP2	Formate dehydrogenase 1, mitochondrial	*Oryza sativa*	–	6.20/39.3	6.6/40
488	P52901	Pyruvate dehydrogenase E1 component subunit α-1	*Arabidopsis thaliana*	–	6.42/39.6	6.4/41
493	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*	–	5.04/42.6	5.9/41
498	P52902	Pyruvate dehydrogenase E1 component subunit	*Pisum sativum*	–	–	6.2/42
499	Q9SAJ4	Phosphoglycerate kinase	*Arabidopsis thaliana*	−1.4	5.49/42.1	6.1/41
511	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*	–	5.04/42.6	5.5/43
536	Q7Y0W9	NADP-specific isocitrate dehydrogenase	*Lupinus albus*	–	6.13/46.1	6.0/46
551	Q7Y0W8	NADP-specific isocitrate dehydrogenase	*Lupinus albus*	–	5.99/46.0	6.0/47
557	B0FGG5	Monodehydroascorbate reductase	*Vaccinium corymbosum*	–	5.78/47.4	6.3/48
561	P93033	Fumarate hydratase 1	*Arabidopsis thaliana*	–	6.65/49.9	7.3/48
562	B0FGG5	Monodehydroascorbate reductase	*Vaccinium corymbosum*	–	5.78/47.4	6.1/49
572	A9SGH3	Enolase	*Physcomitrella patens*	–	5.22/46.1	5.7/50
588	Q9FFR3	6-phosphogluconate dehydrogenase, decarboxylating	*Arabidopsis thaliana*	–	5.62/53.3	6.1/50
599	Q9FFR3	6-phosphogluconate dehydrogenase, decarboxylating	*Arabidopsis thaliana*	–	5.62/53.3	5.7/52
607	Q9LI00	6-phosphogluconate dehydrogenase, decarboxylating	*Oryza sativa*	–	5.85/52.7	6.0/53
611	Q9LEJ0	Enolase 1	*Hevea brasiliensis*	–	5.57/47.8	6.1/73
626	Q40079	V-type proton ATPase subunit B2	*Hordeum vulgare*	–	5.12/53.7	4.9/54
631	Q9FNN5	Subunit of complex I	*Arabidopsis thaliana*	–	8.46/53.4	7.0/55
636	P12862	ATP synthase subunit α	*Triticum aestivum*	–	5.70/55.3	6.1/55
640	P12862	ATP synthase subunit α	*Triticum aestivum*	–	5.70/55.3	5.8/55
641	P49357	Serine hydroxymethyltransferase 1	*Flaveria pringlei*	–	8.15/53.6	6.8/55
646	P12862	ATP synthase subunit α	*Triticum aestivum*	–	5.70/55.3	5.0/43
660	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*	–	6.80/51.7	7.0/56
662	B9SH74	Aldehyde dehydrogenase, putative	*Ricinus communis*	–	5.87/42.0	6.1/57
700	Q42919	Glucose-6-phosphate 1-dehydrogenase	*Medicago sativa*	–	5.85/58.9	6.5/63
738	O82663	Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1	*Arabidopsis thaliana*	–	5.58/66.0	5.8/71
739	P31405	V-type proton ATPase catalytic subunit A	*Gossypium hirsutum*	+	5.36/68.5	5.5/77
771	Q9FGI6	NADH-ubiquinone oxidoreductase 75 kDa subunit	*Arabidopsis thaliana*	–	5.72/77.9	8.1/29
780	P49608	Aconitate hydratase	*Cucurbita maxima*	–	5.74/98.0	5.9/135

(*continued on next page*)

Table 3 (*continued*)

ID [a]		Protein identification [b]	Species	FC	pI/MW (kDa)	
					Predicted [c]	Exp
Energy pathways						
783	P49608	Aconitate hydratase	*Cucurbita maxima*	–	5.74/98.0	5.9/138
784	P49608	Aconitate hydratase	*Cucurbita maxima*	–	5.74/98.0	6.0/138
785	P49608	Aconitate hydratase	*Cucurbita maxima*	–	5.74/98.0	6.1/136
786	P49608	Aconitate hydratase	*Cucurbita maxima*	–	5.74/98.0	6.0/138
788	P49608	Aconitate hydratase	*Cucurbita maxima*	–	5.74/98.0	5.7/143
790	P49608	Aconitate hydratase	*Cucurbita maxima*	–4.9	5.74/98.0	5.8/140
Protein metabolism						
134	O49886	Peptidyl-prolyl *cis–trans* isomerase	*Lupinus luteus*	–	8.71/18.3	9.6/17
136	Q40682	Elongation factor 1-δ 2	*Oryza sativa*	–	4.40/24.5	4.2/32
247	Q94JX9	Nascent polypeptide-associated complex subunit α-like protein 2	*Arabidopsis thaliana*	+	4.37/23.7	5.6/32
259	Q9LS40	CND41, chloroplast nucleoid DNA binding protein-like	*Arabidopsis thaliana*	+	5.27/53.2	5.0/48
291	O49886	Peptidyl-prolyl *cis–trans* isomerase	*Lupinus luteus*	+	8.71/18.3	8.7/17
332	Q3HVM0	Proteasome subunit α type	*Solanum tuberosum*	–	5.40/28.1	5.9/26
345	A9TVH1	Proteasome subunit α type	*Physcomitrella patens*	–	5.92/27.2	5.7/27
352	A5AXI5	Proteasome subunit α type	*Vitis vinifera*	–	6.11/27.2	5.8/27
354	A9TVH1	Proteasome subunit α type	*Physcomitrella patens*	–	5.91/27.3	5.9/27
512	A9PEP6	Predicted protein	*Populus trichocarpa*	2.0	4.94/45.3	5.0/43
513	Q9ZRU6	Elongation factor Tu	*Catharanthus roseus*	–	–	6.0/43
573	A0FH76	EBP1	*Solanum tuberosum*	–	6.26/42.8	6.4/50
584	Q0DDX2	26S protease regulatory subunit 7	*Oryza sativa*	–	6.03/47.7	6.3/50
645	Q6K669	Leucine aminopeptidase 2	*Oryza sativa*	–	5.50/55.0	5.7/55
693	P21239	RuBisCO large subunit-binding protein subunit α	*Brassica napus*	–2.2	4.78/57.0	4.9/61
694	P21239	RuBisCO large subunit-binding protein subunit α	*Brassica napus*	–	4.78/57.0	5.9/61
699	Q940P8	Putative uncharacterized protein	*Arabidopsis thaliana*	–	5.59/57.3	5.6/63
701	P21239	RuBisCO large subunit-binding protein subunit α	*Brassica napus*	–	4.78/57.0	4.9/63
705	Q93ZM7	Chaperonin CPN60-like 2	*Arabidopsis thaliana*	–	5.32/57.1	6.0/64
707	Q05045	Chaperonin CPN60-1	*Cucurbita maxima*	–	5.09/57.4	5.3/63
710	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*	+	5.26/58.1	5.6/64
713	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*	–	5.26/58.1	5.6/65
715	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*	–	5.26/58.1	5.3/65
716	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*	–	5.26/58.1	5.3/65
720	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*	–	6.03/61.2	6.0/65
722	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*	–	6.03/61.2	6.7/66
725	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*	–	6.03/61.2	5.8/67
728	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*	–	6.03/61.2	5.0/69
732	Q9M888	Putative uncharacterized protein	*Arabidopsis thaliana*	–	5.83/58.9	5.9/70
749	P37900	Heat shock 70 kDa protein	*Pisum sativum*	+	5.18/66.7	5.8/66
750	Q43468	Heat shock protein STI	*Glycine max*	–	5.81/63.6	5.7/77
755	P37900	Heat shock 70 kDa protein	*Pisum sativum*	–	5.18/66.7	5.3/80
760	P11143	Heat shock 70 kDa protein	*Zea mays*	–	5.22/70.6	5.3/89
762	Q39043	Luminal-binding protein 2	*Arabidopsis thaliana*	–	5.08/71.1	5.2/87
763	Q39043	Luminal-binding protein 2	*Arabidopsis thaliana*	–	5.08/71.1	5.2/88
791	Q9LZF6	Cell division control protein 48 homolog E	*Arabidopsis thaliana*	–	5.08/90.0	5.3/142
795	O23755	Elongation factor 2	*Beta vulgaris*	–	5.93/93.8	5.9/146
799	O23755	Elongation factor 2	*Beta vulgaris*	–	5.93/93.8	5.8/150
Defense response						
233	P52779	Protein LlR18B	*Lupinus luteus*	+	5.35/16.6	4.7/15
234	Q93XI0	Pathogenesis-related 10	*Lupinus albus*	+	4.87/16.9	6.8/18
276	Q93XI0	Pathogenesis-related 10	*Lupinus albus*	–	4.87/16.9	4.6/15
287	Q93XI0	Pathogenesis-related 10	*Lupinus albus*	–	4.87/16.9	4.6/15
318	Q0PN10	Glutathione S-transferase	*Caragana korshinskii*	–	6.86/25.8	6.3/25
327	Q9SXM5	Acidic chitinase	*Glycine max*	+	5.01/31.9	4.7/26
430	P23535	Glucan endo-1,3-β-glucosidase, basic isoform	*Phaseolus vulgaris*	–	8.75/35.2	6.4/36
Transcription						
314	Q5EI63	Quinone reductase 2	*Triticum monococcum*	–	5.95/21.7	6.7/24
Amino acids metabolism						
393	A3RM06	Cysteine synthase	*Glycine max*	–	5.29/34.7	5.4/32
520	P54260	Aminomethyltransferase	*Solanum tuberosum*	–	7.28/40.9	7.1/44

Table 3 (*continued*)

ID [a]		Protein identification [b]	Species	FC	pI/MW (kDa)	
					Predicted [c]	Exp
521	Q40108	Aspartate aminotransferase	*Lupinus angustifolius*	–	8.36/45.8	6.8/44
616	Q9SP37	Adenosylhomocysteinase	*Lupinus luteus*	–	5.64/53.3	5.8/53
773	P93263	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	*Mesembryanthemum crystallinum*	–	5.90/84.8	6.0/114
776	P93263	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	*Mesembryanthemum crystallinum*	–	5.90/84.8	6.0/119
778	P93263	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	*Mesembryanthemum crystallinum*	–	5.90/84.8	5.9/116
Cell wall metabolism						
267	P34105	NADP-dependent malic enzyme	*Populus trichocarpa*	+	6.50/65.2	6.4/61
518	Q93VR3	GDP-mannose 3,5-epimerase	*Arabidopsis thaliana*	–	5.85/42.8	6.0/44
673	Q96558	UDP-glucose 6-dehydrogenase	*Glycine max*	–	5.74/52.9	5.9/58
734	A9PGL9	Malic enzyme	*Populus trichocarpa*	–	7.61/54.6	6.0/70
745	P34105	NADP-dependent malic enzyme	*Populus trichocarpa*	–	6.50/65.2	6.0/75
747	P34105	NADP-dependent malic enzyme	*Populus trichocarpa*	–	6.50/65.2	6.0/75
Cytoskeleton biosynthesis						
182	Q1G0Z1	Putative spindle disassembly related protein CDC48	*Nicotiana tabacum*	–	5.13/89.9	5.2/149
183	Q1G0Z1	Putative spindle disassembly related protein CDC48	*Nicotiana tabacum*	+	5.13/89.9	7.4/10
207	P20363	α-3/α-5 tubulin chain	*Arabidopsis thaliana*	+	4.95/49.7	5.4/49
262	Q9STD0	β-tubulin	*Zinnia elegans*	+	4.75/50.1	4.9/49
331	P41916	GTP-binding nuclear protein Ran-1	*Arabidopsis thaliana*	–	6.39/25.3	6.7/26
336	P41916	GTP-binding nuclear protein Ran-1	*Arabidopsis thaliana*	+	6.39/25.3	7.4/26
Other metabolic processes						
391	Q8LQJ6	Ethylene-responsive protein 2-like	*Oryza sativa*	–	10.86/12.6	6.0/31
574	Q7M1Z8	Globulin-2	*Zea mays*	–	6.16/49.9	6.3/50
596	P19595	UTP-glucose-1-phosphate uridylyltransferase	*Solanum tuberosum*	–	5.71/51.7	6.1/52
682	P15590	Globulin-1S allele	*Zea mays*	–	6.75/55.1	6.3/60
768	Q7SIC9	Transketolase	*Zea mays*	–	5.47/73.0	6.0/88
769	Q7SIC9	Transketolase	*Zea mays*	–	5.47/73.0	6.0/32
770	Q7SIC9	Transketolase	*Zea mays*	–	5.47/73.0	5.9/95
Unknown biological processes						
141	Q8LPE5	Fructokinase-like protein	*Cicer arietinum*	–	–	5.1/35
237	Q9M328	Putative uncharacterized protein T18D12.90	*Arabidopsis thaliana*	+	5.66/17.8	5.1/20
246	Q8GYY8	Putative germin	*Arabidopsis thaliana*	+	8.39/23.5	4.4/30
353	Q2V987	Transcription factor APFI-like	*Solanum tuberosum*	–	7.05/29.1	5.8/27
384	Q9SMK5	Plasma membrane intrinsic polypeptide	*Cicer arietinum*	–	4.95/23.3	5.2/30
549	A5CB20	Putative uncharacterized protein	*Vitis vinifera*	–	8.42/54.2	6.7/47
671	Q7XCL2	Ubiquitin domain containing protein	*Oryza sativa*	–	4.71/59.3	4.9/58
678	Q94IC1	Betaine aldehyde dehydrogenase	*Hordeum vulgare*	–2.2	5.47/54.5	5.2/58

[a] Spot numbers are corresponding to the numbers in Fig. 4.
[b] Protein identification according to the UniProt database (http://www.uniprot.org).
[c] Predicted pI and MW (kDa) were calculated by using an ExPASy tool (http://www.expasy.org).

mannose 3,5-epimerase (spot 518), involved in the carbohydrate metabolism directed for the cell wall biosynthesis were suppressed due to B deficiency. Several malic enzyme isoforms (spots 734, 745 and 747) were suppressed under B deficiency, and this enzyme is described to provide the NADPH used for the production of H_2O_2 in lignin biosynthesis [44]. Lignin production that results from the hydroxycinnamyl alcohols polymerization by peroxidases [45] could be compromised by B deficiency. The suppression of several ascorbate peroxidases isoforms (spots 340, 346 and 347), and the previously observation of ascorbate peroxidase inhibition in B-deficient squash roots [5] could be related with the increased content of phenolic compounds described for B-deficient plants [46] and with the lower degree of lignification observed in some trees growing in low B content soils [47].

3.3.5. *Defense responses*

Several proteins related with defense responses were *de novo* expressed due to B deficiency, namely PR-10 (spot 234) and LIR18B protein (spot 233), both belonging to the PR-10 family, and an acidic chitinase (spot 327) that belongs to the PR-8 family [48]. The PR family proteins are known to be induced by several biotic and abiotic stresses [49]. An uncharacterized T18D12.90 protein (spot 237) and a putative germin-like protein (spot 246), that were *de*

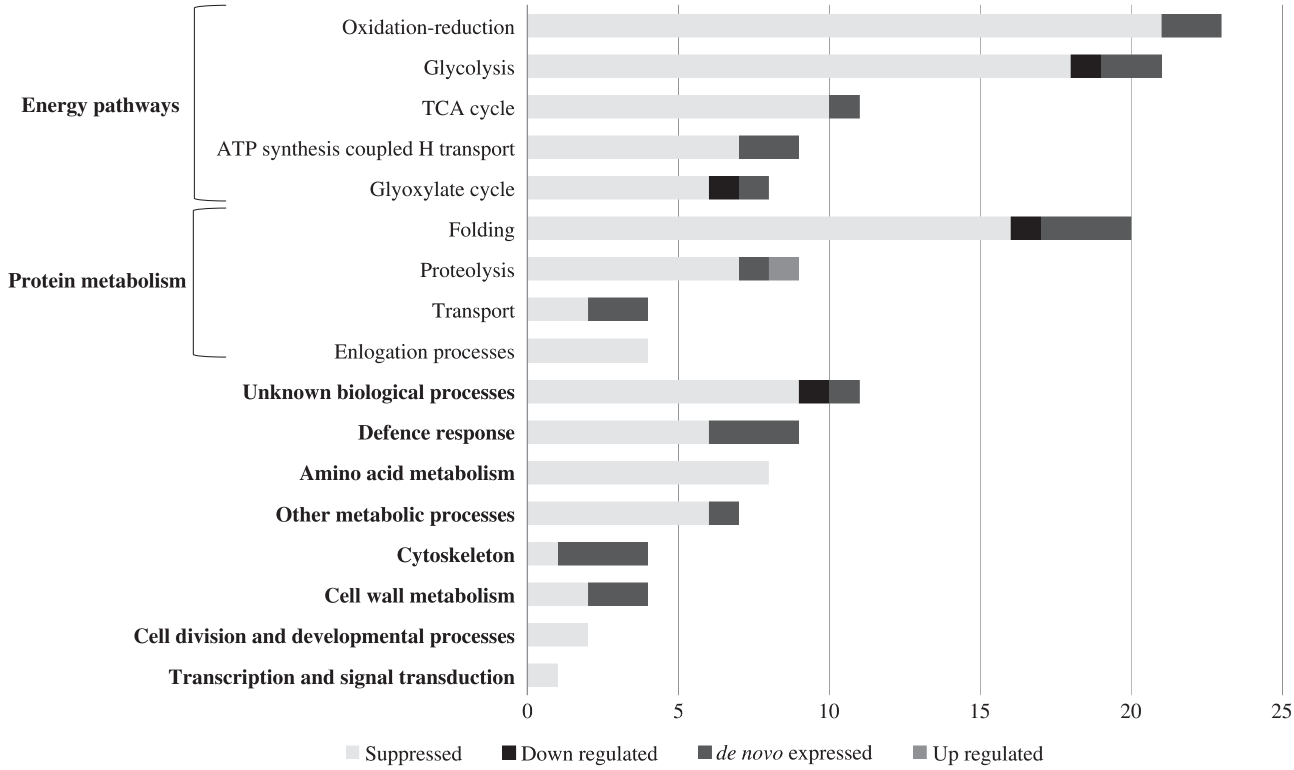

Fig. 5 – Functional classification of the *Lupinus albus* root proteins responsive to B deficiency. The proteins were grouped according to the biological functions described in databases.

novo expressed under B deficiency, have unknown biological functions, however, they have been also associated with various stress responses. For example, in *Arabidopsis thaliana* the protein T18D12.90 is described to be part of the universal stress protein (USP) family [50] and germin as well as germin-like proteins, besides their involvement in stress responses, have been described to participate in a wide range of activities related to developmental processes and cell wall biosynthesis [51]. Several other studies had already reported increased defense proteins in association with B deficiency [19,42,52]. Updated evidence shows that PR proteins and other stress responsive proteins, may display additional functions in growth and developmental processes, by modulating signal molecules [53,54], however the association of these defense proteins with B is not yet understood.

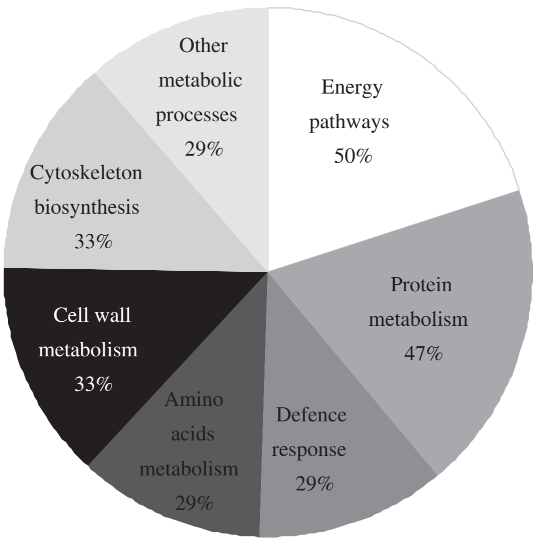

Fig. 6 – Percentage of protein isoforms identified in each metabolic class, of proteins responsive to B deficiency in *Lupinus albus* roots (see Table 3).

3.3.6. *Cytoskeleton biosynthesis*

Several proteins related with cytoskeleton biosynthesis were affected by B deficiency. Under B deficiency we detected *de novo* expression of tubulins (spots 207 and 262), which are major components of microtubules. Another *de novo* expressed protein, which could be involved in the regulation of cytoskeletal assembly and organization, is a GTP-binding nuclear protein Ran-1 (spot 336) [55,56]. The *de novo* expression of a putative spindle disassembly-related protein CDC48 (spot 183) is probably the result of protein degradation processes since this protein spot has a considerable lower molecular mass than that one annotated in the database. Additionally, several other proteins related with cytoskeleton biosynthetic process, were found to be suppressed due to B deficiency. The putative proteins, still uncharacterized, from *A. thaliana* (spots 699 and 732) and from *Vitis vinifera* (spots 725, 720, 722 and 728) are described in the UniProt database to have sequence similarities to the TCP-1 chaperonin family that, in association with the Hsp70 molecular chaperones, can interact with cytoskeleton components [57]. Elongation factors (spots 136 and 513), besides their participation in the translational apparatus, appear to have a second role as a regulator of cytoskeleton rearrangements [58]. Previous studies on altered cytoskeleton features were reported as increased levels of tubulins, actins and altered polymerization patterns of these cytoskeleton proteins in higher plants subjected to B deficiency [59,60]. Cytoskeleton is involved in diverse important cellular aspects, such as mitotic spindle formation, intracellular transport and control of cell shape [61]. So, modified cytoskeleton biosynthesis could still be a missing explanation for the B role in higher plants. Indeed, a possible role for B in cytoskeleton is supported by previous findings that B deficiency primarily disrupts processes where active cytoskeleton remodeling is required, such as the initial phases of differentiation, including pollen tube growth, anther development [62,63], somatic embryo formation [64] and early nodulation processes [65].

3.3.7. *Protein isoforms in stress responses*

One striking feature of this proteomic study is the detection of several protein isoforms associated with B deficiency. Indeed, a numerous group of proteins showed slight changes in pI and/or MW in response to the deficiency. The class with the major percentage of protein isoforms (Fig. 6) was that of energy pathways (50%) followed by the class of protein metabolism (47%). As previously discussed, the plant metabolism seems to be modified in a controlled manner in response to the long-term B deficiency, rather than being just impaired as a whole. Different protein isoforms were also found to have a crucial role in fungal infection and symbiosis studies in *Medicago truncatula*, and in the hydrogen peroxide responses of the rice seedling leaves [66,67]. The evidence for the participation of protein isoforms in several stress responses, points out for active functioning in regulatory processes that could be determinant for plants to cope with adverse conditions. This is an important and a very complex matter that is now emerging, and that in the near future may bring new insight on plant stress responses [68]. So, this could be a future in-depth study to perform in relation to B deficiency.

4. Conclusions

There appears to be a metabolic adjustment of the biosynthetic fluxes of the lupin root in response to B deficiency. The adaptive responses to the deficiency resulted in a reduction of important metabolic processes, namely, energy and protein metabolic processes, in which a higher number of protein isoforms was observed. Other common adaptive stress responses are related with defense proteins. Several other metabolic processes affected by the deficiency, such as cell wall metabolism, are in accordance with the known B participation in plant cell wall structure, and cytoskeleton biosynthesis. The high requirement of B in active cytoskeleton remodeling, such as in initial phases of differentiation [64], in reproductive processes [62,63] and in nodulation processes [69], is consistent with a possible role for B in cytoskeleton biosynthetic processes.

Supplementary materials related to this article can be found online at doi:10.1016/j.jprot.2011.03.002.

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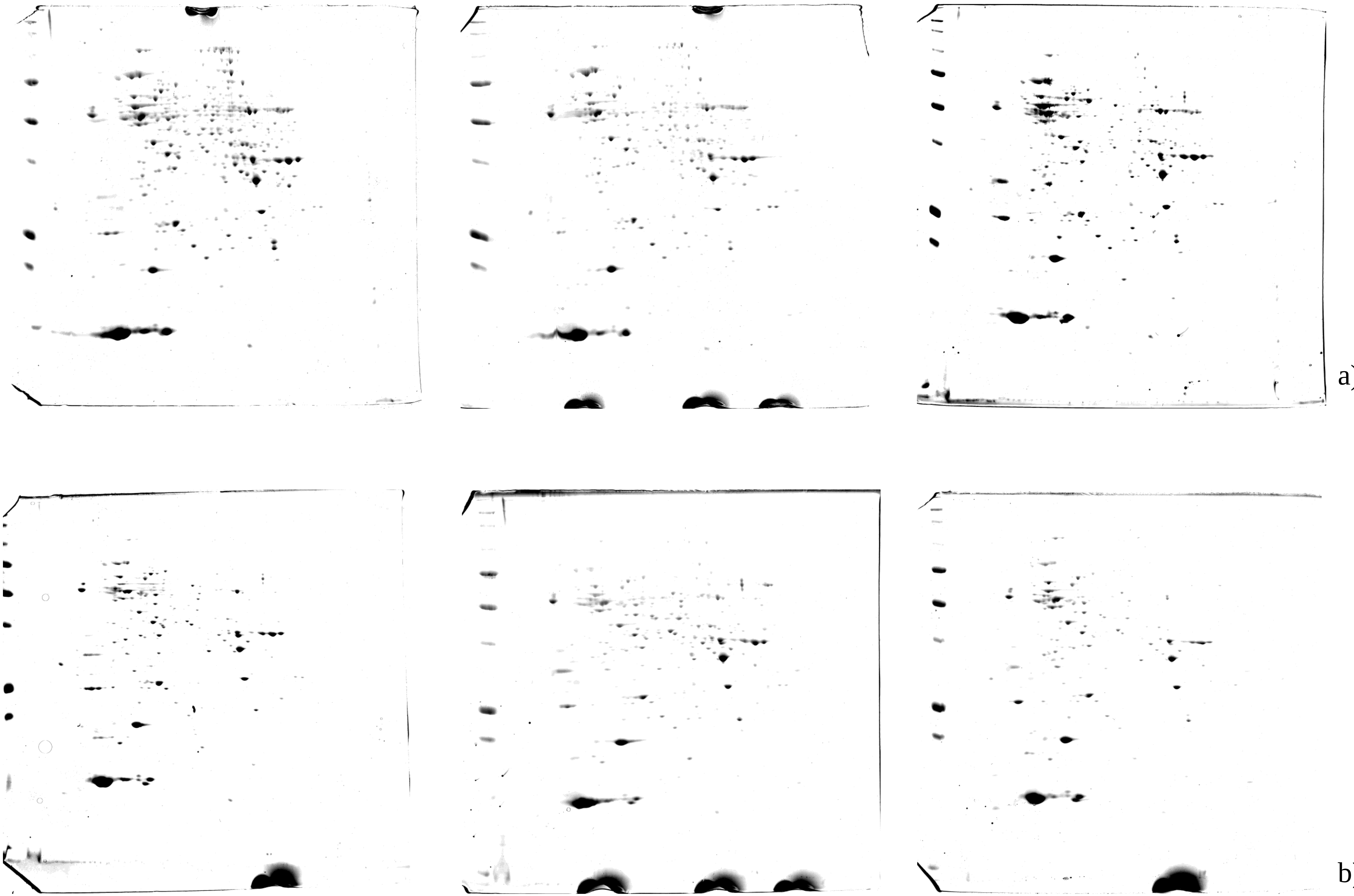
a)
b)

Supplementary Table 1.

ID		Protein identification[a]	Species	FC	pI/MW (kDa) Predicted[b]	pI/MW (kDa) Exp	Xcorr[c]
225	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*	+	6.80/51.7	6.4/84	36.14
	O23264	Selenium-binding protein 1	*Arabidopsis thaliana*		5.37/54.1		20.16
252	Q10DV7	Actin-1	*Oryza sativa*	+	5.30/41.8	6.4/36	10.21
	Q96533	Alcohol dehydrogenase class-3	*Arabidopsis thaliana*		6.51/41.0		10.17
254	Q8GZN3	Malate dehydrogenase	*Lupinus albus*	+	6.10/35.6	6.3/38	60.19
	Q40676	Aldolase	*Oryza sativa*		6.55/38.7		16.20
255	Q9ZR33	Reversibly glycosylated polypeptide	*Triticum aestivum*	+	5.82/41.5	4.5/15	10.17
	Q8S3Q3	Putative uncharacterized protein	*Oryza sativa*		5.10/37.9		10.13
	A2Q396	Galactose mutarotase-like	*Medicago truncatula*		5.82/35.8		10.13
	D7SQC7	Unnamed protein product	*Vitis vinifera*		---		10.13
	P93819	Malate dehydrogenase	*Arabidopsis thaliana*		6.11/35.6		10.12
	Q40676	Fructose-bisphosphate aldolase	*Oryza sativa*		6.55/38.7		8.14
263	P12459	Tubulin β-1 chain	*Glycine max*	+	4.88/50.9	6.4/53	10.18
	Q9LEJ0	Enolase 1	*Hevea brasiliensis*		5.57/47.8		10.17
341	A9PHK1	Predicted protein	*Populus trichocarpa*	-	8.65/27.5	7.2/26	30.18
	Q3HVM0	Proteasome subunit α type	*Solanum tuberosum*		5.40/28.1		20.17
	Q9FMV1	Uncharacterized protein	*Arabidopsis thaliana*		9.01/27.6		20.14
	Q8H1K7	Ascorbate peroxidase	*Retama raetam*		5.88/23.6		16.19
357	Q7M1Z8	Globulin-2	*Zea mays*	-	6.16/49.9	6.6/26	30.14
	A9PHK1	Predicted protein	*Populus trichocarpa*		8.65/27.5		28.19
	Q9FMV1	Uncharacterized protein	*Arabidopsis thaliana*		9.01/27.6		20.16
	Q8S3Q3	Putative uncharacterized protein	*Oryza sativa*		5.10/37.9		18.19
358	A9U1X9	Predicted protein	*Physcomitrella patens*	-	6.75/31.1	6.2/28	10.18
	A9NZX3	Putative uncharacterized protein	*Picea sitchensis*		6.72/29.9		10.17

	P08477	Glyceraldehyde-3-phosphate dehydrogenase	*Hordeum vulgare*		---		10.15
363	P40941	ADP/ATP translocase 2	*Arabidopsis thaliana*	-	9.80/33.8	6.3/28	10.19
	Q9M7G2	Class I chitinase	*Arabis lignifera*		---		10.12
367	Q6W2J3	VDAC1.3	*Lotus japonicus*	-	6.71/29.6	7.8/29	40.21
	Q9SXU1	Proteasome subunit α type-7	*Cicer arietinum*		6.86/27.1		30.17
368	O24616	Proteasome subunit α type-7-B	*Arabidopsis thaliana*	-	8.73/27.3	6.0/29	10.15
	Q949H3	Putative class I chitinase	*Hevea brasiliensis*		---		10.15
	A9PI22	Putative uncharacterized protein	*Populus trichocarpa*		7.80/26.4		10.14
377	Q9SWE7	V-type proton ATPase subunit E	*Citrus limon*	-	7.13/26.3	5.3/30	20.16
	Q8W593	Probable lactoylglutathione lyase	*Arabidopsis thaliana*		5.27/32.2		20.15
	Q8S3Q3	Putative uncharacterized protein	*Oryza sativa*		5.10/37.9		18.13
410	Q8LPE5	Fructokinase-like protein	*Cicer arietinum*	2.2	---	5.1/34	30.15
	A2VC28	Spermidine synthase	*Lotus japonicus*		---		20.20
	P50346	60S acidic ribosomal protein P0	*Glycine max*		5.15/34.2		20.17
	P15590	Globulin-1 S allele	*Zea mays*		6.75/55.1		20.13
416	Q6VWJ5	Fructokinase 3	*Solanum lycopersicum*	-	5.57/41.5	7.5/34	30.17
	O80944	Aldo-keto reductase family 4 member C8	*Arabidopsis thaliana*		6.52/34.7		30.15
	O04397	Ferredoxin-NADP reductase	*Nicotiana tabacum*		8.10/35.4		20.16
418	A7LH72	GEM-like 1	*Vitis vinifera*	-	5.85/31.0	5.8/35	10.12
	Q39243	Thioredoxin reductase 1	*Arabidopsis thaliana*		6.96/39.6		8.16
420	Q9SPB8	Malate dehydrogenase	*Glycine max*	-	8.23/36.1	5.6/35	10.19
	Q0JGZ6	Fructokinase-1	*Oryza sativa*		5.07/34.7		10.14
422	Q94JJ0	Fructose-bisphosphate aldolase	*Oryza sativa*	-	8.81/42.0	7.0/35	30.18
	Q7Y256	Cysteine synthase	*Betula pendula*		6.38/38.2		18.12
428	A9P8P5	Putative uncharacterized protein	*Populus trichocarpa*	-1.6	4.94/35.3	3.4/35	20.18
	Q6Z1G7	Pyruvate dehydrogenase E1 component subunit β	*Oryza sativa*		5.25/39.9		20.11
431	Q6Z1G7	pyruvate dehydrogenase E1 component subunit β	*Oryza sativa*	-	5.25/39.9	5.3/36	20.16
	A9P8P5	Putative uncharacterized protein	*Populus trichocarpa*		4.94/35.3		20.11

446	Q8GZN2	Malate dehydrogenase	*Lupinus albus*	-	6.01/35.5	6.0/37	70.22
	P40691	Auxin-induced protein PCNT115	*Nicotiana tabacum*		7.10/33.9		18.16
452	Q8GZN2	Malate dehydrogenase	*Lupinus albus*	-	6.01/35.5	6.2/37	30.22
	Q40676	Fructose-bisphosphate aldolase	*Oryza sativa*		6.55/38.7		16.18
457	Q8GZN2	Malate dehydrogenase	*Lupinus albus*	-1.9	6.01/35.5	7.0/37	30.17
	Q94JJ0	Fructose-bisphosphate aldolase	*Oryza sativa*		8.81/42.0		20.14
	P08477	Glyceraldehyde-3-phosphate dehydrogenase	*Hordeum vulgare*		---		16.20
461	Q9M4M9	Fructose-bisphosphate aldolase	*Persea americana*	-	6.48/38.6	6.3/37	40.22
	Q8GZN2	Malate dehydrogenase	*Lupinus albus*		6.01/35.5		20.17
	Q9SMJ5	DTDP-glucose 4-6-dehydratase	*Cicer arietinum*		7.13/38.9		16.20
465	Q8GZN2	Malate dehydrogenase	*Lupinus albus*	-	6.01/35.5	6.0/38	40.18
	Q9M4M9	Fructose-bisphosphate aldolase	*Persea americana*		6.48/38.6		30.23
466	Q9ZR33	Reversibly glycosylated polypeptide	*Triticum aestivum*	-	5.82/41.5	5.7/38	20.18
	Q9M4M9	Fructose-bisphosphate aldolase	*Persea americana*		6.48/38.6		20.14
	A5B7D2	Putative uncharacterized protein	*Vitis vinifera*		5.26/40.6		20.11
471	O82705	RGP1 protein	*Oryza sativa*	+	8.21/39.5	5.6/39	10.19
	Q96533	Alcohol dehydrogenase class-3	*Arabidopsis thaliana*		6.51/40.7		10.16
	Q8S3Q3	Putative uncharacterized protein	*Oryza sativa*		5.10/37.9		10.14
	Q40676	Fructose-bisphosphate aldolase	*Oryza sativa*		6.55/38.7		8.19
476	O81796	Isocitrate dehydrogenase [NAD] regulatory subunit 3	*Arabidopsis thaliana*	-	6.13/37.1	6.5/52	20.22
	O82705	RGP1 protein	*Oryza sativa*		8.21/39.5		20.17
477	Q7XTJ3	Putative uncharacterized protein	*Oryza sativa*	-	6.16/46.1	5.9/40	30.22
	O81796	Isocitrate dehydrogenase [NAD] regulatory subunit 3	*Arabidopsis thaliana*		6.13/37.1		20.18
	O22263	Protein disulfide-isomerase like 2-1	*Arabidopsis thaliana*		5.65/37.2		20.18
487	Q96533	Alcohol dehydrogenase class-3	*Arabidopsis thaliana*		6.51/40.7	5.2/41	10.18
	B4FRH5	Succinyl-CoA ligase β-chain	*Zea mays*		6.08/45.2		10.18
	Q9XEF6	Hypothetical EIF-2-α	*Arabidopsis thaliana*		5.13/41.6		10.14
490	Q852R9	Pyruvate dehydrogenase E1 α subunit	*Beta vulgaris*	-	8.34/43.8	6.7/41	40.19

	Q9FM47	Ribonucleoprotein-like	*Arabidopsis thaliana*		6.02/42.4		24.20
496	Q852R9	Pyruvate dehydrogenase E1 α subunit	*Beta vulgaris*	-	8.34/43.8	6.5/41	70.19
	P19168	Chalcone synthase 3	*Glycine max*		5.89/42.4		20.15
	Q9SXP2	Formate dehydrogenase 1, mitochondrial	*Oryza sativa*		6.20/39.3		18.17
497	P52903	Pyruvate dehydrogenase E1 component subunit α	*Solanum tuberosum*	-	6.38/40.4	6.1/41	50.17
	Q30D01	Putative 3-dehydroquinate synthase	*Fagus sylvatica*		8.38/50.1		40.17
	A9NUF2	Putative uncharacterized protein	*Picea sitchensis*		8.65/49.5		20.17
500	Q96255	Phosphoserine aminotransferase	*Arabidopsis thaliana*	-	---	6.7/42	40.15
	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*		5.04/42.6		20.25
501	Q30D01	Putative 3-dehydroquinate synthase	*Fagus sylvatica*	-	8.38/50.1	6.4/42	20.18
	Q852R9	Pyruvate dehydrogenase E1 α subunit	*Beta vulgaris*		8.34/43.8		20.16
	A5B2Z7	Putative uncharacterized protein	*Vitis vinifera*		7.17/43.9		20.16
502	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*	-	5.04/42.6	6.2/42	30.24
	B5AGU9	12-oxophytodienoate reductase-like protein	*Artemisia annua*		7.72/43.2		20.21
	A5B6G3	Putative uncharacterized protein	*Vitis vinifera*		8.12/49.4		20.14
503	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*	-	5.04/42.6	5.7/42	30.22
	Q9XQ94	Glutamine synthetase	*Medicago sativa*		5.25/41.7		18.19
504	O82478	Alcohol dehydrogenase Adh-1	*Glycine max*	-	---	5.9/42	40.18
	Q852R9	Pyruvate dehydrogenase E1 α subunit	*Beta vulgaris*		8.34/43.8		20.16
	A5B2Z7	Putative uncharacterized protein	*Vitis vinifera*		7.17/43.9		20.16
507	O82478	Alcohol dehydrogenase Adh-1	*Glycine max*	-	---	6.2/42	30.19
	P30074	Chalcone synthase 2	*Medicago sativa*		5.97/42.7		30.17
	P52902	Pyruvate dehydrogenase E1 component subunit α	*Pisum sativum*		---		20.17
	A5B2Z7	Putative uncharacterized protein	*Vitis vinifera*		7.17/43.9		20.16
509	Q9FUZ6	Elongation factor Tu	*Zea mays*	-	5.99/48.5	6.0/43	60.19
	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*		5.04/42.6		20.25
510	P26563	Aspartate aminotransferase P2	*Lupinus angustifolius*	-	6.23/44.7	6.6/43	68.23
	A9PGP7	Chorismate synthase	*Populus trichocarpa*		8.96/47.0		20.22

	Q96255	Phosphoserine aminotransferase	*Arabidopsis thaliana*		---		20.18
534	Q9SA73	T5I8.3 protein	*Arabidopsis thaliana*	-	6.35/44.5	6.7/46	40.16
	Q9LDQ7	S-adenosylmethionine synthase	*Camellia sinensis*		5.34/42.8		20.12
547	Q7Y0W8	Isocitrate dehydrogenase	*Lupinus albus*	-	5.99/46.0	6.1/47	28.15
	Q5KT13	Tryptophan synthase β subunit	*Polygonum tinctorium*		6.45/51.8		20.21
553	Q9XFS9	1-deoxy-D-xylulose 5-phosphate reductoisomerase	*Arabidopsis thaliana*	-	---	5.8/47	20.17
	Q9LJL7	DNA/RNA binding protein-like	*Arabidopsis thaliana*		5.73/54.3		20.17
556	Q7Y0W8	Isocitrate dehydrogenase	*Lupinus albus*	-	5.99/46.0	5.9/47	46.23
	Q9XFS9	1-deoxy-D-xylulose 5-phosphate reductoisomerase	*Arabidopsis thaliana*		---		30.20
566	A9PHT1	Putative uncharacterized protein	*Populus trichocarpa*	-	6.9/54.0	6.5/49	20.22
	A0FH76	EBP1	*Solanum tuberosum*		6.26/42.8		20.15
569	A9SGH3	Enolase	*Physcomitrella patens*	-	5.22/46.1	6.3/49	20.15
	P35683	Eukaryotic initiation factor 4A-1	*Oryza sativa*		5.37/47.1		18.24
578	A7PRX3	Putative uncharacterized protein	*Vitis vinifera*	4.0	8.44/55.4	7.3/50	20.18
	A9PHT1	Putative uncharacterized protein	*Populus trichocarpa*		6.90/54.0		20.17
585	A9SGH3	Enolase	*Physcomitrella patens*	-	5.22/46.1	5.7/50	20.16
	Q9FFR3	6-phosphogluconate dehydrogenase	*Arabidopsis thaliana*		5.62/53.3		18.14
592	O23960	Acetyl-CoA carboxylase	*Glycine max*	-	7.22/58.9	6.0/51	78.16
	A7PFD2	Putative uncharacterized protein	*Vitis vinifera*		6.56/53.3		40.16
593	Q9M434	Enolase	*Lupinus luteus*	-	5.14/47.8	5.2/50	50.20
	P17614	ATP synthase subunit β	*Nicotiana plumbaginifolia*		5.13/54.1		30.18
600	Q8W557	UDP-glucose pyrophosphorylase	*Amorpha fruticosa*	-	6.07/51.6	5.7/52	30.17
	O49169	Elongation factor 1-α	*Manihot esculenta*		9.20/49.4		20.16
604	A9PCX3	Serine hydroxymethyltransferase	*Populus trichocarpa*	+	7.18/51.9	5.5/51	38.20
	P19023	ATP synthase subunit β	*Zea mays*		5.19/54.1		28.17
	Q8W557	UDP-glucose pyrophosphorylase	*Amorpha fruticosa*		6.07/51.6		20.18
	P17614	ATP synthase subunit β	*Nicotiana plumbaginifolia*		5.13/54.1		20.17
608	Q56XG6	DEAD-box ATP-dependent RNA helicase 15	*Arabidopsis thaliana*	-	5.42/48.3	6.5/52	30.18

	O49169	Elongation factor 1-α	*Manihot esculenta*		9.20/49.4		20.16
	P68172	Adenosylhomocysteinase	*Nicotiana sylvestris*		5.51/53.1		18.15
613	Q9ZTB2	Nodulin	*Glycine max*	-	5.74/52.6	5.9/53	40.16
	Q9SP37	Adenosylhomocysteinase	*Lupinus luteus*		5.64/53.3		20.18
619	P93508	Calreticulin	*Ricinus communis*	-1.4	4.36/45.5	4.3/52	38.18
	O04275	ATP synthase subunit β	*Pisum sativum*		6.63/60.2		20.17
621	Q9LEJ0	Enolase 1	*Hevea brasiliensis*	-	5.57/47.8	5.4/54	20.20
	O04275	ATP synthase subunit β	*Pisum sativum*		6.63/60.2		20.17
622	P19023	ATP synthase subunit β	*Zea mays*	-	5.19/54.1	5.3/53	28.19
	Q9LEJ0	Enolase 1	*Hevea brasiliensis*		5.57/47.8		20.16
624	O04275	ATP synthase subunit β	*Pisum sativum*	-1.6	6.63/60.2	5.2/52	30.19
	Q9LEJ0	Enolase 1	*Hevea brasiliensis*		5.57/47.8		20.23
625	Q40079	V-type proton ATPase subunit B 2	*Hordeum vulgare*	+	5.12/53.7	4.8/53	58.20
	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*		6.80/51.7		36.19
	Q9M5K3	Dihydrolipoyl dehydrogenase 1	*Arabidopsis thaliana*		6.24/49.9		30.17
628	Q8H2T7	Putative NADH dehydrogenase	*Oryza sativa*	-	8.31/55.3	6.9/55	78.24
	Q5F2M7	Pyruvate kinase	*Glycine max*		6.80/54.4		48.22
	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*		6.80/51.7		26.20
632	Q40079	V-type proton ATPase subunit B 2	*Hordeum vulgare*	+	5.12/53.7	5.6/53	58.18
	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*		6.80/51.7		48.22
	O23264	Selenium-binding protein 1	*Arabidopsis thaliana*		5.37/54.1		40.19
	A8IKE1	Alanine aminotransferase 1	*Glycine max*		5.32/53.3		30.21
	P31023	Dihydrolipoyl dehydrogenase	*Pisum Sativum*		6.06/49.7		30.18
	Q9LEJ0	Enolase 1	*Hevea brasiliensis*		5.57/47.8		20.22
634	P93508	Calreticulin	*Ricinus communis*	-	4.36/45.5	4.3/55	28.13
	Q70Z18	Nucleosome assembly protein 1-like protein 2	*Nicotiana tabacum*		4.34/43.2		20.23
637	Q9FNN5	NADH dehydrogenase	*Arabidopsis thaliana*	-	8.46/53.4	6.7/55	30.18
	P12862	ATP synthase subunit α	*Triticum aestivum*		5.70/55.3		30.14

638	P12862	ATP synthase subunit α	*Triticum aestivum*	-	5.70/55.3	6.2/55	40.18
	Q9M5K3	Dihydrolipoyl dehydrogenase 1	*Arabidopsis thaliana*		6.24/49.9		20.17
639	Q9ZTB2	Nodulin	*Glycine max*	-	5.74/52.6	5.9/55	40.17
	P12862	ATP synthase subunit α	*Triticum aestivum*		5.70/55.3		20.14
644	O23264	Selenium-binding protein 1	*Arabidopsis thaliana*	-2.2	5.37/54.1	5.7/55	30.19
	Q9SSV4	Inositol-3-phosphate synthase	*Nicotiana paniculata*		5.44/56.4		20.18
652	Q9FNN5	NADH dehydrogenase	*Arabidopsis thaliana*	-	8.46/53.4	7.1/55	60.19
	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*		6.80/51.7		54.21
	Q9ZWH7	Catalase	*Oryza sativa*		7.36/56.2		20.20
653	P31023	Dihydrolipoyl dehydrogenase	*Pisum Sativum*	-	6.06/49.7	6.4/55	40.18
	P12862	ATP synthase subunit α	*Triticum aestivum*		5.70/55.3		30.17
656	P31023	Dihydrolipoyl dehydrogenase	*Pisum Sativum*	-	6.06/49.7	6.9/56	50.17
	P12862	ATP synthase subunit α	*Triticum aestivum*		5.70/55.3		30.12
	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*		6.80/51.7		26.16
657	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*	-	6.80/51.7	6.6/56	26.21
	P31023	Dihydrolipoyl dehydrogenase	*Pisum Sativum*		6.06/49.7		20.16
661	P12862	ATP synthase subunit α	*Triticum aestivum*	-	5.70/55.3	6.2/57	30.16
	Q9C5J7	6-phosphofructokinase 7	*Arabidopsis thaliana*		6.87/53.5		18.12
669	Q96558	UDP-glucose 6-dehydrogenase	*Glycine max*	-	5.74/52.9	5.7/58	36.18
	P12862	ATP synthase subunit α	*Triticum aestivum*		5.70/55.3		30.16
670	P12862	ATP synthase subunit α	*Triticum aestivum*	-	5.70/55.3	6.0/58	30.14
	A7Q2D6	Putative uncharacterized protein	*Vitis vinifera*		6.04/58.3		14.18
672	Q9FZE1	T1K7.6 protein	*Arabidopsis thaliana*	-	5.84/53.0	6.0/58	20.17
	A7Q2D6	Putative uncharacterized protein	*Vitis vinifera*		6.04/58.3		14.17
677	B4F972	Glutamate decarboxylase	*Zea mays*	-	5.64/55.2	5.3/59	10.11
	Q9LEJ0	Enolase 1	*Hevea brasiliensis*		5.57/47.8		10.11
680	A7R2K3	Putative uncharacterized protein	*Vitis vinifera*	-	5.09/44.0	5.4/59	10.10
	A5ASG9	Putative uncharacterized protein	*Vitis vinifera*		8.82/57.9		10.10

709	Q05045	Precursor Chaperonin CPN60-1, mitochondrial	*Cucurbita maxima*	-1.7	5.09/57.4	5.4/62	184.23
	Q76E42	Glucose-6-phosphate isomerase	*Oryza sativa*		5.88/68.3		28.19
711	P21343	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit β	*Solanum tuberosum*	-	6.2/60.4	6.0/65	60.19
	P15590	Globulin-1 S allele	*Zea mays*		6.75/55.1		30.19
	Q653F6	Putative t-complex protein 1 theta chain	*Oryza sativa*		6.16/60.3		20.20
719	P21343	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit β	*Solanum tuberosum*	-	6.20/60.4	6.0/65	40.15
	Q653F6	Putative t-complex protein 1 theta chain	*Oryza sativa*		6.16/60.3		30.19
	P15590	Globulin-1 S allele	*Zea mays*		6.75/55.1		30.18
724	Q9FMP3	Dihydropyrimidinase	*Arabidopsis thaliana*	-	5.58/58.0	5.9/66	10.21
	Q9LIR4	Putative dihydroxyacid dehydratase	*Arabidopsis thaliana*		5.85/64.9		10.13
	A9P0C2	Putative uncharacterized protein	*Picea sitchensis*		5.84/34.7		10.12
740	P31405	V-type proton ATPase catalytic subunit A	*Gossypium hirsutum*	-3.5	5.36/68.5	5.7/73	98.22
	Q9ZSQ4	Phosphoglucomutase	*Populus tremula*		5.49/63.1		58.19
	Q38931	70 kDa peptidyl-prolyl isomerase	*Arabidopsis thaliana*		5.24/61.5		20.16
741	B9RHV0	ATP synthase α	*Ricinus communis*	-	5.31/63.2	5.5/74	20.19
	Q38931	70 kDa peptidyl-prolyl isomerase	*Arabidopsis thaliana*		5.24/61.5		20.16
744	B8PUQ5	Malic enzyme	*Triticum aestivum*	-	6.51/71.0	6.2/74	28.15
	P15590	Globulin-1 S allele	*Zea mays*		6.75/55.1		20.17
772	Q43644	NADH-ubiquinone oxidoreductase 75 kDa subunit	*Solanum tuberosum*	-	5.52/77.1	6.0/106	10.17
	Q6K8J4	Putative uncharacterized protein	*Oryza sativa*		5.64/82.2		10.14
792	O23755	Elongation factor 2	*Beta vulgaris*	-	5.93/93.8	6.0/142	60.16
	P49608	Aconitate hydratase	*Cucurbita maxima*		5.74/98.0		30.13

[a] Protein identification according to the UniProt database (http://www.uniprot.org)
[b] Predicted pI and MW (kDa) were calculated by using an ExPASy tool (http://www.expasy.org)
[c] Cross-correlation score (Xcorr)

Supplementary Table 2.

ID[a]	Protein identification[b]		Species	MH+	Z	P[c]	Xcorr[d]	Cov (%)	UnPep
	Polypetides								
	Energy pathways								
146	P08477	Glyceraldehyde-3-phosphate dehydrogenase	*Hordeum vulgare*			$3.14X10^{-5}$	18.15	10.8	2
		RVPTVDVSVVDLTVRL		1498.84753	2	$3.14X10^{-5}$	3.04		
		RAASFNIIPSSTGAAKA		1434.75867	2	$1.85X10^{-2}$	2.69		
216	Q8W557	UDP-glucose pyrophosphorylase	*Amorpha fruticosa*			$1.03X10^{-7}$	86.20	18.9	7
		KSAVAGLNQISENEKS		1459.73877	2	$1.03X10^{-7}$	3.93		
		RANPENPTVELGPEFKK		1641.81189	2	$1.82X10^{-5}$	3.29		
		RYLSGEAQHVEWSKI		1533.73328	2	$2.59X10^{-5}$	3.17		
		KLEIPDGAVIANKD		1239.69434	2	$2.49X10^{-3}$	2.94		
		KGGTLISYEGRV		1052.53711	2	$4.15X10^{-2}$	2.64		
		RLVVDDFLPLPSKG		1342.76172	2	$2.11X10^{-2}$	2.60		
		KKVSNFLSRF		950.54181	2	$3.41X10^{-2}$	2.42		
		KVSNFLSRF		822.44684	2	$3.64X10^{-2}$	2.38		
		KYGSNVPLLLMNSFNTHDDTQKI		2410.13435	4	$1.14X10^{-1}$	1.63		
232	P49608	Aconitate hydratase	*Cucurbita maxima*			$3.28X10^{-6}$	30.26	5.9	3
		RSENAVQANMELEFQRN		1781.81229	3	$3.28X10^{-6}$	5.14		
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	3	$3.46X10^{-3}$	2.91		
		KTSLAPGSGVVTKY		1116.62585	2	$1.99X10^{-4}$	2.18		
245	Q41712	Ascorbate peroxidase	*Vigna unguiculata*			$3.49X10^{-5}$	46.23	28.4	5
		KAMGLSDQDIVALSGGHTIGAAHKERS		2550.27291	4	$5.26X10^{-4}$	4.16		
		KAMGLSDQDIVALSGGHTIGAAHKE		2265.12921	4	$3.49X10^{-5}$	3.69		
		RSGFEGPWTSNPLIFDNSYFKE		2306.07642	2	$6.42X10^{-4}$	2.71		
		KTGGPFGTIKH		877.47778	2	$1.39X10^{-1}$	2.30		
		KSYPTVSADYQKA		1258.59497	2	$9.61X10^{-4}$	2.19		
251	Q38799	Pyruvate dehydrogenase E1 component subunit	*Arabidopsis thaliana*			$1.17X10^{-6}$	8.18	5.0	1
		RDALNSAIDEEMSADPKV		1721.75344	2	$1.17X10^{-6}$	3.59		
264	Q40079	V-type proton ATPase subunit B2	*Hordeum vulgare*			$6.38X10^{-5}$	28.15	8.1	3
		KTPVSLDMLGRI		1104.57177	2	$6.38X10^{-5}$	2.98		
		KAVVQVFEGTSGIDNKY		1563.80127	2	$2.15X10^{-4}$	2.73		
		KYQEIVNIRL		1034.56287	2	$2.53X10^{-1}$	2.21		
340	Q41712	Ascorbate peroxidase	*Vigna unguiculata*			$1.64X10^{-4}$	28.23	19.6	3
		KSYPTVSADYQKA		1258.59497	3	$1.08X10^{-3}$	3.37		
		KAMGLSDQDIVALSGGHTIGAAHKE		2265.12921	2	$1.64X10^{-4}$	2.65		
		KTGGPFGTIKH		877.47778	2	$1.54X10^{-3}$	2.33		
346	Q43758	Ascorbate peroxidase	*Glycine max*			$2.11X10^{-4}$	30.17	14.8	3

		KSYPTVSADYQKA		1258.59497	3	$2.52X10^{-2}$	3.43		
		KSYPTVSADYQKA		1258.59497	3	$1.65X10^{-2}$	3.40		
		KTGGPFGTIKH		877.47778	2	$1.21X10^{-2}$	3.18		
		KGSDHLRDVFGKA		1230.62256	2	$2.11X10^{-4}$	2.57		
		KGSDHLRDVFGKA		1230.62256	2	$2.72X10^{-2}$	2.22		
		KSYPTVSADYQKA		1258.59497	2	$6.33X10^{-4}$	2.03		
347	Q8H1K7	Ascorbate peroxidase	*Retama raetam*			$1.41X10^{-4}$	16.21	17.7	2
		KAMGLSDQDIVALSGGHTIGAAHKE		2265.12921	3	$1.41X10^{-4}$	4.12		
		RLAWHSAGTFDVKT		1331.67432	4	$4.47X10^{-2}$	2.63		
421	Q0JGZ6	Fructokinase-1	*Oryza sativa*			$1.35X10^{-7}$	10.17	5.3	1
		KAPGGAPANVAIAVARL		1334.75391	2	$1.35X10^{-7}$	3.43		
442	Q8GZN3	Malate dehydrogenase	*Lupinus albus*			$5.65X10^{-4}$	30.15	11.7	3
		RLNVQVSDVKN		1001.56256	2	$3.81X10^{-3}$	3.07		
		KLDLTAEELSEEKA		1376.67908	2	$6.08X10^{-4}$	2.91		
		KIVQGLGIDEFSRK		1333.71106	2	$5.65X10^{-4}$	2.91		
443	Q8GZN3	Malate dehydrogenase	*Lupinus albus*			$4.74X10^{-6}$	40.19	11.7	4
		KLDLTAEELSEEKA		1376.67908	2	$4.74X10^{-6}$	3.68		
		KIVQGLGIDEFSRK		1333.71106	2	$1.72X10^{-5}$	3.21		
		RLNVQVSDVKN		1001.56256	2	$2.67X10^{-3}$	2.69		
		KKLDLTAEELSEEKA		1504.77405	2	$1.23X10^{-2}$	2.05		
469	Q40676	Fructose-bisphosphate aldolase	*Oryza sativa*			$7.43X10^{-5}$	8.17	4.5	1
		KGILAADESTGTIGKR		1332.70056	2	$7.43X10^{-5}$	3.50		
478	Q9SXP2	Formate dehydrogenase 1, mitochondrial	*Oryza sativa*			$1.81X10^{-5}$	20.22	3.5	1
		KYEEDLDAMLPKC		1084.64734	2	$5.07X10^{-5}$	3.71		
		KYEEDLDAMLPKC		956.55237	2	$1.79X10^{-1}$	2.98		
488	P52901	Pyruvate dehydrogenase E1 component subunit α-1	*Arabidopsis thaliana*			$1.81X10^{-4}$	40.17	9.5	4
		RRMEIAADSLYKA		1312.65656	3	$1.02X10^{-2}$	3.33		
		KRGDYVPGLKV		1004.55237	2	$1.64X10^{-2}$	2.68		
		RMEIAADSLYKA		1140.56055	2	$1.81X10^{-4}$	2.61		
		KGPIILEMDTYRY		1323.66131	2	$1.23X10^{-1}$	2.06		
493	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*			$9.24X10^{-5}$	28.17	9.4	3
		KGVTTIIGGGDSVAAVEKV		1573.84314	2	$4.57X10^{-4}$	2.90		
		KELDYLVGAVSNPKR		1404.73694	2	$9.24X10^{-5}$	2.56		
		KRPFAAIVGGSKV		1102.63672	2	$3.47X10^{-2}$	2.53		
498	P52902	Pyruvate dehydrogenase E1 component subunit	*Pisum sativum*			$3.40X10^{-5}$	40.18	9.6	4
		KGYGVEAFGVDRK		1169.55859	2	$2.98X10^{-2}$	3.64		
		KNGPIILEMDTYRY		1437.70424	2	$3.40X10^{-5}$	2.91		
		KDCIITAYRD		1011.49279	2	$3.19X10^{-1}$	2.51		
		KGYGVEAFGVDRKE		1297.65356	2	$2.05X10^{-3}$	2.46		
499	Q9SAJ4	Phosphoglycerate kinase	*Arabidopsis thaliana*			$4.10X10^{-12}$	66.25	20.0	6
		KFLKPSVAGFLMQKE		1465.82361	3	$1.54X10^{-3}$	4.91		
		KFLKPSVAGFLMQKE		1481.81848	3	$1.43X10^{-2}$	4.85		

		KLAALADVYVNDAFGTAHRA		1903.96606	3	$3.78X10^{-5}$	3.75		
		KKLAALADVYVNDAFGTAHRA		2032.06104	4	$6.40X10^{-3}$	3.58		
		RVDLNVPLDDNSNITDDTRI		2015.95166	2	$4.10E^{-1}2$	3.56		
		KELDYLVGAVANPKK		1388.74207	2	$3.19X10^{-5}$	3.53		
		KYSLKPLVPRL		1072.65137	2	$6.58X10^{-5}$	2.23		
511	P50318	Phosphoglycerate kinase	*Arabidopsis thaliana*			$2.76X10^{-4}$	20.16	7.1	2
		KELDYLVGAVSNPKR		1404.73694	2	$6.18X10^{-4}$	3.26		
		KGVTTIIGGGDSVAAVEKV		1573.84314	2	$2.76X10^{-4}$	2.92		
536	Q7Y0W9	NADP-specific isocitrate dehydrogenase	*Lupinus albus*			$9.69X10^{-6}$	106.21	26.0	9
		KLEAACIGAVESGKM		1304.65148	2	$8.63X10^{-4}$	3.82		
		RAFAEASMTTAYEKK		1435.64097	2	$4.35X10^{-5}$	3.71		
		RLIDDMVAYAVKS		1253.64460	2	$2.43X10^{-4}$	3.68		
		RLIDDMVAYAVKS		1237.64966	2	$1.56X10^{-5}$	3.59		
		KTIESEAAHGTVTRH		1371.68628	2	$9.69X10^{-6}$	3.50		
		KINVANPIVEMDGDEMTRV		1935.87865	3	$8.26X10^{-5}$	2.88		
		RAFAEASMTTAYEKK		1419.64612	2	$1.82X10^{-3}$	2.68		
		KFEAAGIWYEHRL		1378.65381	3	$7.05X10^{-2}$	2.66		
		KYYDLGLPYRD		1159.57825	2	$2.49X10^{-4}$	2.55		
		KLLDFTQKL		864.48254	2	$1.19X10^{-1}$	2.54		
		RAFAEASMTTAYEKKW		1563.73594	2	$4.13X10^{-1}$	2.14		
551	Q7Y0W8	NADP-specific isocitrate dehydrogenase	*Lupinus albus*			$1.67X10^{-4}$	30.24	10.7	3
		KKLEEACIGAVESGKM		1490.75192	3	$3.65X10^{-4}$	4.88		
		RLIDDMVAYAVKS		1253.64460	2	$2.84X10^{-4}$	3.03		
		RAFADASMTTAYEKK		1421.62532	2	$1.67X10^{-4}$	2.82		
557	B0FGG5	Monodehydroascorbate reductase	*Vaccinium corymbosum*			$6.54X10^{-6}$	20.21	2.8	1
		KLTDFGVQGADAKN		1221.61096	2	$6.54X10^{-6}$	2.65		
		KAYLFPESPARL		1150.58911	2	$2.62X10^{-2}$	2.02		
561	P93033	Fumarate hydratase 1	*Arabidopsis thaliana*			$1.27X10^{-5}$	20.17	5.9	2
		RDTFGPIQVPSDKL		1303.65283	2	$1.27X10^{-5}$	3.35		
		KVNMEYGLDPTIGKA		1452.70391	2	$2.12X10^{-2}$	2.23		
562	B0FGG5	Monodehydroascorbate reductase	*Vaccinium corymbosum*			$8.42X10^{-4}$	20.18	2.8	1
		KLTDFGVQGADAKN		1221.61096	2	$8.42X10^{-4}$	3.67		
		KAYLFPESPARL		1150.58911	2	$1.45X10^{-1}$	2.22		
572	A9SGH3	Enolase	*Physcomitrella patens*			$5.78X10^{-4}$	20.18	2.6	1
		RIEEELGNVRY		1058.54761	2	$5.99X10^{-3}$	3.69		
		RGNPTVEVDLVTDRV		1414.71729	2	$5.78X10^{-4}$	2.22		
588	Q9FFR3	6-phosphogluconate dehydrogenase, decarboxylating	*Arabidopsis thaliana*			$4.63X10^{-4}$	18.18	5.1	2
		KICSYAQGMNLLRA		1441.69263	2	$1.68X10^{-2}$	2.88		
		KGFPISVYNRT		1052.55237	2	$4.63X10^{-4}$	2.26		
599	Q9FFR3	6-phosphogluconate dehydrogenase, decarboxylating	*Arabidopsis thaliana*			$4.64X10^{-6}$	24.23	9.0	3
		KGLLYLGMGVSGGEEGARN		1681.82140	2	$4.64X10^{-6}$	4.66		
		KICSYAQGMNLLRA		1441.69263	2	$7.84X10^{-2}$	2.76		
		KGFPISVYNRT		1052.55237	2	$3.95X10^{-1}$	2.42		
607	Q9LI00	6-phosphogluconate dehydrogenase, decarboxylating	*Oryza sativa*			$7.76X10^{-4}$	16.16	2.9	1

		RDRLPANLVQAQRD		1380.77063	3	$4.06X10^{-1}$	3.28		
		KGLLYLGMGVSGGEEGARN		1681.82140	2	$7.76X10^{-4}$	2.48		
611	Q9LEJ0	Enolase 1	*Hevea brasiliensis*			$2.14X10^{-4}$	10.12	3.8	1
		KVNQIGSVTESIEAVKM		1573.84314	2	$2.14X10^{-4}$	2.49		
626	Q40079	V-type proton ATPase subunit B2	*Hordeum vulgare*			$2.29X10^{-4}$	58.19	14.1	6
		KAVVQVFEGTSGIDNKY		1563.80127	2	$2.29X10^{-4}$	3.88		
		RKFVAQGAYDTRN		1255.64294	3	$2.04X10^{-2}$	3.30		
		KFVAQGAYDTRN		1127.54797	2	$1.35X10^{-2}$	3.17		
		KTPVSLDMLGRI		1104.57177	2	$4.51X10^{-4}$	3.12		
		KYQEIVNIRL		1034.56287	2	$1.47X10^{-1}$	2.72		
		RTVSGVAGPLVILDKV		1368.80969	2	$1.04X10^{-2}$	2.15		
631	Q9FNN5	Subunit of complex I	*Arabidopsis thaliana*			$5.16X10^{-5}$	40.18	13.8	4
		KLEEIDMLQEVTKQ		1463.72979	2	$5.16X10^{-5}$	3.61		
		KAVQSGLGTAAVIVMDKS		1575.84107	3	$1.49X10^{-2}$	3.48		
		RASAAYIYIRG		1027.55713	2	$3.97X10^{-4}$	3.27		
		KVSDGRPSYLVVNADESEPGTCKD		2380.10853	3	$6.11X10^{-4}$	2.60		
636	P12862	ATP synthase subunit α	*Triticum aestivum*			$3.51X10^{-4}$	30.16	7.5	3
		RTGSIVDVPAGKA		1043.57312	2	$1.31X10^{-3}$	3.20		
		RVVSVGDGIARV		972.54724	2	$3.51X10^{-4}$	2.85		
		RAAELTTLLESRM		1203.65796	2	$3.53X10^{-3}$	2.68		
640	P12862	ATP synthase subunit α	*Triticum aestivum*			$1.01X10^{-4}$	30.14	7.5	3
		RAAELTTLLESRM		1203.65796	2	$7.28X10^{-2}$	2.80		
		RTGSIVDVPAGKA		1043.57312	2	$2.42X10^{-3}$	2.59		
		RVVSVGDGIARV		972.54724	2	$1.01X10^{-4}$	2.38		
641	P49357	Serine hydroxymethyltransferase 1	*Flaveria pringlei*			$1.60X10^{-5}$	18.17	6.8	2
		KNTVPGDVSAMVPGGIRM		1585.80027	3	$2.69X10^{-2}$	2.92		
		RLNESTGYIDYDQLEKS		1787.83337	2	$1.60X10^{-5}$	2.25		
646	P12862	ATP synthase subunit α	*Triticum aestivum*			$2.54X10^{-4}$	16.17	7.7	4
		RTGSIVDVPAGKA		1043.57312	2	$5.34X10^{-2}$	3.25		
		RAAELTTLLESRM		1203.65796	2	$4.89X10^{-4}$	3.17		
		RVVSVGDGIARV		972.54724	2	$3.60X10^{-4}$	2.71		
		KRTGSIVDVPAGKA		1199.67432	2	$1.45X10^{-2}$	2.58		
660	O23254	Serine hydroxymethyltransferase	*Arabidopsis thaliana*			$1.52X10^{-6}$	26.21	9.3	3
		KANAVALGNYLMSKG		1367.69876	2	$6.89X10^{-6}$	3.97		
		KLLICGGSAYPRD		1206.62995	2	$6.35X10^{-5}$	3.33		
		KISATSIYFESLPYKV		1618.83630	2	$1.52X10^{-6}$	3.10		
662	B9SH74	Aldehyde dehydrogenase, putative	*Ricinus communis*			$4.35X10^{-6}$	10.22	4.4	1
		RSGVESGATLETGGDRF		1435.66589	2	$4.35X10^{-6}$	4.31		
700	Q42919	Glucose-6-phosphate 1-dehydrogenase	*Medicago sativa*			$3.03X10^{-4}$	10.13	2.5	1
		RGPAEADELLEKA		1171.58411	2	$3.03X10^{-4}$	2.53		
738	O82663	Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1	*Arabidopsis thaliana*			$6.48X10^{-4}$	20.13	5.4	2

		KGSDWLGDQDAIQYMCRE		1930.80582	2	$6.48X10^{-4}$	2.59		
		RTQETLEEGCQLIDKA		1663.78434	2	$1.53X10^{-3}$	2.37		
739	P31405	V-type proton ATPase catalytic subunit A	*Gossypium hirsutum*			$1.05X10^{-5}$	60.17	10.9	6
		KLAADTPLLTGQRV		1255.70044	2	$1.05X10^{-5}$	3.49		
		KDTVLELEFQGVKK		1377.72607	2	$8.44X10^{-3}$	3.10		
		RSGDVYIPRG		906.46796	2	$4.67X10^{-2}$	2.57		
		KITYIAPPGQYSLKD		1450.79407	2	$7.02X10^{-2}$	2.41		
		REDYLAQNAFTPYDKF		1674.76465	2	$2.35X10^{-4}$	2.28		
		KRSGDVYIPRG		1062.56909	2	$1.32X10^{-1}$	2.13		
771	Q9FGI6	NADH-ubiquinone oxidoreductase 75 kDa subunit	*Arabidopsis thaliana*			$1.51X10^{-5}$	26.15	6.0	3
		RGSGEEIGTYVEKL		1268.60046	2	$4.94X10^{-2}$	2.69		
		RLNEDINEEWISDKT		1604.74390	2	$1.87X10^{-3}$	2.68		
		RFASEVAGVQDLGILGRG		1631.87512	2	$1.51X10^{-5}$	2.48		
780	P49608	Aconitate hydratase	*Cucurbita maxima*			$6.35X10^{-9}$	40.22	7.0	4
		RSENAVQANMELEFQRN		1781.81229	3	$6.35X10^{-9}$	4.42		
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	3	$1.43X10^{-4}$	4.09		
		KTSLAPGSGVVTKY		1116.62585	2	$1.68X10^{-5}$	2.63		
		KGPMLLGVKA		830.48044	2	$4.07X10^{-1}$	2.56		
783	P49608	Aconitate hydratase	*Cucurbita maxima*			$1.25X10^{-7}$	40.18	7.0	4
		RSENAVQANMELEFQRN		1781.81229	2	$1.25X10^{-7}$	3.42		
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	3	$1.79X10^{-3}$	2.71		
		KTSLAPGSGVVTKY		1116.62585	2	$9.20X10^{-4}$	2.60		
		KGPMLLGVKA		830.48044	2	$2.17X10^{-1}$	2.53		
784	P49608	Aconitate hydratase	*Cucurbita maxima*			$3.92X10^{-5}$	40.17	7.0	4
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	3	$1.05X10^{-3}$	2.58		
		RSENAVQANMELEFQRN		1781.81229	2	$3.92X10^{-5}$	2.57		
		KTSLAPGSGVVTKY		1116.62585	2	$1.93X10^{-4}$	2.44		
		KGPMLLGVKA		830.48044	2	$2.58X10^{-1}$	2.34		
785	P49608	Aconitate hydratase	*Cucurbita maxima*			$1.33X10^{-7}$	30.20	4.6	3
		RSENAVQANMELEFQRN		1781.81229	2	$1.33X10^{-7}$	4.06		
		KTSLAPGSGVVTKY		1116.62585	2	$2.94X10^{-4}$	2.39		
		KGPMLLGVKA		830.48044	2	$2.01X10^{-2}$	2.31		
786	P49608	Aconitate hydratase	*Cucurbita maxima*			$1.49X10^{-4}$	20.14	4.3	2
		RSENAVQANMELEFQRN		1781.81229	2	$1.49X10^{-4}$	2.77		
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	2	$6.51X10^{-4}$	2.66		
788	P49608	Aconitate hydratase	*Cucurbita maxima*			$1.35X10^{-4}$	30.15	5.5	3
		RSENAVQANMELEFQRN		1781.81229	2	$1.35X10^{-4}$	3.05		
		KGPMLLGVKA		830.48044	2	$3.21X10^{-1}$	2.23		
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	2	$3.15X10^{-3}$	2.08		
790	P49608	Aconitate hydratase	*Cucurbita maxima*			$2.30X10^{-7}$	40.21	7.0	4
		RSENAVQANMELEFQRN		1781.81229	2	$2.30X10^{-7}$	3.64		
		KTSLAPGSGVVTKY		1116.62585	2	$2.79X10^{-5}$	2.49		
		KSAGQDTIVLAGAEYGSGSSRD		1925.91992	2	$1.47X10^{-2}$	2.36		
		KGPMLLGVKA		830.48044	2	$4.72X10^{-1}$	2.18		

	Protein metabolism								
134	O49886	Peptidyl-prolyl cis-trans isomerase	*Lupinus luteus*			4.08×10^{-5}	30.15	16.8	2
		RIVMELYADTTPRT		1424.70899	2	4.08×10^{-5}	3.00		
		RIVMELYADTTPRT		1408.71411	2	1.42×10^{-2}	2.63		
		KTSRPVTIADCGQLS		1504.74242	2	1.02×10^{-3}	2.16		
136	Q40682	Elongation factor 1-δ 2	*Oryza sativa*			8.31×10^{-4}	20.16	8.9	2
		KLDEYLLTRS		1022.55170	2	6.43×10^{-2}	3.11		
		RSYISGYQASKD		1103.53674	2	8.31×10^{-4}	2.41		
247	Q94JX9	Nascent polypeptide-associated complex subunit α-like protein 2	*Arabidopsis thaliana*			4.82×10^{-4}	20.18	13.4	2
		KSPHSETYVIFGEAKI		1564.76416	3	3.79×10^{-3}	3.57		
		KNVLFFISKPDVFKS		1553.87268	2	4.82×10^{-4}	2.11		
259	Q9LS40	CND41, chloroplast nucleoid DNA binding protein-like	*Arabidopsis thaliana*			6.19×10^{-6}	10.13	3.4	1
		KATSFSYCLVDRDSGKS		1705.78501	2	6.19×10^{-6}	2.51		
291	O49886	Peptidyl-prolyl cis-trans isomerase	*Lupinus luteus*			6.42×10^{-5}	40.16	22.7	3
		KTSRPVTIADCGQLS		1504.74242	2	6.42×10^{-5}	3.21		
		RIVMELYADTTPRT		1424.70899	2	2.34×10^{-3}	3.11		
		RIVMELYADTTPRT		1408.71411	2	8.94×10^{-4}	2.85		
		KFADENFIKR		983.48328	2	1.92×10^{-1}	2.45		
332	Q3HVM0	Proteasome subunit α type	*Solanum tuberosum*			9.01×10^{-4}	20.16	11.3	2
		KAAAIGANNQAAQSILKQ		1540.84424	3	1.16×10^{-2}	3.16		
		KDGVVLVGEKK		915.51459	2	9.01×10^{-4}	3.06		
345	A9TVH1	Proteasome subunit α type	*Physcomitrella patens*			1.85×10^{-6}	20.17	11.4	2
		KYIGLLATGMTADAKS		1440.74029	2	1.85×10^{-6}	3.31		
		KAAGITSIGVRG		944.55237	2	1.30×10^{-1}	2.16		
352	A5AXI5	Proteasome subunit α type	*Vitis vinifera*			9.71×10^{-8}	50.23	27.7	5
		RDGPQLYMVEPSGVSYRY		1813.84253	2	9.71×10^{-8}	4.31		
		RHSGMAVAGLAADGRQ		1328.63756	2	4.00×10^{-4}	3.17		
		KAVDNSGTVIGIKC		1173.64734	2	3.71×10^{-3}	3.15		
		RVFQIEYAAKA		1068.57239	2	1.29×10^{-3}	2.68		
		KIIYGVHDEAKD		1144.59973	2	1.18×10^{-3}	2.57		
354	A9TVH1	Proteasome subunit α type	*Physcomitrella patens*			4.10×10^{-8}	10.21	6.5	1
		KYIGLLATGMTADAKS		1440.74029	2	2.46×10^{-5}	4.10		
512	A9PEP6	Predicted protein	*Populus trichocarpa*			1.86×10^{-6}	50.21	14.6	4
		KAFVDSGAQSTIISKS		1423.74268	2	1.86×10^{-6}	4.30		
		RYKGIAHGVGQSEILGRI		1684.91296	3	2.77×10^{-3}	4.25		
		RVGGGEVSVPFLQEKD		1445.76343	2	1.89×10^{-2}	4.14		
		RGIAHGVGQSEILGRI		1393.75464	2	2.96×10^{-4}	3.03		
		KLVELGFGRE		890.50940	2	4.45×10^{-2}	2.24		
513	Q9ZRU6	Elongation factor Tu	*Catharanthus roseus*			7.37×10^{-6}	50.22	21.7	4
		RGSALSALQGTNEEIGRK		1602.80823	2	1.54×10^{-3}	4.48		

		KFPGDEIPIIRG		1156.63611	2	$1.40X10^{-4}$	3.09		
		RTADITGKVELPENVKM		1613.87451	2	$7.37X10^{-6}$	2.54		
		KLMDAVDEYIPDPVRV		1648.78870	2	$4.97X10^{-4}$	2.23		
		RGSALSALQGTNEEIGRKA		1730.90320	2	$2.67X10^{-4}$	2.20		
573	A0FH76	EBP1	*Solanum tuberosum*			$9.96X10^{-5}$	20.15	6.7	1
		KVVLSVSNPDTRV		1186.64258	2	$9.96X10^{-5}$	2.95		
		KIVEGVLSHQMKQ		1256.66673	2	$3.97X10^{-2}$	2.90		
584	Q0DDX2	26S protease regulatory subunit 7	*Oryza sativa*			$7.39X10^{-5}$	40.13	13.4	4
		RSVCTEAGMYAIRA		1373.61880	2	$7.39X10^{-5}$	2.46		
		KGVLCYGPPGTGKT		1205.59832	2	$1.10X10^{-2}$	2.40		
		KTYGLGPYSTSIKK		1286.66272	2	$9.88X10^{-2}$	2.05		
		RFDDGVGGDNEVQRT		1407.61353	2	$4.89X10^{-2}$	2.04		
645	Q6K669	Leucine aminopeptidase 2	*Oryza sativa*			$1.03X10^{-4}$	10.15	2.7	1
		KFDMGGSAAVFGAAKA		1344.62526	2	$1.03X10^{-4}$	2.03		
693	P21239	RuBisCO large subunit-binding protein subunit α	*Brassica napus*			$1.09X10^{-7}$	64.20	15.4	7
		KVGAATETELEDRK		1290.61719	2	$4.83X10^{-6}$	4.02		
		KTNDSAGDGTTTASVLARE		1636.77734	2	$1.09X10^{-7}$	3.98		
		RGYISPQFVTNPEKL		1479.74780	2	$1.18X10^{-6}$	3.55		
		KELSETDSVYDSEKL		1501.65405	2	$4.54X10^{-4}$	3.01		
		KDSTTLIADAASKDELQARI		1904.95593	3	$3.04X10^{-7}$	2.87		
		KVGAATETELEDRKL		1418.71216	2	$3.24X10^{-3}$	2.83		
		KDSTTLIADAASKD		1192.60559	2	$2.99X10^{-2}$	2.58		
694	P21239	RuBisCO large subunit-binding protein subunit α	*Brassica napus*			$4.71X10^{-4}$	26.14	9.0	3
		KDSTTLIADAASKDELQARI		1904.95593	2	$4.71X10^{-4}$	2.80		
		RGYISPQFVTNPEKL		1479.74780	2	$3.06X10^{-3}$	2.56		
		KVGAATETELEDRK		1290.61719	2	$8.42X10^{-3}$	2.34		
699	Q940P8	Putative uncharacterized protein	*Arabidopsis thaliana*			$2.47X10^{-4}$	30.20	8.2	3
		RVDEIITCAPRR		1173.59323	2	$2.80X10^{-4}$	3.58		
		RGASHHVLDEAERS		1320.62915	3	$2.47X10^{-4}$	3.36		
		RMASFVGAMAISDLVKS		1555.78586	2	$1.06X10^{-3}$	2.53		
701	P21239	RuBisCO large subunit-binding protein subunit α	*Brassica napus*			$8.30X10^{-8}$	74.20	15.6	8
		KTNDSAGDGTTTASVLARE		1636.77734	2	$8.30X10^{-8}$	4.03		
		RGYISPQFVTNPEKL		1479.74780	2	$2.78X10^{-6}$	3.98		
		KDSTTLIADAASKDELQARI		1904.95593	3	$1.54X10^{-7}$	3.82		
		KVGAATETELEDRK		1290.61719	2	$1.76X10^{-6}$	3.80		
		KELSETDSVYDSEKL		1501.65405	2	$4.99X10^{-5}$	3.02		
		KKELSETDSVYDSEKL		1629.74902	3	$3.00X10^{-2}$	2.98		
		KVGAATETELEDRKL		1418.71216	2	$9.83X10^{-5}$	2.71		
		KDSTTLIADAASKD		1192.60559	2	$4.92X10^{-2}$	2.19		
705	Q93ZM7	Chaperonin CPN60-like 2	*Arabidopsis thaliana*			$6.91X10^{-5}$	30.19	6.3	3
		KSVAAGVNVMDLRV		1247.64125	2	$6.91X10^{-5}$	3.70		
		RVTDALNATRA		960.51086	2	$1.40X10^{-3}$	2.57		
		KLSGGVAVFKV		877.51416	2	$2.06X10^{-3}$	2.26		
707	Q05045	Chaperonin CPN60-1	*Cucurbita maxima*			$3.95X10^{-5}$	124.23	22.4	11

		KIGGASEAEVGEKK		1146.56372	2	$3.95X10^{-5}$	4.51		
		KGVEDLADAVKV		1016.52588	2	$1.28X10^{-2}$	3.16		
		KAAVEEGIVPGGGVALLYASKE		1901.03784	3	$6.29X10^{-2}$	2.97		
		KIGVQIIQNALKT		1196.73608	2	$8.87X10^{-3}$	2.78		
		KLLEQDDPDLGYDAAKG		1662.78577	2	$1.00X10^{-4}$	2.52		
		KEGVITISDGKT		1018.54150	2	$1.32X10^{-2}$	2.48		
		RVTDALNATKA		932.50476	2	$3.17X10^{-3}$	2.45		
		KDDTVILDGAGDKKA		1346.67981	2	$1.30X10^{-1}$	2.27		
		KIGGASEAEVGEKKD		1274.65869	2	$1.03X10^{-3}$	2.16		
		KSVASGMNAMDLRR		1267.57693	2	$7.30X10^{-2}$	2.15		
		KDRVTDALNATKA		1203.63281	2	$1.07X10^{-1}$	2.15		
		KSVASGMNAMDLRR		1283.57185	2	$1.37X10^{-1}$	2.10		
		KSVASGMNAMDLRR		1251.58203	2	$1.27X10^{-2}$	2.01		
710	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*			$5.73X10^{-7}$	40.19	10.2	4
		KYEDLMAAGIIDPTKV		1552.75634	2	$5.73X10^{-7}$	3.80		
		KLADLVGVTLGPKG		1182.70923	2	$1.00X10^{-4}$	3.40		
		REVELEDPVENIGAKL		1541.76929	2	$3.81X10^{-3}$	3.19		
		KVVAAGANPVLITRG		1280.76855	2	$1.43X10^{-3}$	2.20		
713	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*			$8.09X10^{-5}$	30.17	7.5	3
		REVELEDPVENIGAKL		1541.76929	2	$6.86X10^{-3}$	3.39		
		KLADLVGVTLGPKG		1182.70923	2	$8.09X10^{-5}$	3.15		
		KVVAAGANPVLITRG		1280.76855	2	$3.35X10^{-4}$	2.99		
715	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*			$3.69X10^{-4}$	40.17	10.2	4
		REVELEDPVENIGAKL		1541.76929	2	$1.23X10^{-2}$	2.91		
		KLADLVGVTLGPKG		1182.70923	2	$1.73X10^{-3}$	2.77		
		KVVAAGANPVLITRG		1280.76855	2	$1.82X10^{-3}$	2.48		
		KYEDLMAAGIIDPTKV		1552.75634	2	$3.69X10^{-4}$	2.35		
716	P21240	RuBisCO large subunit-binding protein subunit β	*Arabidopsis thaliana*			$2.54X10^{-5}$	40.15	9.7	4
		KLADLVGVTLGPKG		1182.70923	2	$2.54X10^{-5}$	2.94		
		KYEDLMAAGIIDPTKV		1552.75634	2	$6.99X10^{-4}$	2.79		
		REVELEDPVENIGAKL		1541.76929	2	$7.84X10^{-2}$	2.29		
		RKGVVTLEEGKS		1059.60449	2	$2.26X10^{-1}$	2.03		
720	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*			$1.34X10^{-5}$	10.18	3.4	1
		KNSTVVAGGGAIDMEISRY		1692.82212	2	$1.34X10^{-5}$	3.52		
722	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*			$1.03X10^{-4}$	10.16	3.4	1
		KNSTVVAGGGAIDMEISRY		1692.82212	2	$1.03X10^{-4}$	3.11		
725	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*			$6.36X10^{-5}$	10.16	3.4	1
		KNSTVVAGGGAIDMEISRY		1692.82212	2	$6.36X10^{-5}$	3.18		
728	A5BFM5	Putative uncharacterized protein	*Vitis vinifera*			$2.21X10^{-5}$	10.15	3.4	1
		KNSTVVAGGGAIDMEISRY		1692.82212	2	$2.21X10^{-5}$	3.03		
732	Q9M888	Putative uncharacterized protein	*Arabidopsis thaliana*			$2.93X10^{-6}$	40.20	11.2	4

		KEMQIQNPTAIMIART		1647.81929	2	$8.62X10^{-5}$	4.04		
		RLVEGLVLDHGSRH		1294.71143	2	$2.93X10^{-6}$	3.82		
		KTPVVMGDEPDKEILKM		1686.86186	3	$7.93X10^{-3}$	2.55		
		RVLNPNAEVLNKS		1210.67896	2	$2.01X10^{-1}$	2.01		
749	P37900	Heat shock 70 kDa protein	*Pisum sativum*			$7.25X10^{-4}$	36.14	7.4	4
		RIAGLDVQRI		871.49957	2	$9.95X10^{-2}$	2.83		
		KEIEDAVSDLRT		1146.56372	2	$7.25X10^{-4}$	2.82		
		KDVDEVLLVGGMTRV		1419.71481	2	$1.76X10^{-2}$	2.54		
		RTTPSVVAFNQKS		1191.63684	2	$4.13X10^{-2}$	2.03		
750	Q43468	Heat shock protein STI	*Glycine max*			$2.62X10^{-5}$	38.17	9.5	4
		KALELDDEDISYLTNRA		1766.84436	2	$2.62X10^{-5}$	3.32		
		KLGAMPEGLKDAEKC		1374.69334	3	$9.81X10^{-3}$	3.30		
		KELEQQEYFDPKL		1425.65320	2	$1.34X10^{-3}$	2.22		
		RAAVYLEMGKF		997.50229	2	$8.22X10^{-3}$	2.10		
755	P37900	Heat shock 70 kDa protein	*Pisum sativum*			$2.93X10^{-6}$	40.19	8.7	4
		RIINEPTAAALSYGMNNKE		1822.90038	2	$2.93X10^{-6}$	3.60		
		KDVDEVLLVGGMTRV		1419.71481	2	$1.06X10^{-3}$	2.87		
		RTTPSVVAFNQKS		1191.63684	2	$1.64X10^{-3}$	2.80		
		KEIEDAVSDLRT		1146.56372	2	$5.59X10^{-3}$	2.72		
760	P11143	Heat shock 70 kDa protein	*Zea mays*			$8.73X10^{-6}$	10.16	2.0	1
		KNALENYAYNMRN		1374.61068	2	$8.73X10^{-6}$	3.24		
762	Q39043	Luminal-binding protein 2	*Arabidopsis thaliana*			$2.78X10^{-7}$	50.18	9.0	5
		KDAGVIAGLNVARI		1155.64807	2	$1.59X10^{-4}$	3.30		
		RARFEELNNDLFRK		1523.76013	2	$2.78X10^{-7}$	2.76		
		KVFSPEEISAMILTKM		1580.82402	2	$3.59X10^{-3}$	2.56		
		RFEELNNDLFRK		1296.62195	2	$3.51X10^{-2}$	2.31		
		KNGHVEIIANDQGNRI		1536.75134	2	$2.59X10^{-4}$	2.25		
763	Q39043	Luminal-binding protein 2	*Arabidopsis thaliana*			$1.71X10^{-4}$	58.21	12.9	7
		RARFEELNNDLFRK		1523.76013	3	$1.03X10^{-2}$	4.20		
		KDAGVIAGLNVARI		1155.64807	2	$1.71X10^{-4}$	3.94		
		KNGHVEIIANDQGNRI		1536.75134	3	$5.45X10^{-4}$	3.91		
		RFEELNNDLFRK		1296.62195	2	$1.54X10^{-3}$	3.33		
		KSQIDEIVLVGGSTRI		1473.79077	2	$8.76X10^{-3}$	2.81		
		KEAEEFAEEDKKV		1324.59033	2	$3.20X10^{-3}$	2.15		
		KFDLTGVPPAPRG		1169.63135	2	$7.02X10^{-2}$	2.10		
791	Q9LZF6	Cell division control protein 48 homolog E	*Arabidopsis thaliana*			$1.28X10^{-6}$	50.18	6.8	5
		KYQAFAQTLQQSRG		1440.72302	2	$2.55X10^{-2}$	3.54		
		KYTQGFSGADITEICQRA		1845.84359	2	$1.28X10^{-6}$	2.87		
		RKYQAFAQTLQQSRG		1568.81799	2	$3.94X10^{-4}$	2.84		
		KLAEDVDLERI		1059.53174	2	$1.14X10^{-2}$	2.68		
		KDFSTAILERK		1051.54187	2	$1.25X10^{-1}$	2.33		
795	O23755	Elongation factor 2	*Beta vulgaris*			$1.46X10^{-4}$	50.15	8.1	5
		KDLQDDFMGGAEIIKS		1567.73085	2	$2.69X10^{-3}$	2.97		
		RGFVQFCYEPIKQ		1387.67148	2	$5.67X10^{-2}$	2.51		

		RIMGPNYVPGEKKD		1348.69295	2	$6.45X10^{-2}$	2.38		
		RVFYASQLTAKPRL		1380.76343	2	$1.46X10^{-4}$	2.18		
		RIRPVLTVNKM		1039.66223	2	$2.13X10^{-2}$	2.09		
799	O23755	Elongation factor 2	*Beta vulgaris*			$8.19X10^{-4}$	30.14	3.3	3
		RRVFYASQLTAKPRL		1536.86450	3	$8.19X10^{-4}$	2.87		
		RVFYASQLTAKPRL		1380.76343	2	$5.07X10^{-3}$	2.49		
		RGFVQFCYEPIKQ		1387.67148	2	$1.33X10^{-2}$	2.23		
	Defence response								
233	P52779	Protein LlR18B	*Lupinus luteus*			$1.93X10^{-5}$	50.16	29.5	5
		KFHTKGDVLSDAVRE		1444.75427	3	$5.84X10^{-2}$	3.22		
		KGDVLSDAVREEAKA		1388.70154	2	$2.71X10^{-2}$	2.74		
		KLLSGPDGGSIGKI		1100.59460	2	$1.93X10^{-5}$	2.73		
		KGDVLSDAVRE		931.48431	2	$4.57X10^{-2}$	2.67		
		KAVEGYVLANPNY		1309.64233	2	$2.89X10^{-5}$	2.52		
234	Q93XI0	Pathogenesis-related 10	*Lupinus albus*			$5.74X10^{-6}$	86.28	51.9	9
		KAIENYLSAHPEYN		1520.70154	2	$2.13X10^{-7}$	3.89		
		KLVEGVNGGSIGKV		1129.62122	2	$6.04X10^{-6}$	3.59		
		KKLTLIEGGETKY		1188.68347	2	$4.39X10^{-4}$	3.49		
		KALVKDADTIIPKA		1283.75696	2	$5.74X10^{-6}$	3.45		
		KAVEAIQSVETVEGNGGPGTIKK		2056.05566	2	$8.19X10^{-6}$	3.39		
		KAVEAIQSVETVEGNGGPGTIKKL		2184.15063	3	$6.14X10^{-3}$	3.19		
		KLTLIEGGETKY		1060.58850	2	$2.46X10^{-4}$	2.87		
		KVRGDAFFKA		939.50470	2	$6.36X10^{-2}$	2.32		
		KDADTIIPKA		872.47235	2	$1.01X10^{-1}$	2.23		
276	Q93XI0	Pathogenesis-related 10	*Lupinus albus*			$1.45X10^{-6}$	56.25	44.3	6
		KAVEAIQSVETVEGNGGPGTIKK		2056.05566	3	$1.45X10^{-6}$	5.03		
		KAIENYLSAHPEYN		1520.70154	2	$4.02X10^{-6}$	3.44		
		KLVEGVNGGSIGKV		1129.62122	2	$1.99X10^{-5}$	3.44		
		KLTLIEGGETKY		1060.58850	2	$1.15X10^{-3}$	2.98		
		KKLTLIEGGETKY		1188.68347	2	$8.54X10^{-3}$	2.61		
		KDADTIIPKA		872.47235	2	$1.78X10^{-1}$	2.34		
287	Q93XI0	Pathogenesis-related 10	*Lupinus albus*			$4.84X10^{-5}$	50.16	34.8	5
		KAIENYLSAHPEYN		1520.70154	2	$4.84X10^{-5}$	2.75		
		KLVEGVNGGSIGKV		1129.62122	2	$4.16X10^{-2}$	2.67		
		KLTLIEGGETKY		1060.58850	2	$1.06X10^{-1}$	2.52		
		KKLTLIEGGETKY		1188.68347	2	$3.58X10^{-2}$	2.43		
		KALVKDADTIIPKA		1283.75696	2	$2.44X10^{-1}$	2.31		
318	Q0PN10	Glutathione S-transferase	*Caragana korshinskii*			$7.49X10^{-5}$	18.16	6.4	1
		KSPLLPSDPYQRA		1272.65833	3	$1.68X10^{-1}$	2.78		
		KGIKYEYKEEDLRN		1542.77991	2	$7.49X10^{-5}$	2.78		
327	Q9SXM5	Acidic chitinase	*Glycine max*			$6.51X10^{-4}$	20.17	3.7	1
		KYGGVMLWNRF		1095.54041	2	$6.51X10^{-4}$	3.31		
		KYGGVMLWNRF		1111.53533	2	$8.37X10^{-3}$	3.24		
430	P23535	Glucan endo-1,3-β-glucosidase, basic isoform	*Phaseolus vulgaris*			$5.46X10^{-5}$	20.12	8.9	2

		RNVLNFWPSVKI		1203.65210	2	$3.73X10^{-2}$	2.49		
		RDISLPYALFTSPNVVVRD		1891.03235	2	$5.46X10^{-5}$	2.47		
	Transcription								
314	Q5EI63	Quinone reductase 2	*Triticum monococcum*			$8.81X10^{-4}$	10.14	6.4	1
		KAFFDATGGLWRE		1240.61096	2	$8.81X10^{-4}$	2.13		
	Amino acids metabolism								
393	A3RM06	Cysteine synthase	*Glycine max*			$2.34X10^{-4}$	10.15	4.6	1
		RAFGAEVYLTDPAKG		1381.69983	2	$2.34X10^{-4}$	2.74		
520	P54260	Aminomethyltransferase	*Solanum tuberosum*			$1.15X10^{-5}$	20.16	6.9	2
		RVGFFSSGPPPRS		1147.58948	2	$1.15X10^{-5}$	3.15		
		RAEGGFLGAEVILKQ		1303.72559	2	$5.69X10^{-2}$	2.62		
521	Q40108	Aspartate aminotransferase	*Lupinus angustifolius*			$1.60X10^{-6}$	88.22	22.4	8
		KLIFGADSPAIQENRV		1530.79114	2	$9.27X10^{-6}$	4.46		
		RNKEYLPIVGVADFNKL		1706.91125	3	$3.77X10^{-3}$	4.03		
		RRVEQQLVNEASRN		1428.75537	2	$1.60X10^{-6}$	3.77		
		RVGALSIVSKS		873.54041	2	$1.08X10^{-3}$	3.35		
		KEYHIYLTSDGRI		1353.64331	2	$1.20X10^{-3}$	3.17		
		RVEQQLVNEASRN		1272.65430	2	$4.28X10^{-3}$	2.83		
		RTEEGKPLVLNVVRR		1453.83728	3	$6.46X10^{-4}$	2.62		
		RVTTVQCLSGTGSLRV		1478.76315	2	$2.44X10^{-2}$	2.44		
		RQQLFDALQSRG		1205.62732	2	$5.28X10^{-3}$	2.13		
616	Q9SP37	Adenosylhomocysteinase	*Lupinus luteus*			$1.42X10^{-6}$	20.16	5.6	2
		RVVGVSEETTTGVKR		1305.68970	2	$1.42X10^{-6}$	3.25		
		RSEFGPSQPFKG		1123.54187	2	$6.37X10^{-4}$	2.27		
773	P93263	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	*Mesembryanthemum crystallinum*			$5.10X10^{-5}$	48.17	8.9	5
		KYLFAGVVDGRN		1096.57861	2	$5.10X10^{-5}$	3.32		
		KAGINVIQIDEAALRE		1482.82751	2	$5.23X10^{-5}$	3.09		
		RIPPTEELADRI		1140.58948	2	$6.20X10^{-4}$	2.62		
		KFALESFWDGKS		1199.57312	2	$4.81X10^{-2}$	2.17		
		KYGAGIGPGVYDIHSPRI		1658.82849	2	$3.35X10^{-3}$	2.05		
776	P93263	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	*Mesembryanthemum crystallinum*			$1.90X10^{-5}$	20.20	3.9	2
		KYGAGIGPGVYDIHSPRI		1658.82849	2	$1.90X10^{-5}$	2.96		
		KYLFAGVVDGRN		1096.57861	2	$7.67X10^{-4}$	2.79		
778	P93263	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	*Mesembryanthemum crystallinum*			$1.81X10^{-4}$	48.17	8.9	5
		KYLFAGVVDGRN		1096.57861	2	$1.81X10^{-4}$	3.34		
		KYGAGIGPGVYDIHSPRI		1658.82849	2	$5.52X10^{-2}$	2.93		
		KAGINVIQIDEAALRE		1482.82751	2	$1.83X10^{-2}$	2.61		
		KFALESFWDGKS		1199.57312	2	$4.92X10^{-3}$	2.17		
		KISEEEYVKA		996.48840	2	$1.68X10^{-1}$	2.01		
	Cell wall metabolism								

267	P34105	NADP-dependent malic enzyme	*Populus trichocarpa*			4.15X10^{-6}	20.18	5.1	2
		KAIFASGSPFDPVEYEGKV		1813.86426	2	4.15X10^{-6}	3.51		
		KAYELGLATRL		993.53638	2	1.82X10^{-1}	2.30		
518	Q93VR3	GDP-mannose 3,5-epimerase	*Arabidopsis thaliana*			7.72X10^{-4}	30.13	9.0	3
		KHYNKDFGIECRI		1438.65321	3	2.47X10^{-3}	2.50		
		RFEMWGDGLQTRS		1355.60486	2	7.72X10^{-4}	2.25		
		KLATEELCKH		963.48156	2	9.30X10^{-2}	2.03		
673	Q96558	UDP-glucose 6-dehydrogenase	*Glycine max*			2.00X10^{-5}	18.18	6.0	2
		KAADLTYWESAARM		1353.64331	2	2.00X10^{-5}	3.57		
		RILTTNLWSAELSKL		1475.81042	2	3.07X10^{-4}	2.78		
734	A9PGL9	Malic enzyme	*Populus trichocarpa*			1.36X10^{-6}	10.18	3.4	1
		KAIKPTVLIGTSGVGKT		1440.87842	2	1.36X10^{-6}	3.58		
745	P34105	NADP-dependent malic enzyme	*Populus trichocarpa*			6.88X10^{-6}	20.16	4.2	2
		KAYELGLATRL		993.53638	2	4.03X10^{-3}	3.23		
		KSIQVIVVTDGERI		1315.72156	2	6.88X10^{-6}	2.75		
747	P34105	NADP-dependent malic enzyme	*Populus trichocarpa*			1.13X10^{-5}	20.17	4.2	2
		KSIQVIVVTDGERI		1315.72156		1.13X10^{-5}	3.38		
		KAYELGLATRL		993.53638		2.57X10^{-3}	3.13		
	Cytoskeleton biosynthesis								
182	Q1G0Z1	Putative spindle disassembly related protein CDC48	*Nicotiana tabacum*			2.11X10^{-5}	60.19	8.5	5
		REDENRLDEIGYDDVGGVRK		2050.93115	3	1.20X10^{-4}	3.58		
		RGILLYGPPGSGKT		1158.65173	2	2.11X10^{-5}	3.38		
		KYQAFAQTLQQSRG		1440.72302	2	8.68X10^{-4}	3.24		
		RKYQAFAQTLQQSRG		1568.81799	3	4.52X10^{-2}	2.67		
		KYTQGFSGADITEICQRA		1845.84359	2	2.62X10^{-2}	2.27		
		RLGDVVSVHQCPDVKY		1552.77880	2	4.86X10^{-2}	2.11		
183	Q1G0Z1	Putative spindle disassembly related protein CDC48	*Nicotiana tabacum*			1.26X10^{-4}	40.19	7.8	3
		REDENRLDEIGYDDVGGVRK		2050.93115	3	5.51X10^{-2}	3.80		
		RLVVDEAINDDNSVVALHPDTMEKL		2540.21847	3	1.76X10^{-3}	3.10		
		KYTQGFSGADITEICQRA		1845.84359	2	1.26X10^{-4}	2.40		
		RGILLYGPPGSGKT		1158.65173	2	8.07X10^{-2}	2.15		
207	P20363	α-3/ α-5 tubulin chain	*Arabidopsis thaliana*			5.35X10^{-4}	24.16	11.6	3
		RAVCMISNNTAVAEVFSRI		1884.89424	3	4.94X10^{-3}	2.90		
		RSLDIERPTYTNLNRL		1691.87109	3	5.35X10^{-4}	2.74		
		RAVFVDLEPTVIDEVRT		1701.90576	2	1.38X10^{-3}	2.40		
262	Q9STD0	β-tubulin	*Zinnia elegans*			2.65X10^{-4}	8.14	3.8	1
		RAVLMDLEPGTMDSIRS		1679.79788	2	2.65X10^{-4}	2.79		
		RAVLMDLEPGTMDSIRS		1679.79788	2	8.20X10^{-2}	2.11		
331	P41916	GTP-binding nuclear protein Ran-1	*Arabidopsis thaliana*			5.02X10^{-6}	18.14	11.3	2
		KNLQYYEISAKS		1228.62085	2	7.36X10^{-3}	2.83		
		RFYCWDTAGQEKF		1404.58888	2	5.02X10^{-6}	2.74		

336	P41916	GTP-binding nuclear protein Ran-1	*Arabidopsis thaliana*			$9.79X10^{-5}$	18.13	11.3	2
		KNLQYYEISAKS		1228.62085	2	$1.75X10^{-3}$	2.50		
		RFYCWDTAGQEKF		1404.58888	2	$9.79X10^{-5}$	2.32		
	Other metabolic processes								
391	Q8LQJ6	Ethylene-responsive protein 2-like	*Oryza sativa*			$5.51X10^{-4}$	8.12	12.4	1
		RIAAPYDLVMQTKQ		1365.70826	2	$5.51X10^{-4}$	2.09		
574	Q7M1Z8	Globulin-2	*Zea mays*			$6.36X10^{-5}$	70.17	18.9	7
		KQSKGEITTASEEQIRE		1676.84497	3	$4.49X10^{-2}$	3.34		
		KVFLAGTNSALQKM		1248.69470	2	$2.48X10^{-1}$	3.16		
		RVVMLLSPVVSTSGRF		1460.81413	2	$6.36X10^{-5}$	2.90		
		KGEITTASEEQIRE		1333.65942	2	$2.81X10^{-3}$	2.88		
		RVAELEAAPRA		955.52069	2	$3.85X10^{-4}$	2.83		
		KEGEGVIVLLRG		1084.63611	2	$3.19X10^{-1}$	2.27		
		RLLDMDVGLANIARG		1416.75153	2	$9.92X10^{-3}$	2.19		
596	P19595	UTP-glucose-1-phosphate uridylyltransferase	*Solanum tuberosum*			$5.83X10^{-6}$	20.19	6.3	2
		KSAVAGLNQISENEKS		1459.73877	2	$5.83X10^{-6}$	3.79		
		KLEIPDGAVIANKD		1239.69434	2	$2.80X10^{-4}$	2.43		
682	P15590	Globulin-1 S allele	*Zea mays*			$1.88X10^{-5}$	20.17	4.7	2
		KAEEVDEVLGSRR		1203.58521	2	$1.88X10^{-5}$	3.42		
		KVFLAGADNVLQKL		1274.71033	2	$2.22X10^{-3}$	2.67		
768	Q7SIC9	Transketolase	*Zea mays*			$5.82X10^{-6}$	20.18	4.1	2
		KVTTTIGFGSPNKA		1221.64734	2	$9.35X10^{-5}$	3.59		
		KANSYSVHGSALGAKE		1361.68079	2	$5.82X10^{-6}$	2.25		
769	Q7SIC9	Transketolase	*Zea mays*			$8.39X10^{-5}$	20.18	3.4	2
		KVTTTIGFGSPNKA		1221.64734	2	$8.39X10^{-5}$	2.42		
		KNPYWFNRD		996.46863	2	$2.23X10^{-2}$	2.35		
770	Q7SIC9	Transketolase	*Zea mays*			$8.77X10^{-5}$	10.16	2.1	1
		KVTTTIGFGSPNKA		1221.64734	2	$8.77X10^{-5}$	3.25		
	Unknown biological processes								
141	Q8LPE5	Fructokinase-like protein	*Cicer arietinum*			$1.82X10^{-5}$	40.15	22.3	4
		KFANACGAITTTKK		1254.61470	2	$1.04X10^{-2}$	2.97		
		KIVDDQSILEDEARL		1502.73328	2	$4.79X10^{-5}$	2.88		
		RTALAFVTLRA		991.59351	2	$2.82X10^{-3}$	2.70		
		RLPLWPSPEEARN		1294.67896	2	$1.82X10^{-5}$	2.63		
237	Q9M328	Putative uncharacterized protein T18D1290	*Arabidopsis thaliana*			$2.81X10^{-4}$	14.15	6.9	1
		KLDSIVMGSRG		977.50842	2	$2.81X10^{-4}$	3.00		
		KLYWGDARQ		880.43115	2	$5.56X10^{-2}$	2.01		
246	Q8GYY8	Putative germin	*Arabidopsis thaliana*			$1.17X10^{-5}$	18.21	12.3	2

		RIDYAPGGLNPPHTHPRA		1741.87683	2	1.17X10^{-5}	3.26		
		RGLVHFQKN		828.47266	2	8.36X10^{-2}	2.31		
353	Q2V987	Transcription factor APFI-like	*Solanum tuberosum*			1.76X10^{-4}	30.19	10.1	2
		KNAMVAAGALVRQ		1088.58809	2	7.06X10^{-3}	3.70		
		KDEEYDSMLGVVRE		1428.63114	2	1.76X10^{-4}	3.16		
		KNAMVAAGALVRQ		1072.59314	2	1.35X10^{-3}	2.99		
384	Q9SMK5	Plasma membrane intrinsic polypeptide	*Cicer arietinum*			4.64X10^{-4}	10.12	5.8	1
		KVSTFIVTEEKV		1152.61462	2	4.64X10^{-4}	2.43		
549	A5CB20	Putative uncharacterized protein	*Vitis vinifera*			1.22X10^{-4}	18.20	3.6	1
		KAGGVCIADEVQTGFGRT		1636.77478	2	1.22X10^{-4}	4.03		
		RHDIIGDVRG		924.48975	2	1.21X10^{-2}	2.97		
671	Q7XCL2	Ubiquitin domain containing protein	*Oryza sativa*			2.51X10^{-4}	10.12	3.1	1
		RAMSNIESSPEGFNMLRR		1814.80476	2	2.51X10^{-4}	2.38		
678	Q94IC1	Betaine aldehyde dehydrogenase	*Hordeum vulgare*			2.55X10^{-5}	10.13	2.8	1
		RLGPVVSEGQYEKI		1305.66846	2	2.55X10^{-5}	2.63		

[a] Spot numbers are corresponding to the numbers in Figure 4.
[b] Protein identification according to the UniProt database (http://www.uniprot.org)
[c] Probability of a false identification (P)
[d] Cross-correlation score (Xcorr)