

The Proteome of Seed Development in the Model Legume *Lotus japonicus*^{1[C][W]}

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We have characterized the development of seeds in the model legume *Lotus japonicus*. Like soybean (*Glycine max*) and pea (*Pisum sativum*), *Lotus* develops straight seed pods and each pod contains approximately 20 seeds that reach maturity within 40 days. Histological sections show the characteristic three developmental phases of legume seeds and the presence of embryo, endosperm, and seed coat in desiccated seeds. Furthermore, protein, oil, starch, phytic acid, and ash contents were determined, and this indicates that the composition of mature *Lotus* seed is more similar to soybean than to pea. In a first attempt to determine the seed proteome, both a two-dimensional polyacrylamide gel electrophoresis approach and a gel-based liquid chromatography-mass spectrometry approach were used. Globulins were analyzed by two-dimensional polyacrylamide gel electrophoresis, and five legumins, LLP1 to LLP5, and two convicilins, LCP1 and LCP2, were identified by matrix-assisted laser desorption/ionization quadrupole/time-of-flight mass spectrometry. For two distinct developmental phases, seed filling and desiccation, a gel-based liquid chromatography-mass spectrometry approach was used, and 665 and 181 unique proteins corresponding to gene accession numbers were identified for the two phases, respectively. All of the proteome data, including the experimental data and mass spectrometry spectra peaks, were collected in a database that is available to the scientific community via a Web interface (<http://www.cbs.dtu.dk/cgi-bin/lotus/db.cgi>). This database establishes the basis for relating physiology, biochemistry, and regulation of seed development in *Lotus*. Together with a new Web interface (<http://bioinfoserver.rsbs.anu.edu.au/utis/PathExpress4legumes/>) collecting all protein identifications for *Lotus*, *Medicago*, and soybean seed proteomes, this database is a valuable resource for comparative seed proteomics and pathway analysis within and beyond the legume family.

Legumes constitute the third largest plant family and are an important source of food, feed, and natural compounds of industrial importance. Most legumes possess the ability to form symbiosis with both nitrogen-fixing rhizobia and phosphate-retrieving mycorrhiza, which makes the legumes very useful in pastures and for soil improvement schemes (Graham

and Vance, 2003). The crop legumes account for 27% of the world's primary agricultural crop production, with grain legumes contributing 33% of daily protein nitrogen intake of humans (Graham and Vance, 2003). Legume seed proteins are rich in Lys, complementing the nutritional profiles of cereals and tubers in the diet, but are low in sulfur-containing amino acids (Duranti and Gius, 1997).

Most of the stored nitrogen and sulfur and some of the carbon is found in the protein fraction, mainly in the storage proteins. These proteins accumulate in protein bodies in the cotyledonary parenchyma cells until they undergo hydrolysis upon germination (Tabe et al., 2002). Storage proteins are synthesized on the rough endoplasmic reticulum, and a signal peptide guides transport to the endoplasmic reticulum (zur Nieden et al., 1984). Storage proteins are devoid of catalytic activity and play no structural role in the tissue. Apart from proteins, carbon is stored in lipids

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and starch. The levels of protein, lipids, and starch vary between legume species. Soybean (*Glycine max*) and peanut (*Arachis hypogaea*) are oil crops, whereas beans (*Phaseolus vulgaris*), lentils (*Lens culinaris*), peas (*Pisum sativum*), and chickpeas (*Cicer arietinum*) are major staple foods (Domoney et al., 2006).

A typical mature legume seed consist mainly of the embryo. Seed development proceeds through three distinct phases: histodifferentiation, seed filling, and desiccation. Growth of the embryo is characterized by cell division in the histodifferentiation phase and by cell enlargement in the seed-filling phase. Histodifferentiation can be further divided into two phases, where cell division is confined to endosperm and seed coat in the first phase and to the embryo in the second phase (Wang and Hedley, 1993). The endosperm first develops into a syncytium and then cellularizes. The mitotic activity of the seed in the cell division phase has been proposed to be controlled by hormones, environmental factors, and carbon and nitrogen supply (Egli et al., 1989; Munier-Jolain and Ney, 1998; Ozga et al., 2002). During the cell enlargement (seed-filling) phase, seed nitrogen accumulation and protein composition depend on both symbiotic N₂ fixation and nitrogen from the soil. Carbon derives mainly from recent photosynthate rather than from remobilized sources (for review, see Domoney et al., 2006).

Proteins involved in cell division are abundant during early stages of seed development, and the level decreases before the accumulation of the major storage proteins during seed filling (Gallardo et al., 2003).

In legumes, the terms “storage protein” and “globulin” have become synonymous, because the large majority of the storage proteins are soluble in high-salt solution but insoluble in water and as such are globulins according to Osborne’s classical definitions (Chittenden et al., 1908). There are two main groups of globulins. They evolved from a common single-domain ancestor and have sedimentation coefficients of 7S and 11S (Shutov et al., 1995). In pea, 7S and 11S globulins are called vicilins and legumins, respectively, and are often referred to as vicilin- and legumin-like globulins in other legumes. Vicilins are trimeric structures consisting of subunits of approximately 50 kD. Some but not all of the approximately 50-kD polypeptides are proteolytically processed at one or both of two cleavage sites. These cleavage sites are not strictly conserved, but processing occurs at the carboxyl side of an Asn residue. A subset of the processed polypeptides may also be glycosylated. Most vicilins lack Cys, so no disulfide bonds are formed. Convicilins (approximately 70 kD) are homologous to vicilin but contain a polar insert and do not appear to be post-translationally processed besides removal of the signal peptide (Higgins and Spencer, 1981).

The legumins are hexamers composed of subunits of 60 to 80 kD. The legumins consist of disulfide bonded subunits formed by proteolytic cleavage of a single polypeptide precursor at an Asn-Gly or alternatively

an Asn-Phe cleavage site into acidic (approximately 40 kD) and basic (approximately 20 kD) polypeptides (March et al., 1988). In contrast to vicilins, the legumins are rarely glycosylated. For a review of legume seed development, see Weber et al. (2005).

Here, we present data on the seed development and protein composition in the model legume *Lotus japonicus*. Based on the newly released genome sequence, we present a detailed catalogue of proteins present in the seeds at two time points during development and a more detailed analysis of the storage proteins. This work will create the basis for relating physiological development to detailed proteome analysis.

RESULTS

Characterization of the Developing *Lotus* Seed

L. japonicus ecotype Gifu (hereafter referred to as *Lotus*) seeds were collected at 3-d intervals between 7 and 43 d after flowering (DAF; Fig. 1). At each developmental stage, fresh and dry weight of the seeds were measured and water content was calculated in order to define the major phases of seed formation and maturation (Fig. 1). In parallel, seeds were fixed, sectioned,

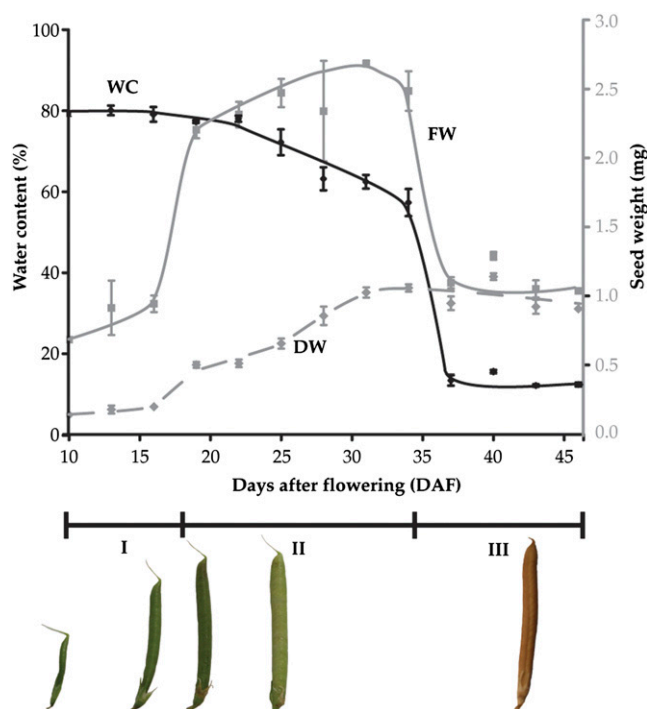


Figure 1. Water content, fresh weight, and dry weight of developing seeds. The graph at top represents the fresh weight (FW; gray line), dry weight (DW; dashed line), and water content (WC; black line) of the developing seeds from 10 to 46 DAF. Error bars represent sd for five replicates. The histodifferentiation (I), seed-filling (II), and desiccation (III) phases are indicated at bottom. Pods representing 7, 16, 19, 25, and 43 DAF are shown.

and stained with toluidine blue to describe the developmental changes at the cellular level (Figs. 2 and 3). The seed weight increased rapidly at 16 to 19 DAF (Fig. 1), and the embryo size also increased dramatically at this stage, indicating the transition from histodifferentiation dominated by cell divisions to seed filling, which is dominated by cell enlargements in the embryo (Fig. 2). The accumulation of storage proteins in the seeds became visible at 25 DAF (Fig. 4). The seed-filling phase ended around 34 DAF, when seeds enter the desiccation phase and dry out (Fig. 1). As expected, the amount of protein in the seeds increased dramatically during seed filling and remained constant in the mature seed (Fig. 4).

At 7 DAF, the embryo in the transition stage occupies only a fraction of the embryo sac, which is filled by the mainly liquid endosperm (Figs. 2 and 3A). At 10 DAF, the embryo is in the heart stage (Figs. 2 and 3B). The embryo is in early torpedo stage at 16 DAF, when the embryo cells are beginning to elongate (Fig. 3C). At 19 DAF, the embryo is in the torpedo stage (Figs. 2 and 3D).

The endosperm has only formed one or two cell layers encircling the embryo sac at 7 DAF (Fig. 3E). Between 7 and 10 DAF, the endosperm cellularizes and fills the embryo sac (Figs. 2 and 3F). The mature seed is high in protein and dominated by the embryo, which takes up most of the embryo sac. In contrast to faba bean (*Vicia faba*) and pea seeds, for example, but like *Medicago*, well-developed endosperm tissue is found in the mature seed (Fig. 3G; Borisjuk et al., 1995, 2002; Abirached-Darmency et al., 2005).

The outer layer of the seed coat consists of one layer of epidermis followed by a layer of hypodermis and several layers of parenchyma cells at 7 DAF (Fig. 3H). At 16 DAF, the epidermis cells are elongated and differentiated almost to macrosclereid cells and hypodermis cells have started to thicken the cell wall (Fig. 3I). At 19 DAF, the seed coat epidermis has differentiated into macrosclereid cells and the hypodermis has differentiated into hourglass-shaped osteosclereid

cells (Fig. 3J). In the seed coat, the macrosclereid cells have become more impenetrable (Ma et al., 2004) and efficiently protect the embryo (Fig. 3K).

Components in Mature *Lotus* Seeds

The main components of legume seeds are starch, protein, and oil. As a prelude to the detailed investigation of proteins involved in seed physiology, biochemistry, and development, the content of these components was determined in mature *Lotus* seed (Table I). In addition, ash and phytic acid contents were determined.

In contrast to peas, in which up to 50% of the dry weight in mature seeds is starch, the mature *Lotus* seeds contained only 0.6% starch. The starch content in *Lotus* is thus more similar to the level found in mature soybean seeds, in which the content varies between 0.19% and 0.91% in different soybean cultivars (Wilson et al., 1978).

The protein content in mature *Lotus* seed is approximately 43% (Table I). For soybean, the protein content is 43.7% (Prakash and Misra, 1988), while the protein level in eight *Medicago* genotypes is between 30% and 40% of the dry weight (Djemel et al., 2005). In contrast, the protein level in pea is between 22% and 26%. Again, *Lotus* is more similar to soybean than to pea.

Lipids constitute approximately 7% of the dry weight of the mature *Lotus* seed. In pea, the lipid content is between 1.4% and 3.3%, while the lipid content in soybean can be higher than 20%. In seven underutilized legumes, the crude lipid content was between 3.77% and 7.04% (Vadivel and Janardhanan, 2000). The fatty acid composition of the lipid fraction was further analyzed (Table II). *Lotus* lipid is composed of approximately 11% C16:0 (palmitate), 4% C18:0 (stearate), and 46% C18:2 (linoleate), which is similar to the values obtained for soybean (Shen et al., 1997). The content of C18:1 (oleate) and C18:3 ω 3 (linolenate) in *Lotus* is approximately 11% and 25%, respectively. For oleate, this is less than half of the level

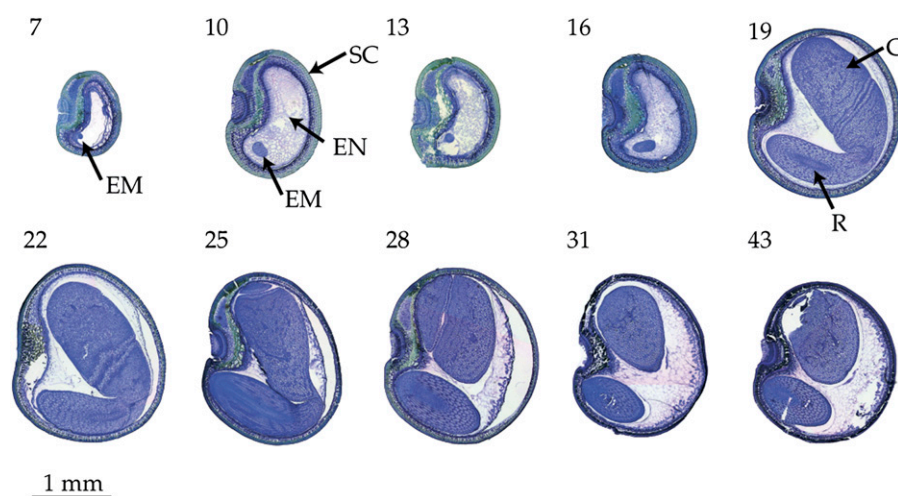


Figure 2. Thin sections of seeds in different developmental stages. The seeds were harvested from 7 to 43 DAF, fixed, sectioned into 5- μ m slices, and stained with toluidine blue. The numbers indicate DAF. The embryo only takes up a small part of the embryo sac at 7 DAF. The endosperm cellularizes between 7 and 10 DAF. Consistent with the increase in fresh weight (Fig. 1), the seed size increases dramatically at 16 to 19 DAF and the embryo expands to occupy most of the seed. This indicates the transition from histodifferentiation to seed filling. At 43 DAF, the seed is mature and desiccated. Some endosperm tissue is still found in the mature seed. C, Cotyledon; EM, embryo; EN, endosperm; R, radicle; SC, seed coat.

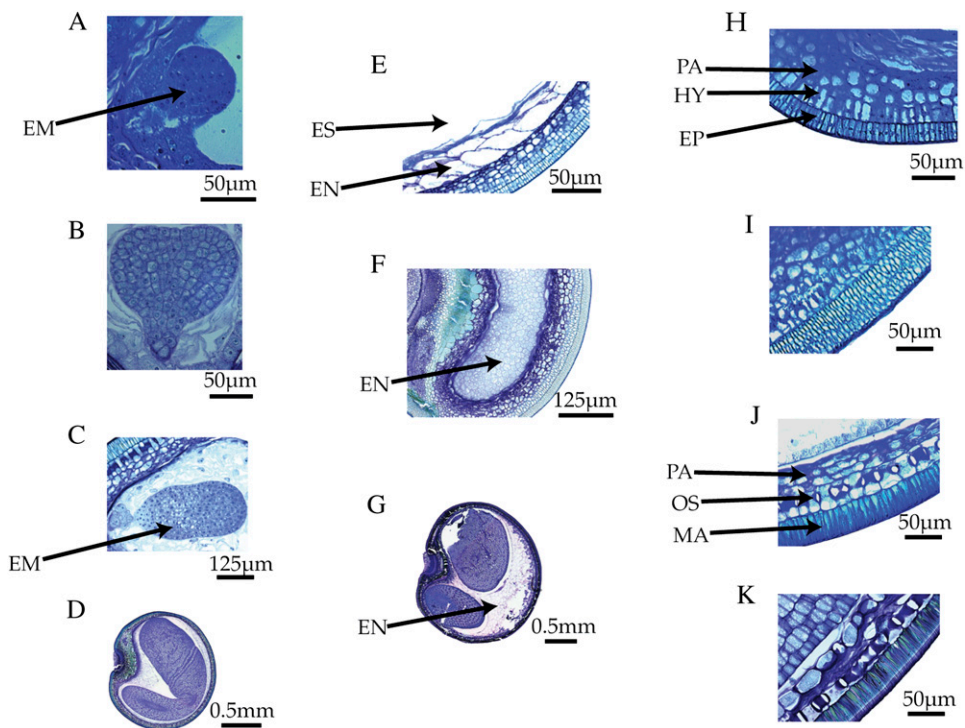


Figure 3. Detailed development of embryo, endosperm, and seed coat. A to D, Thin sections of the embryo at 7, 10, 16, and 22 DAF. At 7 DAF, the embryo is in the transition stage. The embryo (EM) has developed into the heart stage at 10 DAF and close to the torpedo stage at 16 DAF. At 22 DAF, the embryo is in the torpedo stage and the cells are now elongating instead of dividing. E to G, Thin sections showing endosperm tissue at 7, 10, and 43 DAF. The endosperm (EN) has begun to cellularize at 7 DAF and forms one or two cell layers encircling the embryo sac (ES). The endosperm is cellularized at 10 DAF, when it fills the embryo sac. Finally, in the mature seed (43 DAF), the mature embryo occupies most of the embryo sac, but some endosperm tissue is still present. H to K, Thin sections of the seed coat at 7, 16, 19, and 43 DAF. At 7 DAF, the outer layer of the seed coat consists of one layer of epidermis (EP), followed by a layer of hypodermis (HY), and several layers of parenchyma cells (PA). The epidermis cells have elongated and the hypodermis cells have increased their cell wall at 16 DAF. At 19 DAF, the epidermis cells differentiate into macrosclereid (MA) cells and the hypodermis cells differentiate into osteosclereid (OS) cells (hourglass shape). Finally, in the mature seed (43 DAF), the macrosclereid cells have finished differentiation.

in soybean and pea, while the linolenate is more than three times higher in *Lotus*. Compared with *Medicago*, the stearate and linoleate levels are higher in *Lotus*, while the palmitate and oleate levels are lower (Djemel et al., 2005). The relative composition of saturated and unsaturated fatty acid is an important characteristic of

edible oil. Oil with high levels of polyunsaturated fatty acids has nutritional benefits but decreased stability (Liu and White, 1992). Therefore, *Lotus* is a useful model for studying the genetic regulation of pathways responsible for fatty acid synthesis, degradation, and modification, such as desaturation of stearic acid to

Figure 4. Protein profile of seed development. A 5% to 15% gradient SDS-PAGE scan of protein extracted from seeds is shown. The numbers above each lane indicate DAF. Each lane contains protein extracted from 1 mg of seeds (dry weight). Globulins were selectively extracted from mature seeds (43 DAF) and loaded in lane G. The bands that start to show up at 25 DAF and become highly dominant at 43 DAF are in the globulin fraction; indeed, they have been identified as globulins (data not shown).

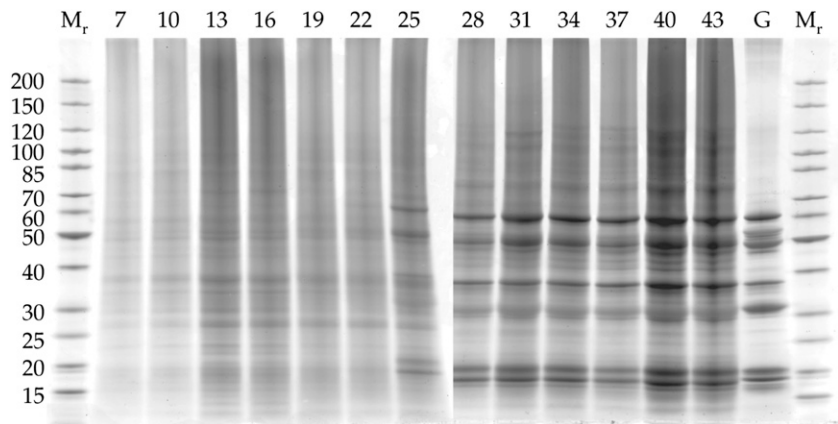


Table I. Components in mature *Lotus* seeds

Compound	Percentage of Dry Matter
Nitrogen	6.89% (approximately 43% protein)
Lipids	6.76%
Starch	0.61%
Phytic acid	0.188%
Ash	4.71%

oleic acid by the plastid stearyl-acyl carrier protein desaturase and establishment of additional double bonds by plastidial and microsomal ω -3 and ω -6 desaturases (Somerville and Browse, 1991). In *Lotus*, the level of ash is approximately 5%. The ash contains both major and minor minerals and an important supply of minerals for food and feed. A chemical analysis of seven different legumes showed ash levels ranging from 3.98% to 6.42% (Vadivel and Janardhanan, 2000).

Characterization of Globulins

Seed globulins were extracted by grinding mature seeds in liquid nitrogen followed by extraction of water-soluble proteins. The supernatant containing soluble proteins was discarded, and the pellet was resuspended in buffer containing 1 M NaCl to dissolve the globulins. Following separation on an isoelectric focusing (IEF) pH 3 to 10 gel in the first dimension and SDS-PAGE in the second dimension, 15 distinct protein spots marked in Figure 5 were analyzed by matrix-assisted laser desorption/ionization quadrupole/time-of-flight mass spectrometry (MALDI-Q-TOF MS; Table III). Between five and 22 peptides were identified for each protein identification, and the MS peptide data were utilized to identify the corresponding gene accession numbers in the *Lotus* genome and the derived protein. For the globulins, a signal peptide was predicted from the corresponding gene model using the TargetP 1.1 software (Emanuelsson et al., 2007). In addition, N-terminal sequences were obtained from 10 of the identified protein spots.

Five *Lotus* legumin storage proteins (LLPs) and two *Lotus* convicilin storage proteins (LCPs) were identified. LLP1, LLP2, LLP3, LCP1, and LCP2 were represented by two spots, whereas LLP4 and LLP5 were represented by one spot on the gel (Figure 5; Table III; Supplemental Figure S1; Supplemental Table S1). Scanning of Coomassie Brilliant Blue-stained spots estimated that LLPs and LCPs contribute approximately 90% and 10% of the total globulins, respectively (data not shown).

The LLP1 precursor in Supplemental Figure S1 was assembled from the C-terminal fragment identified in spot 12 and the N-terminal fragment identified in spot 6. Cleavage at the Asn-Gly-Leu-Glu-Glu-X-X-Cys motif (Supplemental Fig. S1) between Asn-289 and Gly-290 is confirmed by the N-terminal sequence of spot

12. The initial 21 amino acid residues in the LLP1 precursor protein is a signal peptide, and in agreement with this prediction, the N-terminal sequence of spot 6 commences at amino acid residue 22. The C-terminal and N-terminal fragments of the LLP2 and LLP3 precursor proteins were identified in spots 13 and 14 and spots 2 and 1, respectively. Cleavage of LLP2 at Asn-394 and Gly-395 and LLP3 at Asn-425 and Gly-426 was confirmed by the N-terminal sequences of proteins 13 and 14, and signal peptide cleavage was confirmed by the N-terminal sequences of spots 2 and 1, respectively (Supplemental Fig. S1). The processed LLP4 was identified from spot 4. The predicted signal peptide is in agreement with the N-terminal sequence of spot 4. All of the identified peptides are positioned N terminal to the Asn-378 and Ala-379 cleavage site (Supplemental Fig. S1), and the C-terminal fragment of the LLP4 precursor was not found in this study. The processed LLP5 was identified from spot 7, and all of the identified peptides were located N terminal to the Asn-290 and Gly-291 cleavage site (Supplemental Fig. S1).

The criteria used to assign LLP1 to LLP5 as legumins was based on similarity toward globulins from other legume species. LLP1 to LLP5 are 68% to 82% similar to 11S globulins in other legumes. Processing of legumin precursors normally results in a basic protein corresponding to the C-terminal fragment, which was observed for the LLP1 to LLP3 C-terminal proteins in spots 12, 13, and 14 (Fig. 5).

The processed LCP1 was identified from peptides in spots 3 and 15. The predicted signal peptide was not in agreement with the N-terminal sequence of protein 15, which commences from amino acid residue 59 (Supplemental Fig. S1). The most N-terminal peptide identified in spot 3 commences at amino acid residue 9 (Supplemental Fig. S1). This indicated precursor processing rather than signal peptide cleavage. The processed LCP2 was identified from spots 5 and 9. Peptides were identified throughout the precursor protein for spot 5, whereas C-terminal peptides were only identified in spot 9. The criteria used to assign LCP as convicilins was based on similarity toward globulins from other legume species. LCP1 and LCP2 are 79% to 81% similar to 7S globulins in other legumes. 7S globulins are divided into two subgroups: vicilins and convicilins. Convicilins differ from vicilins by an additional intrinsically unstructured sequence rich in polar residues located adjacent to the signal peptide. The additional sequence is often between 99

Table II. Fatty acid analysis in mature *Lotus* seeds

Fatty Acid	Percentage of Fatty Acid
C16:0 (palmitate)	11.3%
C18:0 (stearate)	4.4%
C18:1 (oleate)	10.8%
C18:2 (linoleate)	46.3%
C18:3w3 (linolenate)	24.9%
C20 or more	>1%

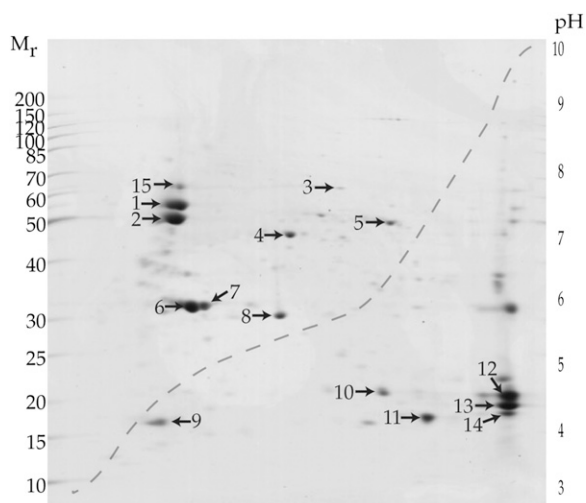


Figure 5. Storage proteins separated by 2-D PAGE. Globulins were extracted from mature seeds (43 DAF) separated on a nonlinear pH 3 to 10 gradient in the first dimension and by 5% to 15% gradient SDS-PAGE in the second dimension. The pH gradient is indicated by the dashed line. The dominant proteins (indicated by arrows) were analyzed (Table III).

and 196 amino acid residues long and increases the average molecular mass of convicilin to approximately 70 kD (Sáenz de Miera et al., 2008). Molecular masses of around 70 kD suggest that LCP1 and LCP2 are convicilins. In addition, a stretch of polar amino acid residues of Gln and Asn is found adjacent to the putative signal peptide.

The remaining spots analyzed were not related to globulins. A lectin was identified in spot 8, with 32% peptide coverage of the precursor protein (Supplemental Fig. S1). A ripening-related protein was identified in spot 11, with 65% peptide coverage. In the gel-based liquid chromatography-mass spectrometry (GeLC-MS/MS) approach (see below), this ripening-related protein was identified as hit 30 in mature seeds. In total for the MALDI and electrospray ionization approaches, 81.5% of spot 11 was covered by peptide identifications. The data obtained for spot 10 did not correspond to any predicted protein.

The Gene Structure of Globulin Genes

The relationship between the proteins and the processing of LLP1 to LLP5 and LCP1 to LCP2 precursor proteins predicted from the protein analysis was further substantiated by determining the structure of the corresponding genes. Sequencing and annotation of the *Lotus* genome was not completed when the gene models used for peptide identification were created. Genome sequences covering approximately 315 Mb of gene space of the *L. japonicus* MG20 ecotype (Sato et al., 2008) were available. To finalize our analysis, unsequenced genome segments and cDNAs were sequenced.

Partial and full-length cDNA sequences corresponding to LLP3 and LLP5 from *Lotus* were obtained by sequencing of EST clones. Alignments toward the genome sequence determined the exon-intron structure shown in Supplemental Figure S2. For LLP5, the exon-intron structure confirmed the gene model predicted by the additional genome sequence obtained by bacterial artificial chromosome sequencing and confirmed the protein sequence shown in Supplemental Figure S1 by adding 178 amino acid residues to the N terminus of the LLP5 protein and one amino acid residue to the C terminus. For LLP3, the partial (346 nucleotides of the 5' end is missing) cDNA sequence from Gifu was not identical with the predicted gene model from the MG20 genome sequence. The *Llp3* gene, therefore, was amplified from Gifu and MG20 and aligned toward the cDNA. This alignment added 32 amino acid residues to the LLP3 protein by removing an intron predicted in the gene model (Supplemental Fig. S1). In addition, five nucleotide mismatches in the exons were identified, corresponding to three amino acid residue differences in LLP3 from Gifu and MG20 (Supplemental Fig. S1).

Alignment of the genome sequence of the *Llp2* genes from the two ecotypes identified 11 nucleotide differences. This resulted in five amino acid residue differences in LLP2 between the two ecotypes (Supplemental Fig. S1).

The *Llp4* gene was completed by additional genome sequencing, and exon-intron predictions were made (Supplemental Fig. S1). The initial Met residue was not predicted in the gene model used for protein identification for LLP4, and in total, 279 amino acid residues were added to the LLP4 protein prediction (Supplemental Fig. S1).

Alignment of a full-length *Lcp1* cDNA from Gifu and MG20 genome sequences confirmed the prediction of exon-intron structure, while alignment of a cDNA lacking the initial 99 nucleotides toward the genome sequence added 27 amino acid residues to the LCP2 protein (Supplemental Fig. S1) by removing a predicted intron. An alignment of *Lcp2* genome sequence of the two ecotypes identified an additional TTC sequence corresponding to Ser-162 in exon 1 of the Gifu sequence (Supplemental Fig. S1).

Combining proteome and genome analysis identification of the LLP and LCP globulins shown in Supplemental Figure S1 was completed, and the corresponding genes were annotated. The LLPs are encoded by genes consisting of three introns except for the *Llp4* gene, which has two introns. The LCP proteins are encoded by genes with five introns.

Large-Scale Protein Identification of Two Developmental Stages

As a first approach toward a full protein profile of the seeds, proteins were extracted from two distinct developmental stages, 16 to 25 DAF (green seeds) and 43 DAF (mature seeds). The proteins were separated

Table III. 2-D-based identifications by MALDI-Q-TOF

Spot ID corresponds to the protein number in Figure 5. The observed M_r and pI values are calculated from the 2-D gel. RRP, Ripening-related protein.

Spot ID	Theoretical M_r /pI	Observed M_r /pI	Protein Identity	Peptides Matched	Sequence Coverage	MOWSE Score	Expected Value	Protein Name
1	66,770/5.43	60,000/4.9	chr5.LjT15N12.20.nc	7	16%	146	1.7e-10	LLP3
2	66,833/5.43	55,000/4.9	chr5.LjT15N12.10.nc	7	16%	85	0.00022	LLP2
3	64,937/6.35	68,000/5.7	chr5.CM0357.580.nc	20	47%	261	5.5e-22	LCP1
4	32,990/6.24	49,000/5.5	LjSGA_091288.1	7	38%	84	0.00028	LLP4
5	65,108/5.84	54,000/6.3	chr5.CM0357.560.nc	22	38%	373	3.5e-33	LCP2
6	54,596/6.32	33,000/5.0	chr1.CM0295.260.nd	8	20%	143	3.5e-10	LLP1
7	33,837/7.96	33,000/5.1	LjSGA_030216.1	6	25%	200	6.9e-16	LLP5
8	30,904/5.73	31,000/5.4	chr5.LjT43D06.110.nd	6	32%	138	1.1e-09	Lectin
9	65,108/5.84	16,000/4.8	chr5.CM0357.560.nc	5	10%	237	1.4e-19	LCP2
11	17,551/5.90	16,000/6.9	chr3.CM0110.130.nc	9	65%	241	5.5e-20	RRP
12	54,596/6.32	20,000/8.1	chr1.CM0295.260.nd	11	33%	232	4.3e-19	LLP1
13	66,833/5.43	18,000/8.1	chr5.LjT15N12.10.nc	5	11%	209	8.7e-17	LLP2
14	66,770/5.43	17,000/8.1	chr5.LjT15N12.20.nc	7	12%	188	1.1e-14	LLP3
15	64,937/6.35	68,000/4.9	chr5.CM0357.580.nc	14	35%	150	6.9e-11	LCP1

by gradient 5% to 15% SDS-PAGE. For each of the two stages, the whole gel lane was cut into approximately 40 slices and subjected to in-gel tryptic digestion, and peptides were identified using a GeLC-MS/MS approach. Two sets of databases, one *Lotus* specific and one containing general protein data, were used for peptide identification. The *Lotus* amino acid (AA) database, the *Lotus* nucleotide (NT) database, and the EST database downloaded from The Institute for Genomic Research (TIGR) belong to one set. The other set consisted of the Swiss-Prot (SPROT) and National Center for Biotechnology Information (NCBI) databases. Individual peptide sequences were verified by inspection of the peptide spectra (see "Materials and Methods" for the criteria used). A total of 665 and 181 protein identifications from green and mature seeds, respectively, corresponded to unique gene accession numbers (Table IV; Supplemental Table S2). Some peptides correspond to more than one gene accession number, either because the accessions represent duplicated genes or gene family members or because all regions of the *Lotus* genome sequence have not been assembled completely. Taking these nonunique protein identifications into account, 920 and 264 proteins were identified from green and mature seeds, respectively, using the *Lotus* AA, NT, and EST contigs (Supplemental Table S2). The overlap between protein identifications from the two developmental stages was assessed by dividing identifications into three subgroups: only green, only mature, and intersection between green and mature seeds. These three subgroups contain 764, 108, and 156 protein identifications, respectively.

For the 920 and 264 protein identifications for green and mature seeds, the molecular process was predicted. Gene Ontology (GO) annotations for the complete set of gene accession numbers from *Lotus* AA, NT, and EST contigs were obtained through a BLAST analysis against UniProt. The subdivisions into classes are

shown in Figure 6. The four dominant molecular processes (primary metabolic process, cellular metabolic process, macromolecule metabolic process, and biosynthetic process) are slightly overrepresented in the mature seeds; however, no big difference is found between green and mature seeds (Fig. 6). For the minor categories, the green seeds generally have a more uniform or higher representation than mature seeds (Fig. 6). The three categories "generation of precursor metabolites and energy," "transport," and "cellular component organization and biogenesis" are relatively lower in the mature seeds (Fig. 6). For the category "carbon utilization," the relative level is about 2-fold higher in mature seeds than in green seeds.

Pathway Analysis

GO annotations based on the 920 and 264 identifications were subsequently used for assigning proteins to biochemical pathways using Cytoscape (Shannon et al., 2003). To establish the background, the complete set of GO annotations for the gene accession numbers from *Lotus* AA, NT, and EST contigs was used. A positive set of protein identifications from, for example, mature seeds (264 gene accession numbers) were

Table IV. Summary of GeLC-MS/MS data

The unique gene accession numbers corresponding to the number of protein identifications from the search in different databases are shown.

Unique Gene Accession Nos. From:	Green Seeds	Mature Seeds
<i>Lotus</i> (AA and NT databases)	556	153
EST database TIGR	76	17
SPROT	17	6
NCBI	16	5
Total	665	181

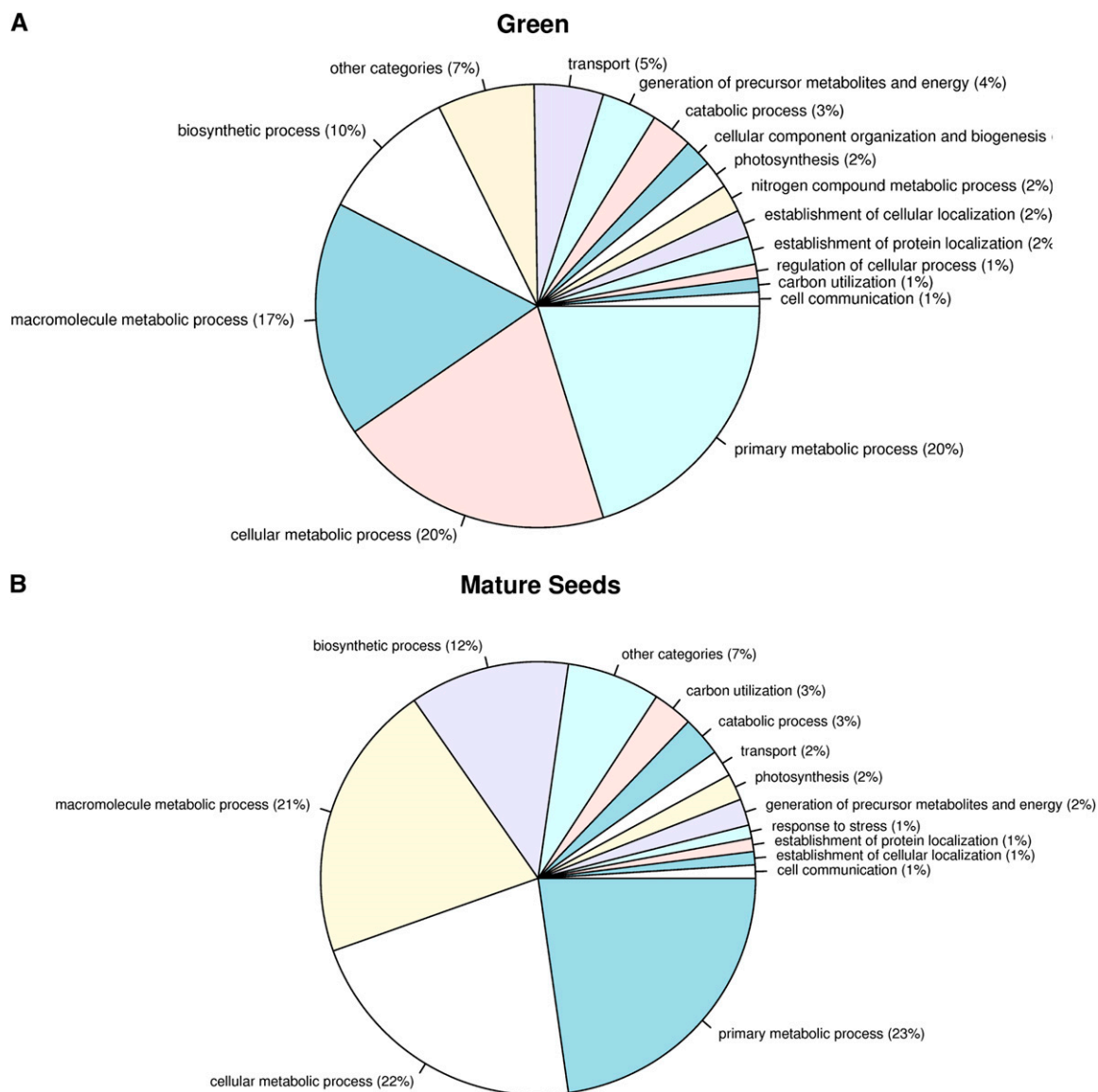


Figure 6. The molecular process of protein identifications. In A and B, the molecular processes of the protein identifications in green and mature seeds, respectively, found using the AA, NT, and EST downloaded from TIGR. Note that it is possible for the same protein to be counted in several categories if it has assignments descending from more than one of the categories depicted. [See online article for color version of this figure.]

compared against the background of the complete set of GO annotations. The biochemical pathways that were thus found to be above the background data are determined as up-regulated pathways in the individual data sets.

As an example of the pathway analysis for green seeds, 25 identified proteins with the corresponding GO annotation “amino acid biosynthesis” were found (Supplemental Table S3). Five of these are predicted to encode Gln synthetase (GS). Of the five GS genes used for identification, three are predicted to be full length and two are predicted to be partial (Supplemental

Table S3). The two partial GS genes correspond to the N and C termini, respectively; however, PCR amplification indicates that the proteins originate from two different genes (data not shown). Four of the five GS are predicted to be located in the cytosol, whereas the fifth GS is predicted to be located in plastids. Three of the protein identifications are predicted to encode a dihydrodipicolinate synthase, which is involved in the biosynthesis of Lys (Supplemental Table S3). In contrast, only one (a Met synthase) of the 25 protein identifications with the predicted GO annotation “amino acid biosynthesis” was found in mature seeds.

Web Interface to the Database

The results presented here may be further investigated using the Web interface found at <http://www.cbs.dtu.dk/cgi-bin/lotus/db.cgi>. This site has a number of options for views and cross-referencing. Guests may log in using the guest user account following the online instructions.

An analysis is associated with the sample on which it is carried out and the experiment that it is part of and may be found by navigating to either one using the tree menu on the left side. The GeLC-MS/MS analyses (divided by tissue type and database in which the peaks were identified) may thus be found by going to *Misc* | *Tissue/Organ Types* | *Green Seeds* | *GeLC-MS/MS green* or *Misc* | *Tissue/Organ Types* | *Mature Seeds* | *GeLC-MS/MS mature*. Alternatively, they can all be accessed from *Misc* | *Experiments* | *GeLC-MS/MS Experiment*. The two-dimensional (2-D) gel separation and associated MALDI-Q-TOF analyses (conducted on 14 selected spots on the gel) are found at *Misc* | *Tissue/Organ Types* | *Mature Seeds* | *2-D_storage_proteins* or *Misc* | *Experiments* | *2-D gel storage proteins*.

When a GeLC-MS/MS or MALDI-Q-TOF analysis is chosen, a node giving access to information on peak peptides will pop out in the tree structure. Furthermore, a node linking to the identified protein (or EST contig or cDNA) will pop out underneath. (Information on peaks and identifications from the GeLC-MS/MS analyses are also listed in Supplemental Table S2.) When a given protein is shown, information on related EST contigs, GO annotations, BLAST (Altschul et al., 1990, 1997) hits against the featured *Lotus* genome, and related experimental analyses in which the protein has been identified is also listed and linked to when relevant. (Data sources are described in "Materials and Methods.") The analyses also link back to the identified proteins, thus making it possible to quickly see in what other analyses that same protein has been identified. EST contig and links to and from related experimental analyses, proteins, and ESTs are shown in a similar way.

DISCUSSION

Model legume studies are important for establishing comparative studies of legume seed development, and we present here the initial microscopical, compositional, and proteome characterization of seed development in *Lotus*. The proteomics analyses established a resource of proteome and genome data that was organized in a database accessible at <http://www.cbs.dtu.dk/cgi-bin/lotus/db.cgi>. This database also holds details of the experimental setup and data from the spectra from the Q-TOF-MS and GeLC-MS/MS. Proteome data obtained from future analyses of seeds and other tissues will also be uploaded to add new information to this resource. Together with seed proteome data from *Medicago* and soybean, our *Lotus* seed proteome database will contribute to establishing the

platform for comparative legume proteomics. So far, 746 unique gene accession numbers identified from green and mature seeds constitute the *Lotus* resource. Similar 2-D gel or Sec-MudPIT-based proteomic studies of seed filling in *Medicago* and soybean identified 226 and 647 unique proteins, respectively (Gallardo et al., 2003, 2007; Hajduch et al., 2005; Agrawal et al., 2008). Comparing these *Medicago* and soybean proteins against the identified *Lotus* seed proteins (BLASTP $e \leq 1 \times 10^{-6}$), 39% of the proteins from *Lotus* were also identified in *Medicago*, and with soybean the overlap was 60%. Comparing our *Lotus* data set with all four proteomic studies from *Medicago* and soybean (873 protein identifications), approximately 27% of the *Lotus* proteins had not been identified previously. Altogether, this shows that further studies are necessary for coverage of the legume seed proteome.

Taking advantage of the 1,619 proteins so far identified in the *Lotus*, *Medicago*, and soybean seed proteomic studies, we attempted to estimate the scope of comparative legume proteomics in predicting biochemical pathways. Of the 1,619 proteins, 1,299 proteins found a homolog in UniprotKB ($e \leq 1 \times 10^{-6}$; Supplemental Table S4). Of these, 612 proteins could be assigned to 213 different enzymatic functions, defined by their Enzyme Commission numbers, and metabolic networks could be derived using the KEGG LIGAND database. In total, enzymes from 123 pathways were identified, and for 42 pathways, five or more enzymes were identified (Supplemental Table S5). Approximately 30% of the pathways in Supplemental Table S5 are involved in amino acid metabolism.

None of the 123 identified pathways are fully covered; however, the merge of proteome data from three legume species increases the coverage for most of the pathways. Although *Lotus*, *Medicago*, and soybean are separate species, we suggest that comparing and compiling proteome data sets can contribute toward a better understanding of seed development and function in legumes. Further details of the pathways assembled from *Lotus*, *Medicago*, and soybean are available at <http://bioinfo.rsb.anu.edu.au/utis/PathExpress4legumes/>.

Globulin Seed Storage Proteins and Globulin Genes in *Lotus*

The overall seed development for *Lotus* is similar to that of other legumes; however, the timing of the shifts between the three growth phases and the presence of endosperm in mature seeds differ between legume species (Borisjuk et al., 1995; Gallardo et al., 2003). The content and composition of lipid, nitrogen, starch, phytic acid, and ash in mature *Lotus* seeds are more similar to those in soybean than in pea. The legumins LLP1 to LLP5 are the major part of the globulins in mature *Lotus* seeds (Fig. 5). This is in contrast to pea, in which the vicilins are the major part of globulins. Tzitzikas et al. (2006) found that two-thirds or more of

the globulins were vicilins for 50 of 59 pea lines; however, in soybeans, the legumins are the major part of the globulins (Yaklich, 2001).

Globulins were identified using a 2-D gel approach, while the proteome was investigated using a GeLC-MS/MS approach. Posttranslational processing of precursor proteins was discovered in the globulins, but in general our methods were not directed toward detection of posttranslational modifications such as phosphorylation and glycosylation. Indications of such modifications were observed, however. For the N-terminal fragments of LLP2, LLP3, and LLP4, the observed molecular masses are approximately 12, 13, and 8 kD, respectively, higher than the theoretical molecular masses (Supplemental Table S1). Glycosylations could cause this molecular mass difference. Glycosylations are normally not found in legumins; however, glycosylated legumins are found in lupin (*Lupinus albus*) and Japanese red cedar (*Cryptomeria japonica*; Duranti et al., 1988; Wind and Häger, 1996). The common N-glycosylation motif, Asn-X-Ser/Thr, is lacking in LLP2 and LLP3. LLP4 has an Asn-X-Ser glycosylation motif at amino acid residues 86 to 88, but a peptide overlapping this potential glycosylation site was identified, indicating that glycosylation at this site may be absent or incomplete (see "Materials and Methods"). The theoretical pI values for the C-terminal fragment of LLP1, LLP2, and LLP3 are higher than the observed pI values (Supplemental Table S1). This could be caused by modification but is rather due to the limited resolution in the high pH range of the IEF strips used for the first dimension.

The N-terminal sequence of LCP1 (spot 15) and identification of LCP2 in spots 5 and 9 indicate that *Lotus* convicilins are processed. This is unusual, since no posttranslational modification other than signal peptide cleavage has been reported for convicilins (Croy et al., 1980; Newbigin et al., 1990). Degradation during extraction cannot be excluded; therefore, processing of LCP1 and LCP2 needs further investigation.

The ancestral angiosperm gene structure for 11S globulin has four introns, while present day 11S globulins have three introns (Häger et al., 1996). Further loss of an intron has given rise to the two-intron genes found in several angiosperms (Häger et al., 1996). In accordance, we found that the *Lotus* *Llp1*, *Llp2*, *Llp3*, and *Llp5* genes have three introns, whereas *Llp4* has two introns.

Legume 7S globulin genes have five introns (Weschke et al., 1987; McHenry and Fritz, 1992), while genes from monocots such as maize (*Zea mays*) have four introns (Belanger and Kriz, 1991). The five-intron structure of the *Lotus* LCPs and the length of the exons correspond to convicilins from pea and bean (Sáenz de Miera et al., 2008).

DNA polymorphism between the *L. japonicus* Gifu and MG20 ecotypes used in this study is generally located outside of the coding regions (Kawaguchi et al., 2001). Therefore, it was interesting to compare the conservation of globulin genes, in which selection

for protein function is less stringent even though protease sites involved in processing and the Cys residue responsible for the assembly of disulfide bonds are maintained (Staswick et al., 1984; Scott et al., 1992; Jung et al., 1998). The genome sequences of the *Llp2*, *Llp3*, and *Lcp2* genes were completed for both ecotypes, and differences in the gene sequences were observed. For *Lcp2*, an insertion/deletion of three nucleotides corresponding to a Ser occurred at nucleotide 483 in the coding sequence. For the *Llp2* and *Llp3* genes located head to head on chromosome 5, the situation is more complex. As shown in Supplemental Figures S3 and S4 these two genes most likely originate from duplication of an ancestral gene that occurred prior to the separation of the Gifu and MG20 ecotypes. According to this hypothesis, changes in the ancestral gene sequence that accumulated in the progenitor of the two ecotypes would be shared between the *Llp2* and *Llp3* genes from the ecotypes. These 156 nucleotide differences are marked with green in Supplemental Figure S4. Subsequent nucleotide changes occurring in the individual ecotypes are marked in gray. Interestingly, these nucleotide changes were found in exons of *Llp2* from Gifu and *Llp3* from MG20, while no mutations were found in the corresponding *Llp2* from MG20 and *Llp3* from Gifu. The second intron of MG20 *Llp3* (Supplemental Fig. S4) is unique in that there is an unusual accumulation of insertions and mutations compared with intron 2 for the three other genes (Supplemental Fig. S4). Only one position in the alignment (marked with yellow in Supplemental Figure S4) does not support the above-described hypothesis. However, a single nucleotide mutation in the *Llp2* or *Llp3* gene of Gifu or MG20 followed by gene conversion is a possible explanation for the observed difference.

Protein Identifications

For the large-scale proteome analysis, the GeLC-MS/MS approach was used and up to 920 and 264 proteins were identified from green and mature seeds, respectively. A possible explanation for this relatively large difference in protein identifications is that peptides from globulins will dominate the MS spectra in mature seeds. Supporting this suggestion, the six protein identifications from mature seeds with the highest MOWSE score are globulins (Supplemental Table S2). Overall, 83% and 41% of the protein identifications were seen only in green and mature seeds, respectively, which indicates a large metabolic difference for these stages; however, the molecular process pattern (Fig. 6) of green and mature seeds is similar.

Protein identifications 7, 8, and 9 from mature seeds do not have any GO annotation (Supplemental Table S2); however, a BLAST search for these three proteins identifies them as homologous of late embryogenesis abundant proteins (LEA proteins). LEA proteins are widespread in higher plants, especially in the seeds,

but generally not found elsewhere. The three LEA proteins identified in *Lotus* seem to be most similar to LEA proteins belonging to subgroup 3. In pea, a subgroup 3 LEA protein is found in mitochondria (Grelet et al., 2005; Tolleter et al., 2007). One of the well-characterized molecular processes of LEA proteins is to protect proteins and other molecules from dehy-

dration (Gilles et al., 2007). The LEA proteins identified at protein identifications 8 and 9 are found only in mature seeds, whereas protein identification 7 is also found in green seeds, as is protein identification 31 (Supplemental Table S2).

Protein identification 10 in mature seeds is homologous to oleosin. Oleosin is a structural component of

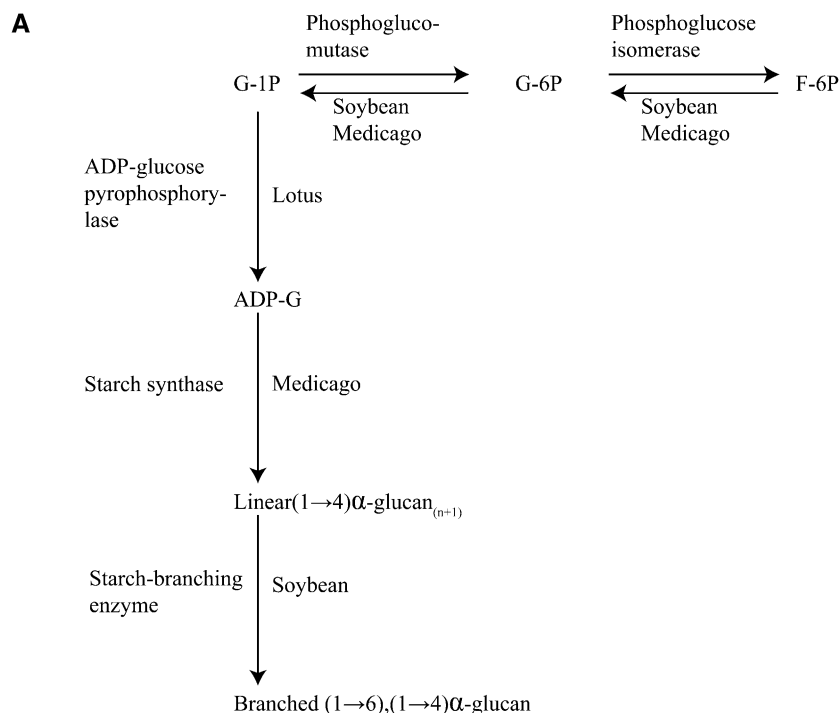
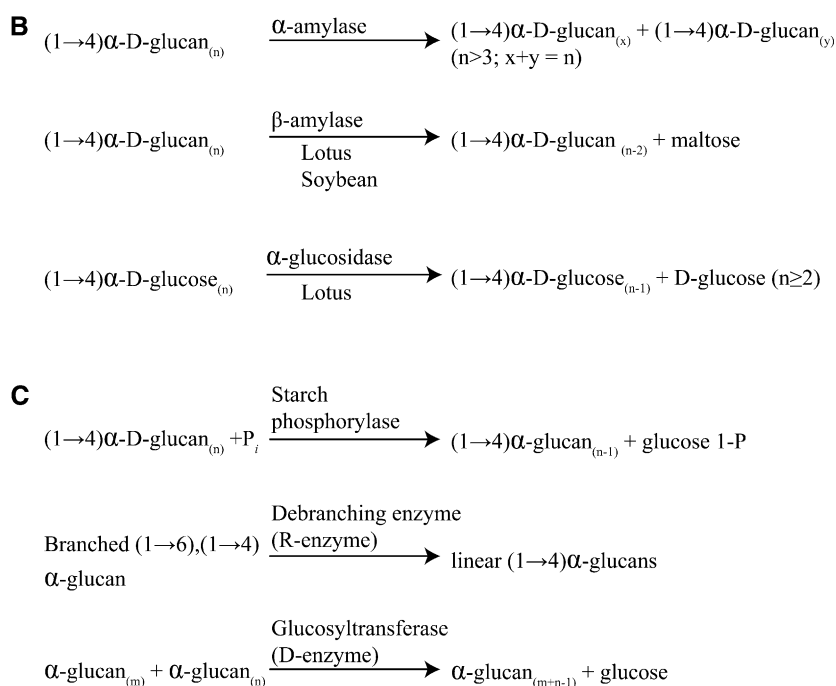


Figure 7. Comparative analysis of starch metabolism in legumes. A, Starch biosynthesis. The key enzyme in starch biosynthesis is ADP-Glc pyrophosphorylase, which converts Glc-1-P (G-1P) to ADP-Glc (ADP-G). B, The irreversible hydrolytic breakdown of starch. C, The phosphorylytic breakdown of starch. *Lotus*, *Medicago*, and soybean indicate the species in which a proteomics-based identification was obtained. F-6P, Fru-6-P; G-6P, Glc-6-P.



the oil body, where it limits coalescence during the cytoplasm compression caused by desiccation.

The 10 protein identifications with the highest MOWSE scores in mature seeds are either globulins or proteins directly or indirectly involved in desiccation, which is in good accordance with the developmental stage of the seed.

Globulins were already found in green seeds as protein identifications 1, 2, 3, 7, and 8. A protein disulfide isomerase PDIL-1 homolog was identified as proteins 6 and 40 in green and mature seeds, respectively, and a PDIL-2 homolog was identified as protein 242 in green seeds. Protein disulfide isomerases play important roles in the formation of disulfide bonds in nascent proteins. Kamauchi et al. (2008) characterized two PDILs in soybean (GmPDIL-1 and GmPDIL-2) that were suggested to be molecular chaperones involved in proper folding or quality of legumins. This may suggest a role for *Lotus* PDILs in disulfide bond formation in the LLPs.

The GO annotations for the identified proteins were used for pathway analysis. For the pathway category "amino acid biosynthesis" in green seeds, five different GS proteins were identified. In plants, GS is encoded by a small multigene family, and cytosolic GS (GS₁) and chloroplastic GS (GS₂) are the two major isoforms. The GS genes are typically expressed in different organs and tissues, and it has been proposed that each GS isoform has a specific function in assimilation and reassimilation of ammonia (Cren and Hirel, 1999). Our data indicate that all of the *Lotus* GS₁ genes were expressed in green seeds. Furthermore, GS₂ was identified in green seeds, and this is to our knowledge the first time that GS₂ was identified in seeds. In pea, three GS₁ genes have been characterized: all are expressed in nodules and two of them are expressed in cotyledons (Tingey et al., 1987). In soybean, only one GS₁ is found in the cotyledons (Morey et al., 2002). Not all 20 amino acids are translocated to the seed coat through the phloem. In bean, mainly Glu and/or Asn are translocated (Mifflin and Lea, 1977), while in pea, mainly Glu, Ala, and Thr are unloaded from the seed coat (25%, 20%, and 15%, respectively). These amino acids are subsequently converted into other amino acids in which GS is an important enzyme synthesizing Gln from Glu. Furthermore, three of the proteins in amino acid biosynthesis are predicted to catalyze a step in the biosynthesis of Lys, which is in good agreement with the high Lys content of legume seeds.

In the mature *Lotus* seed, a Met synthase was identified that is involved in the synthesis of Met from homo-Cys. Met synthase and several other enzymes involved in amino acids metabolism have been identified in *Medicago* seed development (Gallardo et al., 2003, 2007).

Starch Metabolism in *Lotus*, *Medicago*, and Soybean

Histological sections of the *Lotus* seed stained with iodine potassium iodide indicated degradation and/or mobilization of starch from osteosclereid and parenchyma cells at 25 DAF (data not shown), and the

overall starch level decreased prior to desiccation of the *Lotus* seed. In the mature *Lotus* seed, the starch level amounts to 0.6%. A comparably low level was found in the mature soybean and *Medicago* seed, while the pea seed contained approximately 27% starch (Chavan et al., 1998). Interestingly, soybean and *Medicago* also appear to degrade and/or mobilize starch prior to desiccation (Djemel et al., 2005; Stevenson et al., 2006). Refining the bioinformatics-based comparison presented above, we compiled starch enzyme identifications from the five seed proteomic studies (Fig. 7; Gallardo et al., 2003, 2007; Hajdich et al., 2005; Agrawal et al., 2008). Although legume seed starch metabolism may be different from the well-studied processes in leaves and in cereal grains, this approach provided good coverage of known starch biosynthetic and degradation pathways (Fig. 7, A and B). The key regulator enzyme for starch biosynthesis, ADP-Glc pyrophosphorylase, was not identified in any of the legume proteomic studies; however, the enzyme has been identified in a *Lotus* 2-D-PAGE analysis of seeds at 7 DAF (G. Nautrup-Pedersen, S. Dam, B.S. Laursen, A.L. Siegmund, H.H. Stærfeldt, C. Friis, K. Nielsen, N. Goffard, S. Sato, S. Tabata, P. Roepstorff, and J. Stougaard, unpublished data). No enzymes belonging to the phosphorylytic breakdown pathway were detected in the five seed proteomics studies from *Lotus*, *Medicago*, or soybean (Fig. 7C), while enzymes of the irreversible hydrolytic pathway were found. β -Amylases were identified in *Lotus* and soybean (Fig. 7B), and an isoamylase-like enzyme together with an enzyme phosphorylating glucan (EC 2.7.9.4), increasing the activity of β -amylase in leaves (Delatte et al., 2006; Edner et al., 2007), was found in soybean. However, isoamylase is also indispensable in starch biosynthesis (Zeeman et al., 1998). The α -glucosidase enzyme was found in a *Lotus* 2-D-PAGE seed analysis (G. Nautrup-Pedersen, S. Dam, B.S. Laursen, A.L. Siegmund, H.H. Stærfeldt, C. Friis, K. Nielsen, N. Goffard, S. Sato, S. Tabata, P. Roepstorff, and J. Stougaard, unpublished data). Altogether, this comparative approach identified two pathways probably involved in the starch synthesis and the hydrolytic starch breakdown in the three legumes. Interestingly, degradation of starch in germinating mung bean (*Vigna radiata*), which has a starch content of approximately 54% in mature seeds (Mubarak, 2005), is mainly accomplished by the phosphorylytic breakdown pathway (Matheson and Richardson, 1976; Berkel et al., 1991). Both types of starch degradation have thus been described in legume seeds.

Altogether, these observations highlight the need for improved knowledge of the genes and proteins responsible for the difference in protein, oil, and starch content of different legumes.

MATERIALS AND METHODS

Plant Material

Lotus japonicus ecotype Gifu was grown in a greenhouse with a 16-h-light/8-h-dark cycle, and seeds were harvested at different developmental stages

defined by DAF. Seeds were harvested into 70% ethanol for histochemical studies and directly into a mortar placed on dry ice for protein extractions.

Seed fresh and dry weights were determined as five replicates. The seeds were weighed immediately after harvest (fresh weight) and after drying at 65°C for 72 h (dry weight). Afterward, the water content was calculated.

Fixation, Sectioning, and Staining

A small hole was made in the seeds prior to fixation to allow the fixation liquid to penetrate the seed coat of the mature seeds. The seeds were fixed in 4% (w/v) paraformaldehyde in 50 mM potassium phosphate buffer (pH 7.0) for 2 d at room temperature. The seeds were then vacuum infiltrated to remove trapped air and dehydrated in a graded ethanol series (70%, 80%, 90%, and 96%). Finally, the seeds were embedded in Technovit 7100 (Haereus Kluver) according to the manufacturer's instructions. Thin sections (5 μ m) were stained with toluidine blue, and the slides were observed by light microscopy.

DNA Techniques

Genomic DNA was prepared using plant leaf material from *L. japonicus* Gifu and *L. japonicus* MG20 harvested and stored at -20°C until use. Tissue (0.3–0.5 g) was ground in liquid nitrogen. Then, 5 mL of preheated (60°C) extraction buffer (0.1 M Tris-HCl, pH 8.0, 1.4 M NaCl, 0.02 M EDTA, and 2% cetyltrimethyl ammonium bromide) was added and incubated for 30 min. Five milliliters of chloroform:isoamyl alcohol (24:1) was added, mixed, and centrifuged at 9,300g at room temperature. The aqueous phase was transferred to a new tube, and 10 μ g of RNase per milliliter was added and incubated for 30 min at 37°C. The sample was placed on ice for 5 min, and 0.6 volumes of ice-cold isopropanol was added. The genomic DNA was precipitated at -20°C for 20 min and centrifuged at 14,000g at 4°C for 10 min. The DNA pellet was washed with 70% ethanol, air dried, and dissolved in TE buffer (10 mM Tris-HCl, pH 8.0, and 0.1 mM EDTA, pH 8.0).

Approximately 50 ng of genomic DNA was used for each PCR. PCR products were sequenced using Applied Biosystems BigDye version 3.1 and run on an ABI3130 DNA sequencer.

Partial and full-length cDNA clones originating from a *L. japonicus* seed and seed pod library were sequenced as described above. LjPEST3h1 corresponds to LCP1, LjPEST2e7 corresponds to LCP2, LjPEST2h11 corresponds to LLP3, and LjPEST4d11 corresponds to LLP5.

The exon-intron structures of the globulin genes were predicted using the program FGENESH, last modified on July 24, 2007 (<http://linux1.softberry.com/berry.phtml?topic=fgenes&group=programs&subgroup=gfind>).

Components in Mature Seeds

The level of nitrogen was determined by the Kjeldahl method. The level of lipids was determined as described (Stoldt, 1952; Rotenberg and Andersen, 1980). The level of starch was determined as described (Åman and Hesselman, 1984), and the level of phytic acid was determined as described (Haug and Lantzsch, 1983).

Preparation of Protein Extracts

Total protein extracts were prepared essentially as described (Wang et al., 2003). Globulins were extracted as follows. Thirty dry seeds were ground in a mortar, and water-soluble proteins were extracted twice in 1 mL of water (10 min, 4°C) followed by centrifugation for 10 min at 13,000g. The insoluble material was resuspended in 1 mL of 0.1 M Tris, pH 8.0, and 1 M NaCl. The solution was incubated for 10 min, followed by centrifugation for 10 min at 13,000g. The supernatant was transferred to a new tube, and 3 volumes of 10% trichloroacetic acid in acetone was added. Proteins were allowed to precipitate for 1 h at -20°C. The solution was centrifuged for 13,000g for 10 min at 4°C, and the resulting pellet was washed twice with 80% acetone. The final pellet was allowed to dry at room temperature and dissolved in 250 μ L of IEF buffer (5 M urea, 2 M thiourea, 2% CHAPS, 2% SB3-10, 10 mM dithiothreitol, 2 mM EDTA, and 0.5% [w/v] immobilized pH gradient [IPG] buffer, pH 3–10 nonlinear [GE Healthcare]) for IEF.

One- and Two-Dimensional Electrophoresis

Reduced proteins were separated in one dimension by SDS-PAGE on 5% to 15% gradient gels using the Gly/2-amino-2-methyl-1,3-propanediol-HCl system described by Bury (1981).

IPG strips (Immobiline Dry Strips, 7 cm, pH 3–10 nonlinear [GE Healthcare]) were rehydrated overnight with 125 μ L of sample in IEF buffer. IEF was carried out on an IPGphor II system (GE Healthcare) using the following program: 200 V (step) for 20 volt hours (Vh), 3,500 V (gradient) for 2,500 Vh, and 3,500 V (step) for 5,000 Vh. After IEF, the proteins were reduced and alkylated by equilibration of the strips for 15 min in Eq buffer (50 mM Tris, pH 8.8, 6 M urea, 30% glycerol, 2% SDS, and 0.002% bromophenol blue) containing 6.5 mM dithiothreitol followed by 15 min in Eq buffer containing 10 mM iodoacetamide. For separation in the second dimension, IPG strips were loaded on 5% to 15% gradient gels as described above. Proteins were visualized by Coomassie Brilliant Blue R-250 staining.

MS-Based Protein Identification

For MS-based protein identification from 2-D gels, spots were excised, washed in water, dehydrated with 50 μ L of acetonitrile for 15 min, and vacuum dried. In-gel digestions were performed by adding 20 μ L of 12.5 μ g mL⁻¹ modified porcine trypsin (Promega) in 50 mM NH₄HCO₃. The gel pieces absorbed the trypsin solution for 45 min, and the remaining liquid was removed. Finally, 30 μ L of 50 mM NH₄HCO₃ was added and the samples were incubated at 37°C for 16 to 18 h. The resulting tryptic peptides were adsorbed to a POROS 20 R2 resin packed in a homemade microscale column (Kusmann et al., 1997), washed with 10 μ L of 1% trifluoroacetic acid, and eluted on a MALDI sample target using 1 μ L of 0.4% recrystallized α -cyano-4-hydroxycinnamic acid (Sigma) in 70% acetonitrile and 0.1% trifluoroacetic acid. Peptides were analyzed by MALDI-MS using a Q-TOF Ultima Global mass spectrometer (Micromass). The MS spectra were combined, background subtracted (polynomial order 4, 60%–80% below curve, tolerance 0.010) and deisotoped (MaxEnt 3) using Masslynx 4.0 (Micromass). The resulting peak lists were used to search for matches in an in-house-compiled database of annotated *Lotus* genome sequences (lotus_060912aa [68,838 sequences, 20,265,406 residues] and lotus_060912nt [416,940 sequences, 122,006,960 residues]) using Mascot 2.1 (Perkins et al., 1999). For each spot, peptide mass fingerprint data and one to five MS/MS spectra were combined into a single search performed with a peptide tolerance of 50 ppm and a MS/MS tolerance value of 0.6 D. Only peptides produced by trypsin with the possibility of one missed cleavage were considered. Searches were performed with carbamidomethylation as a fixed modification of Cys residues and oxidation on Met residues as a variable modification. Hits were considered to be significant if the MOWSE score was greater than 61 for lotus_060912aa and greater than 69 for lotus_060912nt. If no hit was found, the data were searched in an in-house-compiled database of *Lotus* TC sequences obtained from TIGR (*L. japonicus* Gene Index release 3.0) and finally in SPROT (version 49.7 [219,361 sequences, 80,573,946 residues]) and NCBI nr (version 20060522 [3,651,628 sequences, 1,255,333,329 residues]). Hits were considered to be significant if the MOWSE score was greater than 65 for ESTs downloaded from TIGR, greater than 66 for SPROT, and greater than 78 for NCBI.

GeLC-MS identifications were performed in duplicate on samples of seeds at 16 to 25 DAF and mature seeds. Proteins were extracted and separated by one-dimensional SDS-PAGE as described above. The lanes were cut into approximately 40 slices, and proteins were digested with trypsin as described above, with the exception that 20 μ L of 25 μ g mL⁻¹ trypsin was used. The samples were then acidified by the addition of 1 μ L of CH₃COOH and filtered through a microspin filter (0.2 μ m) prior to LC-MS/MS.

LC-MS/MS was performed using an LC-Packings Ultimate Nano LC system connected online to a Q-TOF Ultima Global mass spectrometer (Micromass). Peptides were trapped and isocratically desalted on a reverse-phase precolumn (LC-Packings PepMap C18, 300 μ m $\times$ 5 mm) and eluted onto a fused-silica emitter (PicoFrit, New Objective, 10 cm $\times$ 75 μ m packed with Zorbax 300 SB C₁₈ 3.5- μ m particles; Agilent). The peptides were separated using a linear gradient from buffer A (0.02% hepta-fluorobutyric acid and 0.5% CH₃COOH in water) to buffer B (0.02% hepta-fluorobutyric acid, 0.5% CH₃COOH, and 75% acetonitrile in water) for 90 min using a flow rate of 200 nL min⁻¹. Survey scans were acquired over the mass-to-charge ratio range 400 to 2,000, and a maximum of three concurrent MS/MS acquisitions were triggered for precursors detected at an intensity above a predefined threshold and with a charge of +2 or +3. Each MS/MS acquisition

was stopped after 6 s or when the precursor intensity dropped below a given threshold. After data acquisition, the MS/MS data were processed using Masslynx 4.0 (Micromass) as follows. Sequential scans from the same precursor were combined, and the resulting data were further processed if the QA score was above 10.00. The Mass Measure algorithm was used for background subtraction and deisotoping (Background subtract: polynomial order 1, below curve 55.00%; Smooth: smooth window (channels) 4.00, number of smooths 1, mode Savitzky Golay; Centroid: minimum peak width at half height 2; Centroid mode: centroid top 80.00%). A very conservative approach for accepting a hit as a positive identification was applied. The peptide tolerance was set to 1.2 D, and the MS/MS tolerance was set to 0.6 D, and only peptides produced by trypsin with the possibility of one missed cleavage were considered. Oxidation of Met residues and propionamide modification of Cys residues were included as possible modifications. Identifications were only considered if the probability that the match was random was less than 0.01. Peptides with scores less than 20 were not considered, and the MS/MS spectra for peptides scoring between 20 and 40 were manually inspected to verify the assignment of peaks by Mascot. Protein identifications based on only one peptide were all verified by manual inspection of the MS/MS spectra. Manually inspected spectra were only considered significant if they contained a peptide sequence tag of at least three consecutive amino acid residues.

N-Terminal Sequencing

For N-terminal sequencing, proteins were first electroblotted from the 2-D gels to a polyvinylidene difluoride membrane and stained with Coomassie Brilliant Blue R-250. Spots were excised from the membrane and analyzed by automated Edman degradation using an Applied Biosystems Procise 491HT sequencer with online phenylthiohydantoin HPLC analysis. The instrument was operated according to the manufacturer's instructions.

The Database and Interface

The *Lotus* database project integrates data from various experimental analyses (including mass spectrometry and protein-protein interactions), GO (Ashburner et al., 2000) annotations, the sequence databases UniProt (Bairoch et al., 2005) and NR (http://www.ncbi.nlm.nih.gov/blast/blast_databases.shtml), *L. japonicus* genome, cDNA, EST contig, and protein data obtained from the Kazusa DNA Research Institute (Sato et al., 2008), and EST contig, EST, and protein data from The Gene Index Databases (Lee et al., 2005; <http://compbio.dfci.harvard.edu/tgi/>). BLAST (Altschul et al., 1990, 1997) was used to align EST contig (BLASTN), cDNA (BLASTN), and protein (TBLASTN) sequences against the unassembled genome data contained in the database and to find provisional GO annotations taking the annotations from the best matching protein in UniProt. The setup is an implementation of LAMP (Linux, Apache Web server, MySQL, and Perl). The Web interface also uses JavaScript and an extended version of Tree Menu (<http://www.treemenu.net/>).

The MySQL database itself was originally designed using DBDesigner4. From the user's point of view, the database schema centers on the relationship between samples, analyses (each belonging to an experiment), data, and annotations of sequences. An overview of the database schema can be seen in Supplemental Figure S5.

The different analysis types have information in their own specific tables: EstAnalysis, ArrayAnalysis, SeparationAnalysis, InteractionAnalysis, MsAnalysis, SageAnalysis, or ModificationProcess, that all inherit from the common Analysis table structure and in most cases have subordinate tables. Additional descriptive features not available in the existing table structure may be added to an entry by defining feature types (keys) and corresponding values contained in separate tables. This can all be done from the Web interface, and the database is thus user extendable.

The Web interface allows new experiments and analyses to be created. Data may then be filled in online in forms or uploaded in different formats (e.g. XML files that describe the analysis and its data). Furthermore, trusted users may modify and expand the Web interface through the creation of user-defined plots and data views. These scripts may be either global (for all users) or for the individual user only.

Accession Numbers

The genome sequences of *L. japonicus* Gifu *Llp2*, *Llp3*, *Lcp1*, and *Lcp2* correspond to accession numbers FM211901, FM211902, FM211903, and

FM211904, respectively. Additional genome sequences of *L. japonicus* MG20 for *Llp4* and *Llp5* correspond to accession numbers AP010875, AP010876, and AP010877, in which the first two accession numbers correspond to *Llp4*. The cDNA sequences of *L. japonicus* Gifu *Llp3*, *Llp5*, *Lcp1*, and *Lcp2* correspond to accession numbers FM211905, FM211906, FM211907, and FM211908, respectively.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. Amino acid sequences and peptide identifications of proteins separated by 2-D PAGE.

Supplemental Figure S2. Exon-intron structures of storage proteins.

Supplemental Figure S3. Hypothesis of evolution of the *Llp2* and *Llp3* genes.

Supplemental Figure S4. ClustalW alignment of *Llp2* and *Llp3* for the two ecotypes MG20 and Gifu.

Supplemental Figure S5. An overview of the database schema.

Supplemental Table S1. Predicted cleavage sites and observed and theoretical molecular weights and pI for 2-D gel.

Supplemental Table S2. Peaks and peptide identifications in the GeLC-MS experiment.

Supplemental Table S3. Pathway analysis of annotation "amino acid biosynthesis" in green seeds.

Supplemental Table S4. Identified proteins in *Lotus*, *Medicago*, and soybean proteomic studies with corresponding identifiers and Enzyme Commission numbers.

Supplemental Table S5. Comparative pathway analysis in legumes.

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Supplemental Figure S1

Spot #6 and #12 (LLP 1)

1	MAKLLVLSLS	FCFLFFGGCF	AIRQSSQQQN	ECQLERLNAL	KPDNRIESEA
51	GFIETWNPTN	NQFRCAGVAF	SRCTLRRNGL	ERPSYSNAPQ	EIFIQQSGSI
101	FGMIFPGCPE	TVEEPFESDQ	QGRRDRHQKV	NRFREGDVIA	VPPGVVFWMY
151	NEEETPVIAV	SLMDTSSYLN	QLDQMPPRRFY	LSGNQENEFL	QYQRQEMRGK
201	EEENQGGNIF	SGFGGEFLEH	ALNIDRDIHV	KLQGKDEEQD	KGAIVRVKGG
251	LSVITPPERQ	SHRRGSEEEE	DEEEDRPSRH	QSRGGSRRNG	LEETICTMRI
301	RMNIGKSSSP	DFYNPQAGRI	KTISSMDFPA	LRWIKLSAEH	GSINRNAMVV
351	PHYNINANSI	IYALRGKAWI	QVVNCKGNRI	FDGELEEGQV	LIVPQNFAIA
401	ARSTSDKFNY	ISFKTHEMPW	MAKLAGAASA	FEAMPLEVIQ	NSFNLERDQA
451	KQIKNNNRFN	FLVPPREQSQ	RRASA		

Spot #2 and #13 (LLP 2)

1	MAKPFVLSLC	LLLFTSTCLA	RSFDWSDRFS	QCQLDRINVL	EPDNRVESEA
51	GLIETWSPSQ	SPELQCAGVS	VVRRTIQPKG	LHLPSFTPSP	QLIMIVQGRG
101	ALGIAIPGCP	ETYEPPQSQS	RQGRRGGSSR	QQRDRHQKIR	HFSPGDIIAI
151	PPGIPWWTYN	YGNPAIAAIS	LIDTSNFANQ	LDQTPRVFYL	AGNPAIEHPE
201	TQSSQRQPRR	ESPGGRRHGQ	HHQESEQEEE	EGGSILSGFG	AEFLQQVFNI
251	DHD TAKQLQS	PDDQRRQIVK	VEGDDLFSFIS	PESADEDEDE	EDEDEDQEQH
301	GRHSRPSGR	TRRPSREEDE	DEDEDEEERQ	GGGRGRGERQ	RHFEEEEEEE
351	REERGPRGRG	KHWQREEEEE	EEESRRRTIPS	RRESRGRGEC	RTRNGLEENF
401	CTLKIHENIN	RPSRADLYNP	RAGRISDINS	LTLPIILRFLG	LSAEYVNLYQ
451	NGIYAPHWNI	NANSIYVVR	GRGRVRIVNC	QGQAVFNDEL	RKGQLLVVPQ
501	NFVVAAQQAQD	EGFEYVVKFT	NARAAVSHVK	QVFRATPAEV	LSNAFGIRQR
551	DVSDLKFSGN	WGPLVNPNT	QSRSRDSVIA	KVA	

Spot #1 and Spot #14 (LLP 3)

1	MAKPFILSLC	LLLFTSTCLA	RSSDWSDRFS	QCQLDRINAL	EPDNRVESEA
51	GLIETWSPRQ	SPELQCAGVS	VVRCTIQPKG	LHLPSFTPSP	QLIMIVQGRG
101	ALGIAIPGCP	ETYEPPQSQS	RQGRRGGSSR	QQRDRHQKIR	HFSPGDIIAI
151	PPGIPWWTYN	YGNPAIAAIS	LIDTSNFANQ	LDQTPRVFYL	AGNPAIEHPE
201	TEQGQRQPRR	ESPGGRRHGQ	HHQESEQEEE	EGGSILSGFG	AEFLQQVFNI
251	DHD TAKQLQS	PDDQRRQIVK	VEGDDLFSFIS	PESADEDEDE	EDEDEDQEQH
301	GRHSRPSGR	TRRPSREEDE	DEDEDEEEDQ	QHGRSRHSG	RRTRRSREE
351	EDEDEDEEEE	RQGRGRGER	QRHFEREEEE	EREERGPRGR	GKHWQREEEE
401	EEEESSRTIP	SRRESRGRGE	CRTRNGLEEN	FCTLKIHENI	NRPSRADLYN
451	PRAGRISDIN	SLTLPIILRFL	GLSAEYVNLY	QNGIYAPHWN	INANSIYV
501	RGRGRVRIVN	CQGQAVFNDE	LRKGQLLVVP	QNFVVAQQAQ	DEGFEYVVK
551	TNARAAVSHV	KQVFRATPAQ	VLANAFGIRQ	RDVSDLKFSG	NWGPLINPDN
601	TQSRSDNVL	AKVA			

Spot #4 (LLP 4)

1	MAKPHSVCFL	FLLFFTCCL	ARHVPTQSQQ	QSQSQSQFKE	CQLDSIDALE
51	PDNSIESEAG	LTETWNAANH	PELRCAGVAI	LRR TINPSGL	HLPSYTIYPE
101	LHFVDQGKGV	IGMVIPGCAE	TYEEPQVQRP	QQQHERDRHQ	KVRYLRHGDV
151	IAVPPGVVYW	TYNYGKNPLV	IITLQDTTNN	LNQLDPTPTR	FYIAGKPEKE
201	HSESESESES	ESESGKRKEK	KKEGGVNMF	GGFDSAFLSR	VLKVKEDLIS
251	KLQSPKDDRK	KQIIHVKGGL	SIIRPPLEQE	IRETEQREEE	EDEPREGEHR
301	EWRRERTRRK	EREGEEGEEE	VVEEKETETK	TKTKTREKHE	RRGEGEGEGE
351	EGEEEEERTR	TRTRERRERH	EGQKGQSNAL	EETVCTMKLH	ENLADPSRAD
401	IFNPRAGRVS	TVNSLTLPVL	KKLNLGAEWV	NLYKNGVYVP	HWINANSVM
451	YVTRGKGRVQ	VVNCEGESVF	DGEVKRGQVV	VVPQGFVAK	QAGSEGLEEI
501	AFKTNMAMI	SPLVGMNSAI	SGTPAEVLGH	AFGLSPEEVR	ELKNNRKESI
551	LASPHDSRED	AYISMV			

Spot #7 (LLP 5)

1	MAYKLFALSL	SFCFLFLGGC	FAIRQQSQQQ	NECQLERLNA	LKPDNRIESE
51	AGYIETWNPT	NNQFRCAGVA	LSRCTLRRNG	LKRPSYSNAP	QEIFIQQGSG
101	IFGMIFPGCP	ETVEEPFESD	QQGRRDRHQK	VNRFREGDVI	AVPPGVVFWM
151	YNEEETPVIA	VSLIDTGSYL	NQLDQMRRF	YLSGNQEDEF	LQYQRQEVRG
201	REEENQGGNI	FSGFGGEFLE	DALNIDRNIV	HKLQGRDEEQ	DKGAIVRVKG
251	GLSVITPPER	QSHRRGSEEE	EDEEEDRPSR	HQSRGGSRR	GLEETICTVR
301	LRMNIGKSSS	PDIFNPQAGR	IKTATGFDFP	ALRFLKLSAE	HGSLNRNAMV
351	VPHYNLNANS	IIYALRGRAW	IQVVNCKGNR	IFDGELEEGQ	VLIVPQNFFV
401	AARMSDKFN	YVAFKTDNDMP	TMAKLAGATS	EIQAMPLEVI	QNAFNLEREQ
451	AKQVKFNNRF	NFLVPPREQS	QRRASA		

Spot #3 and #15 (LCP 1)

1	MASAKIKARL	PLLLLLLGILF	LVSVSLATAS	RQREDPCREQ	GEDERQPWQP
51	RREREHGRE	REEED	EKESR	RPSWERKERT	REWRRESEER
101	EEEESDRPRR	PHRESKERPR	RHQRESEEEE	GSSSSSESSR	RSQRNPFFHF
151	RSSRFQTHFE	NEGHVRLVQ	RFDERSKLFE	NLQNYRILEF	KAKPQTLVLP
201	HHNDADSIIV	ILSGRAILTI	VNPNDRDSYN	LESGDALVIP	AGATAYLANR
251	DNDENLRVVK	LLIPINRPGQ	YQFFFPSSSE	TQESYLNQFS	RNILEASFNA
301	GYDEIERVLL	QREEQRGES	QEQQVIVKAS	QDQIQQLSRH	AKSSSRKRSS
351	SKSEPPNLR	SKPISSNKF	KLFEITPEKN	QQLRDLILL	SEAQIKEGSI
401	FLPHYHSTST	LILVVNEGRG	ELELVAQRRQ	QQRGQEEQEE	EEQPRIEAQR
451	FRARLSPGDV	IVIPASHPFA	VTASSDLNLL	AFGINAENNQ	RNFLAGRDDN
501	VISQIERPVK	ELAFPGSAEE	IESLIKNQRN	SCFASAQPQQ	GEEEGRSGKK
551	DQLSSILGAF	F			

Spot #5 and spot #9 (LCP 2)

1	MASTEMKARF	PLLLLLLGILF	LASVSVCYGI	VSHDKEDDDR	RPWWPEPERE
51	EEKHHQRTRG	SEEKEKEERE	RHQEPGHRER	ARQEKEKEED	ERQPPWQPGR
101	GEEEGEWGRS	RRLEDPDERE	RVRERTERAK	KWRRETEERD	TPRRPHHRES
151	EEEEGSSSSS	SESSRRSQRR	NPFYFRSSSS	RFQTRFQNEY	GYVRVLQRFD
201	ERSKLFENLQ	NYRIFEFKAK	PHTVVLPHHN	DADSIVVILS	GKAIITLVNP
251	NDRESFNLER	GDVLVHPAGT	IAYVANHDDN	ENLRIAKIII	PVNRPGEFQA
301	FYPSNTEPQE	SYLNGFSRNI	LEASFNAEYN	EIERVLLRGG	EQRQEQGLIV
351	KVSRDLIQQL	SRHAKSSSRK	RTSSEPEPFN	LRSRDPISYN	EFGKHFEINP
401	NRNSQLRDFD	IFLSSTEIRE	GSIFLPHYNS	RSTVILVVNE	GRGEFELVAQ
451	RKQQQQRNE	EDEEEEEEQP	RIEAQRFRAR	LSPGDVVVIP	AGHPVAINAS
501	SDLNFIAFGI	NAENNQRHFL	AGGDDNVISQ	IEKVVKIAIF	PGSAEDIERL
551	IKNQRNSHFA	NAQPQGREEG	GHGRRGPLSS	ILGAFTK	

Spot #8 (lectin homolog)

1	KGKCYGARPW	ASCTTHEAIS	GGFKPPETVA	FLFMVNSVEG	VSNFTKFTD
51	DGSLILQGDA	KIWTDGILAL	PSDPLIGKTT	SRVLYATPVP	IWDSNTGSVA
101	SFVSSFVSVV	SDVPGYKISD	GLVFFLAPWG	TTIPPNSEGK	NLGILDEKNG
151	YNQFVAVEFD	SYNNTRDPTF	RHIGIDVNSV	MSMNLVKWNR	VSGALEKVTI
201	IYDSPTKTLS	VVVTHQNGQI	TTVAQQIDLK	VVLPEKESVG	FSATTWNTHR
251	ERHDIHSWSF	TSTFETNYAT	EENIHINHSS		

Spot#11 (ripening related protein homolog to chickpea)

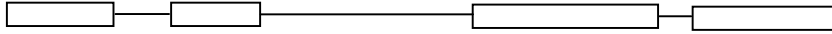
1	MVLAKGLITE	VGVKTPADKF	YNLFTTQLHD	VQKHAKEVHE	TKVHEGDWHG
51	IGSVKHWTYV	VDGKVITCLE	RVEAIDEQNK	TNKYTLFGGD	IDPHYKNFTL
101	ILQVIDNKDS	HAVARWTIEY	EKLHEDIEPP	NGYMEYFNKL	TRDVDNQIHK
151	A				

Supplemental Figure S1: Amino acid sequence and peptide identification of proteins separated by 2-D PAGE.

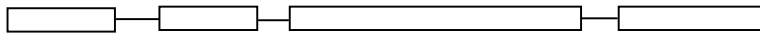
The sequence of each identified protein is shown. The identified peptides are shown in red+bold for N-terminal of LLP's and spot 3, 5, 8 and 11. The identified peptides are shown in bright green+bold for C-terminal of LLP's and spot 9 and 15. The identified peptides are shown in sky blue+bold are overlapping peptide identifications for two spots. Predicted signal peptides are shown in gray boxes. Yellow boxes indicate the N-terminal sequence. The blue boxes indicate the predicted NG cleavage sites. The underlined sequences originate from additional analysis of genome sequences, EST's and gene models which were not included in the data base used for protein identification by Mascot. The italic+bold+underlined letters indicate the difference in the sequence between *L. japonicus* Gifu and *L. japonicus* MG20. For LLP 2 amino acid residues 261, 389, 393, and 552 are Ser, Gly, Ser, Gly, and Ile in *L. japonicus* Gifu sequence. For LLP 3 amino acid residues 202, 204 and 486 are Gln, Ser, and Gly in *L. japonicus* Gifu sequence. For LCP 2 an insert of a Ser at position 161 in the *L. japonicus* Gifu sequence. All the predicted signal peptides are predicted to follow the secretory pathway.

Supplemental Figure S2

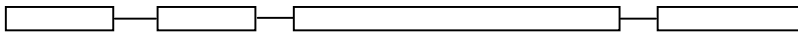
LLP 1



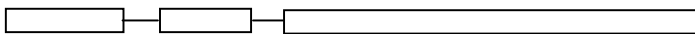
LLP 2



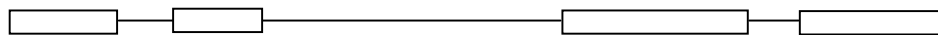
LLP 3



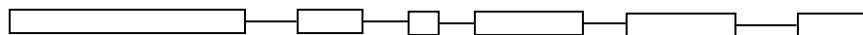
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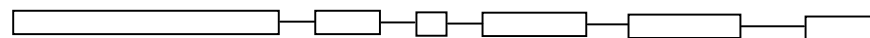
LLP 5



LCP 1



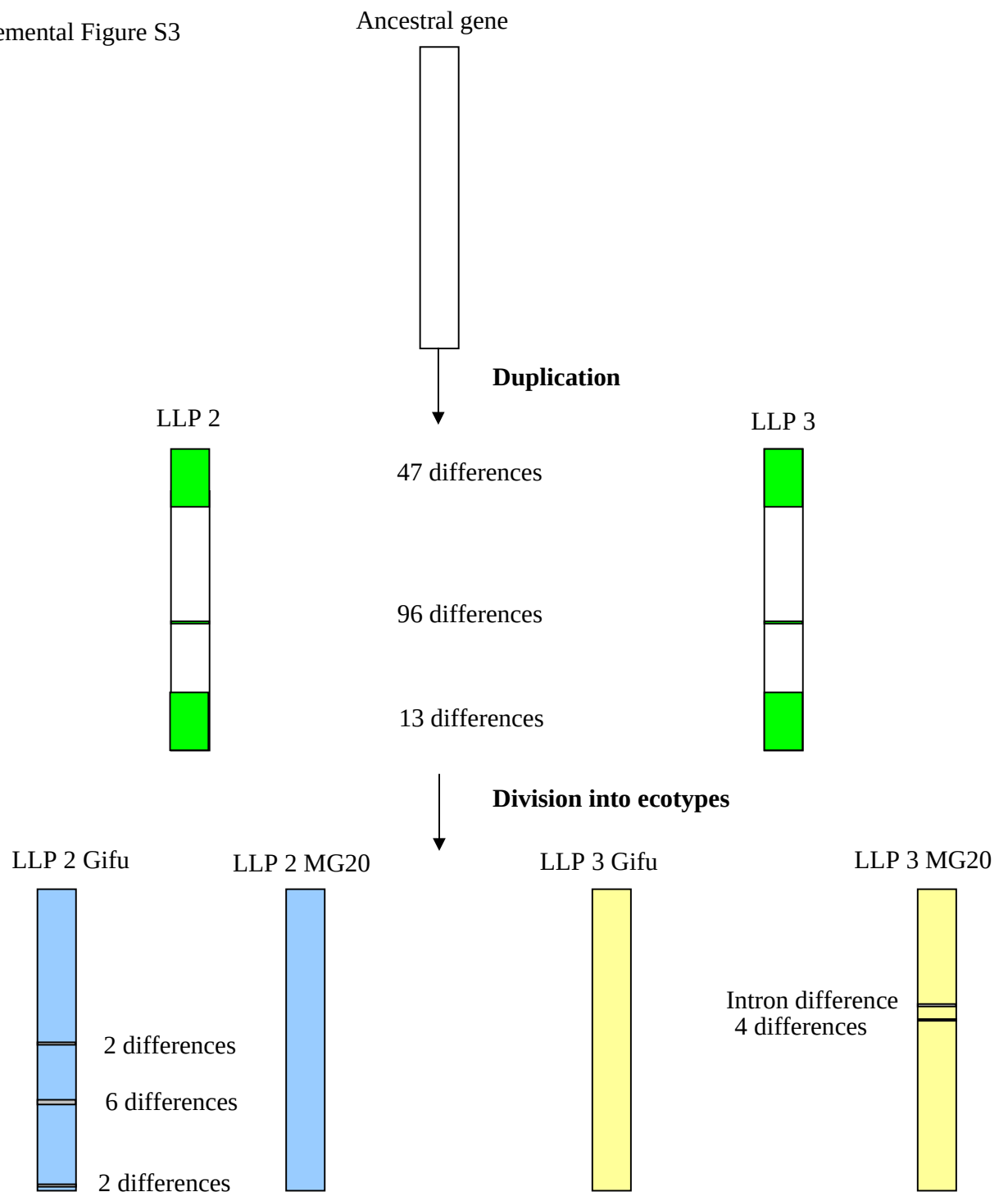
LCP 2



0.2 Kb

Supplemental Figure S2. Exon-intron structure of storage proteins. Exons are boxes and introns are lines. The exons and introns are drawn in scale.

Supplemental Figure S3



Supplemental Figure S3. Hypothesis of evolution of the *Llp 2* and *Llp 3* genes. An ancestral gene was duplicated to *Llp 2* and *Llp 3*. A total of 156 nucleotide differences

located in three regions (green area) occurred in the progenitor of the Gifu and MG20 ecotypes. Further difference between *Llp 2* and *Llp 3* genes marked in grey bars occurred after separation of the two ecotypes. The pale blue and light yellow for *Llp 2* (Gifu and MG20) and *Llp 3* (Gifu and MG20) respectively, symbolised that these sequence are identical except the mutations shown.

Supplemental Figure S4

LLP3MG20	ATGGCCAAACCTTTCTACTCTCTCTTTGCTTACTCTCTTCACGAGCACCTGCTTAGCT	60
LLP3Gifu	ATGGCCAAACCTTTCTACTCTCTCTTTGCTTACTCTCTTCACGAGCACCTGCTTAGCT	60
LLP2MG20	ATGGCCAAACCTTTCTCTCTCTCTTTGCTTACTCTCTTCACGAGCACCTGCTTAGCT	60
LLP2Gifu	ATGGCCAAACCTTTCTCTCTCTCTTTGCTTACTCTCTTCACGAGCACCTGCTTAGCT	60

LLP3MG20	CGGTCTCTGATTGGTCCGACCGATTAGTCAATGCCAGCTTGACAGAATCAACGGTTG	120
LLP3Gifu	CGGTCTCTGATTGGTCCGACCGATTAGTCAATGCCAGCTTGACAGAATCAACGGTTG	120
LLP2MG20	CGGTCTCTGATTGGTCCGACCGATTAGTCAATGCCAGCTTGACAGAATCAACGGTTG	120
LLP2Gifu	CGGTCTCTGATTGGTCCGACCGATTAGTCAATGCCAGCTTGACAGAATCAACGGTTG	120

LLP3MG20	GAGCCTGACAAACGCGTTGAGTCTGAAGCTGGCTTGATTGAGACATGGAGCCCCAGACAG	180
LLP3Gifu	GAGCCTGACAAACGCGTTGAGTCTGAAGCTGGCTTGATTGAGACATGGAGCCCCAGACAG	180
LLP2MG20	GAGCCTGACAAACGCGTTGAGTCTGAAGCTGGCTTGATTGAGACATGGAGCCCCAGACAG	180
LLP2Gifu	GAGCCTGACAAACGCGTTGAGTCTGAAGCTGGCTTGATTGAGACATGGAGCCCCAGACAG	180

LLP3MG20	AGCCCCGAGCTACAATGCGCTGGGGTGTCTGTGTCCGATGCACATCCAACCCAAAGGA	240
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LLP2MG20	AGCCCCGAGCTACAATGCGCTGGGGTGTCTGTGTCCGATGCACATCCAACCCAAAGGA	240
LLP2Gifu	AGCCCCGAGCTACAATGCGCTGGGGTGTCTGTGTCCGATGCACATCCAACCCAAAGGA	240

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LLP2MG20	CTCCACTTGCCATCCTTCACTCCTTCTCCACAGCTGATTATGATCCTCAAGGTAAGTTG	300
LLP2Gifu	CTCCACTTGCCATCCTTCACTCCTTCTCCACAGCTGATTATGATCCTCAAGGTAAGTTG	300

LLP3MG20	ATATATAATTCTTTCTTATAATATATTTCCAATCTAATATATCACTAATTAATATTAA	360
LLP3Gifu	ATATATAATTCTTTCTTATAATATATTTCCAATCTAATATATCACTAATTAATATTAA	360
LLP2MG20	ATATATAATTCTTTCTTATAATATATTTCCAATCTAATATATCACTAATTAATATTAA	357
LLP2Gifu	ATATATAATTCTTTCTTATAATATATTTCCAATCTAATATATCACTAATTAATATTAA	357

LLP3MG20	TTGTTTGTTTGT----TTGGTAACATAAATTAATTTATATATCAGGAGGGGTGCTT	415
LLP3Gifu	TTGTTTGTTTGT----TTGGTAACATAAATTAATTTATATATCAGGAGGGGTGCTT	415
LLP2MG20	TTGTTTGTGCGGTAATTATATAAATTAATTTATATATCAGGAGGGGTGCTT	417
LLP2Gifu	TTGTTTGTGCGGTAATTATATAAATTAATTTATATATCAGGAGGGGTGCTT	417
*** ** *		
LLP3MG20	TAGGAATTGCAATTCTGGGTGTCCTGAGACGTATGAAGAGCCACAATCACAATCAAGAC	475
LLP3Gifu	TAGGAATTGCAATTCTGGGTGTCCTGAGACGTATGAAGAGCCACAATCACAATCAAGAC	475
LLP2MG20	TAGGAATTGCAATTCTGGGTGTCCTGAGACGTATGAAGAGCCACAATCACAATCAAGAC	477
LLP2Gifu	TAGGAATTGCAATTCTGGGTGTCCTGAGACGTATGAAGAGCCACAATCACAATCAAGAC	477

LLP3MG20	AAGGAAGAAGGGGAGGAAGCTCAGGCAGCAAGAGACAGGCACCAGAAGATTCGTCAC	535
LLP3Gifu	AAGGAAGAAGGGGAGGAAGCTCAGGCAGCAAGAGACAGGCACCAGAAGATTCGTCAC	535
LLP2MG20	AAGGAAGAAGGGGAGGAAGCTCAGGCAGCAAGAGACAGGCACCAGAAGATTCGTCAC	537
LLP2Gifu	AAGGAAGAAGGGGAGGAAGCTCAGGCAGCAAGAGACAGGCACCAGAAGATTCGTCAC	537

LLP3MG20	TCAGTCCCAGGTGATATCATTGCCATTCCACCTGGAATCCCTTACTGGACTTACAACACG	595
LLP3Gifu	TCAGTCCCAGGTGATATCATTGCCATTCCACCTGGAATCCCTTACTGGACTTACAACACG	595
LLP2MG20	TCAGTCCCAGGTGATATCATTGCCATTCCACCTGGAATCCCTTACTGGACTTACAACACG	597
LLP2Gifu	TCAGTCCCAGGTGATATCATTGCCATTCCACCTGGAATCCCTTACTGGACTTACAACACG	597

LLP3MG20	GCAATGAACCTGCCATTGCCATCAGTCTCATTGACACCTCCAACCTTGCAAACACGCTTG	655
LLP3Gifu	GCAATGAACCTGCCATTGCCATCAGTCTCATTGACACCTCCAACCTTGCAAACACGCTTG	655
LLP2MG20	GCAATGAACCTGCCATTGCCATCAGTCTCATTGACACCTCCAACCTTGCAAACACGCTTG	657
LLP2Gifu	GCAATGAACCTGCCATTGCCATCAGTCTCATTGACACCTCCAACCTTGCAAACACGCTTG	657

LLP3MG20	ATCAAACCCCAAGAGTATATTAATTATGCAGCATCTCAACTTGGTAAATATAATTGAT	715
LLP3Gifu	ATCAAACCCCAAGAGTATGCATTATATATTATGCACC--ATGTGGATCAACTAAATTAT	712

LLP2MG20	ATCAAACCCCAAGAGTATGCATTATATATTATGCACC--ATGTGGATCAACTAAATTAT	714
LLP2Gifu	ATCAAACCCCAAGAGTATGCATTATATATTATGCACC--ATGTGGATCAACTAAATTAT	714

LLP3MG20	CTACATACAAATTTTCAAATTAATGAATATTATCCATTATTGAATGCAGGTGTTTTATCT	775
LLP3Gifu	AT-CGTGTGTGCTT-----GAAT-CCATTAATTATTGCATGCAGGTGTTTTATCT	760
LLP2MG20	AT-CGTGTGTGCTT-----GAAT-CCATTAATTATTGCATGCAGGTGTTTTATCT	762
LLP2Gifu	AT-CGTGTGTGCTT-----GAAT-CCATTAATTATTGCATGCAGGTGTTTTATCT	762
	* * * * *	
LLP3MG20	TGCCGGGAATCCAGCAATAGAGCACCCAGAGACCCAGCAGGCGCCAGAGGCAACCACGCCG	835
LLP3Gifu	TGCCGGAAATCCAGCGATAGAGCACCCAGAGACCCAGCAGAGCCAGAGGCAACCACGCCG	820
LLP2MG20	TGCCGGAAATCCAGCGATAGAGCACCCAGAGACCCAGCAGAGCCAGAGGCAACCACGCCG	822
LLP2Gifu	TGCCGGAAATCCAGCGATAGAGCACCCAGAGACCCAGCAGAGCCAGAGGCAACCACGCCG	822

LLP3MG20	TGAGTCCCCCGGTGGACGCAGGCATGGCCAGCACCACCAGGAGTCTGAGCAGGAGGAGGA	895
LLP3Gifu	TGAGTCCCCCGGTGGACGCAGGCATGGCCAGCACCACCAGGAGTCTGAGCAGGAGGAGGA	880
LLP2MG20	TGAGTCCCCCGGTGGACGCAGGCATGGCCAGCACCACCAGGAGTCTGAGCAGGAGGAGGA	882
LLP2Gifu	TGAGTCCCCCGGTGGACGCAGGCATGGCCAGCACCACCAGGAGTCTGAGCAGGAGGAGGA	882

LLP3MG20	AGAAGGTGGCAGCATCCTCAGCGGCTTCGGCGCAGAGTTTTTGCAACAAGTTTTCAACAT	955
LLP3Gifu	AGAAGGTGGCAGCATCCTCAGCGGCTTCGGCGCAGAGTTTTTGCAACAAGTTTTCAACAT	940
LLP2MG20	AGAAGGTGGCAGCATCCTCAGCGGCTTCGGCGCAGAGTTTTTGCAACAAGTTTTCAACAT	942
LLP2Gifu	AGAAGGTGGCAGTATCCTCAGCGGCTTCGGCGCAGAGTTTTTGCAACAAGTTTTCAACAT	942

LLP3MG20	CGACCATGACACCGCAAAGCAACTCCAATCCCAGATGATCAGAGGAGGCAAAATTGTGAA	1015
LLP3Gifu	CGACCATGACACCGCAAAGCAACTCCAATCCCAGATGATCAGAGGAGGCAAAATTGTGAA	1000
LLP2MG20	CGACCATGACACCGCAAAGCAACTCCAATCCCAGATGATCAGAGGAGGCAAAATTGTGAA	1002
LLP2Gifu	CGACCATGACACCGCAAAGCAACTCCAATCCTCAGATGATCAGAGGAGGCAAAATTGTGAA	1002

LLP3MG20	GGTGGAGGGCGATGATCTCAGCTTTATTAGCCCCGAAAGTGCAGACGAAGACGAAGATGA	1075
LLP3Gifu	GGTGGAGGGCGATGATCTCAGCTTTATTAGCCCCGAAAGTGCAGACGAAGACGAAGATGA	1060
LLP2MG20	GGTGGAGGGCGATGATCTCAGCTTTATTAGCCCCGAAAGTGCAGACGAAGACGAAGATGA	1062
LLP2Gifu	GGTGGAGGGCGATGATCTCAGCTTTATTAGCCCCGAAAGTGCAGACGAAGACGAAGATGA	1062

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LLP2MG20	AGAAGATGAAGATGAAGATCAAGAGCAACATGGACGCCACTCACGTCCCTCCGGACGAAG	1122
LLP2Gifu	AGAAGATGAAGATGAAGATCAAGAGCAACATGGACGCCACTCACGTCCCTCCGGACGAAG	1122

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LLP2Gifu	AACTAGAAGACCCAGCAGGGAGGAGGACGAAGATGAGGATGAAGATGAAGAAGATGAACA	1182

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LLP2MG20	-----AGGA	1186
LLP2Gifu	-----AGGA	1186

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LLP2MG20	GGAGGA-----CGTGGACGTGGAGAAAG	1209
LLP2Gifu	GGAGGA-----CGTGGACGTGGAGAAAG	1209

LLP3MG20	ACAAAGACATTTTCGAGAGGGAAGAAGAAGAAGAGCGTGAAGAACGTGGACCACGAGGACG	1375
LLP3Gifu	ACAAAGACATTTTCGAGAGGGAAGAAGAAGAAGAGCGTGAAGAACGTGGACCACGAGGACG	1360
LLP2MG20	ACAAAGACATTTTCGAGAGGGAAGAAGAAGAAGAGCGTGAAGAACGTGGACCACGAGGACG	1269
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LLP3MG20	AGGAAAGCATTGGCAGAGGGAAGAAGAAGAGGAAGAAGAAGATCACGCCGGACAATTCC	1435

LLP3Gifu	AGGAAAGCATTGGCAGAGGGAAGAAGAAGAGGAAGAAGAAGAAATCACGCCGGACAATTCC	1420
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LLP2Gifu	ATCTAGGAGAGAGAGCAGGGGAAGGGGAGGATGCAGAACTAGCAATGGTCTTGAGGAAAA	1389

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LLP2MG20	TCCACGCGCAGGTCGCATCAGTGACATCAACAGCCTCACCTCCCAATCCTCCGCTTTTT	1509
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LLP2MG20	GCATGTGCAGAATGGAATCTATGCTCCACACTGGAACATCAATGCAAACAGCATCATTTA	1689
LLP2Gifu	GCATGTGCAGAATGGAATCTATGCTCCACACTGGAACATCAATGCAAACAGCATCATTTA	1689

LLP3MG20	CGTGGTGAGAGGCCGAGGAAGGGTTCGCATAGTGAAGTCCAGGGGCAAGCAGTGTTCAA	1855
LLP3Gifu	CGTGGTGAGAGGCCGAGGAAGGGTTCGCATAGTGAAGTCCAGGGGCAAGCAGTGTTCAA	1840
LLP2MG20	CGTGGTGAGAGGCCGAGGAAGGGTTCGCATAGTGAAGTCCAGGGGCAAGCAGTGTTCAA	1749
LLP2Gifu	CGTGGTGAGAGGCCGAGGAAGGGTTCGCATAGTGAAGTCCAGGGGCAAGCAGTGTTCAA	1749

LLP3MG20	TGACGAGCTCAGGAAGGGACAATTGCTGGTGGTGCCACAGAACTTCGTGGTGCGCAACA	1915
LLP3Gifu	TGACGAGCTCAGGAAGGGACAATTGCTGGTGGTGCCACAGAACTTCGTGGTGCGCAACA	1900
LLP2MG20	TGACGAGCTCAGGAAGGGACAATTGCTGGTGGTGCCACAGAACTTCGTGGTGCGCAACA	1809
LLP2Gifu	TGACGAGCTCAGGAAGGGACAATTGCTGGTGGTGCCACAGAACTTCGTGGTGCGCAACA	1809

LLP3MG20	AGCACAAAGATGAAGGATTCGAGTATGTGGTGTTCAGACCAATGCTAGAGCTGCCGTGAG	1975
LLP3Gifu	AGCACAAAGATGAAGGATTCGAGTATGTGGTGTTCAGACCAATGCTAGAGCTGCCGTGAG	1960
LLP2MG20	AGCACAAAGATGAAGGATTCGAGTATGTGGTGTTCAGACCAATGCTAGAGCTGCCGTGAG	1869
LLP2Gifu	AGCACAAAGATGAAGGATTCGAGTATGTGGTGTTCAGACCAATGCTAGAGCTGCCGTGAG	1869

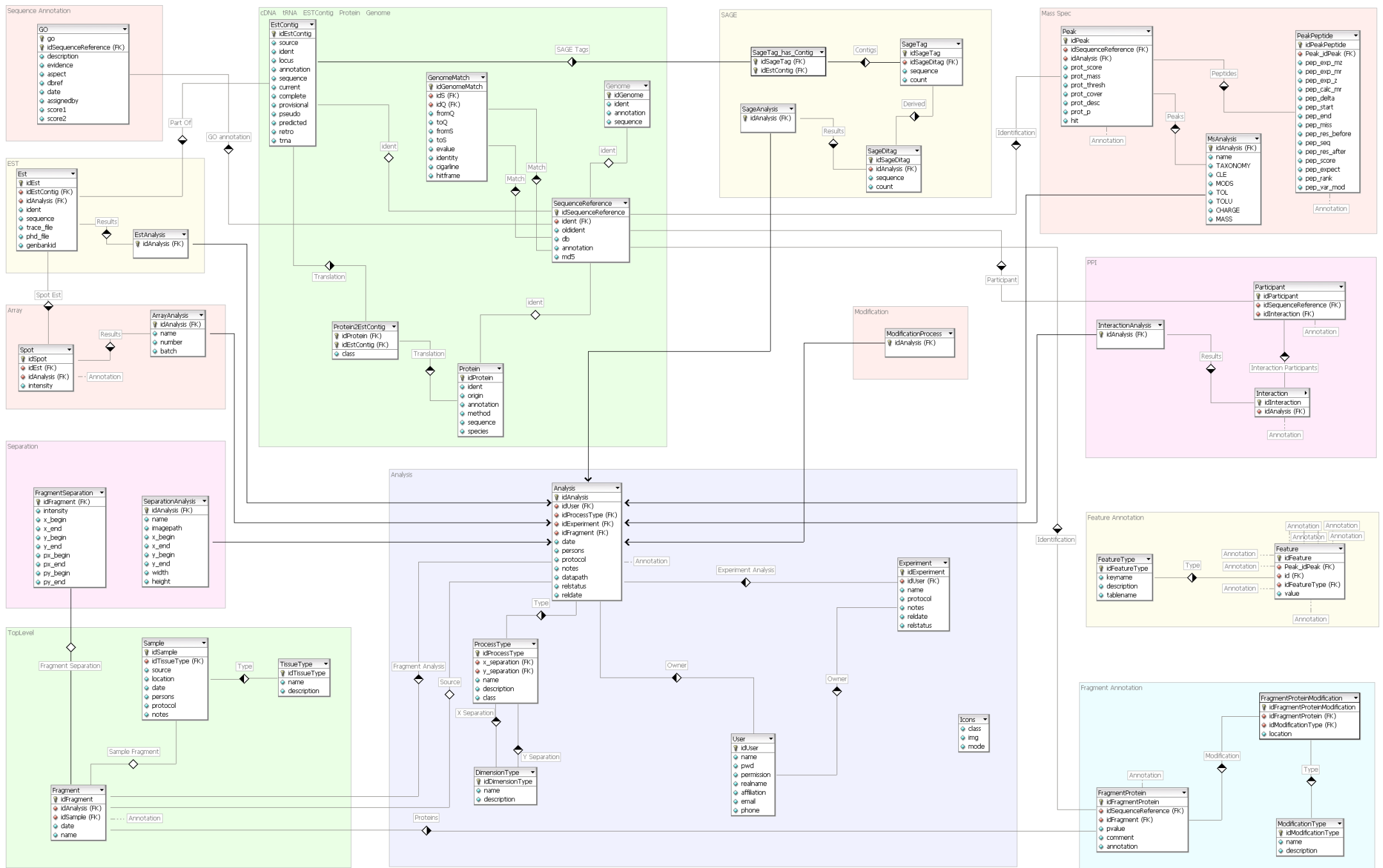
LLP3MG20	CCATGTCAAGCAGGTGTTCAAGGCCACCCCTGCTCAGGTTCTTGCCAATGCCTTCGGCAT	2035
LLP3Gifu	CCATGTCAAGCAGGTGTTCAAGGCCACCCCTGCTCAGGTTCTTGCCAATGCCTTCGGCAT	2020
LLP2MG20	CCATGTCAAGCAGGTGTTCAAGGCCACCCCTGCTCAGGTTCTTGCCAATGCCTTCGGTAT	1929
LLP2Gifu	CCATGTCAAGCAGGTGTTCAAGGCCACCCCTGCTCAGGTTCTTGCCAATGCCTTCGGTAT	1929

LLP3MG20	TCGCCAGCGTGATGTTAGTGATCTCAAGTTCAGCGGAAACTGGGGCCCTCTGATCAACCC	2095
LLP3Gifu	TCGCCAGCGTGATGTTAGTGATCTCAAGTTCAGCGGAAACTGGGGCCCTCTGATCAACCC	2080
LLP2MG20	TCGCCAGCGTGATGTTAGTGATCTCAAGTTCAGCGGAAACTGGGGCCCTCTGATCAACCC	1989
LLP2Gifu	TCGCCAGCGTGATGTTAGTGATCTCAAGTTCAGCGGAAACTGGGGCCCTCTGATCAACCC	1989

LLP3MG20	TGA	<u>AATACCCAATCTCGATCACGAGACA</u>	<u>CGTC</u>	<u>TTGCTAAGGTTGC</u>	TGA	2147
LLP3Gifu	TGA	<u>AATACCCAATCTCGATCACGAGACA</u>	<u>CGTC</u>	<u>TTGCTAAGGTTGC</u>	TGA	2132
LLP2MG20	TGA	<u>AATACCCAATCTCGATCACGAGACAG</u>	<u>TGTC</u>	<u>ATTGCTAAGGTTGC</u>	ATGA	2041
LLP2Gifu	TGA	<u>AATACCCAATCTCGATCACGAGACAG</u>	<u>TGTC</u>	<u>ATTGCTAAGGTTGC</u>	ATGA	2041
	***	*****	***	*****	***	

Supplemental Figure S4. ClustalW alignment of *Llp 2* and *Llp 3* for the two ecotypes MG20 and Gifu. The stars makes nucleotides conserved between the four sequences and the ancestral gene. Green indicates the differences that occurred between the duplication and the diversification into ecotypes. The differences that occurred subsequently to the diversification in ecotypes are marked with gray and only for the gene in which the nucleotide change occurred. The exons are underlined.

Supplemental Figure S5



An overview of the database schema

Supplemental Table S1

Spot ID	Protein name	observed M _r and pI	Predicted cleavage site	Theoretical M _r and pI with predicted cleavages	Difference between observed and theoretical M _r and pI
1	LLP 3	60kDa/4.9	N ₄₂₅ G ₄₂₆	47.0kDa/4.96	13.0kDa/-0.06
2	LLP 2	55kDa/4.9	N ₃₉₄ G ₃₉₅	43.1kDa/4.98	11.9kDa/-0.08
3	LCP 1	68kDa/5.7		62.0kDa/6.07	6.0kDa/-0.37
4	LLP 4	49kDa/5.5	N ₃₇₈ A ₃₇₉	41.3kDa/5.47	7.7kDa/0.03
5	LCP 2	54kDa/6.3		65.3kDa/5.86	-11.3kDa/0.44
6	LLP 1	33kDa/5.0	N ₂₈₉ G ₂₉₀	30.9kDa/5.13	2.1kDa/-0.13
7	LLP 5	33kDa/5.1	N ₂₉₀ G ₂₉₁	30.8kDa/5.21	2.2kDa/-0.11
8	Lectin homolog	31kDa/5.4		26.6kDa/5.42	4.4kDa/-0.02
9	LCP 2	16kDa/4.8		24.6kDa/5.48	-8.6kDa/-0.68
11	Ripening related protein	16kDa/6.9		17.4kDa/5.90	-1.4kDa/1.00
12	LLP 1	20kDa/8.1	N ₂₈₉ G ₂₉₀	21.0kDa/9.65	-1.0kDa/-1.55
13	LLP 2	18kDa/8.1	N ₃₉₄ G ₃₉₅	21.2kDa/9.59	-3.2kDa/-1.49
14	LLP 3	17kDa/8.1	N ₄₂₅ G ₄₂₆	21.2kDa/9.74	-4.2kDa/-1.64
15	LCP 1	68kDa/4.9		58.2kDa/6.21	9.8kDa/-1.31

Supplemental Table S1. Predicted cleavage sites and observed and theoretical M_r and pI for 2-D gel. Spot ID corresponding to the protein number in Figure 5. The protein name is given in relation to homology with other species. The observed M_r and pI is calculated from the 2-D gel. The predicted cleavage site is the cleavage of the LLP's. The theoretical M_r and pI with predicted cleavages are calculated without signal peptide and with cleavage of the predicted cleavage site. For spot ID 9 the theoretical M_r and pI is calculated from the initial identified peptide at amino acid residue 371 (see Fig. 6). The last column is the difference between observed and theoretical M_r and pI.

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Supplemental Table S2.1: The 826 peaks identified in the “green_LotusAA” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.11.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	chr5.CM0357.530.nc	Nutrient reservoir activity.	64823	6.3	32.1	2803	17
2	chr5.LjT15N12.80.nc	Nutrient reservoir activity.	66257	5.4	29.4	2011	16
3	chr5.LjT15N12.90.nc	Nutrient reservoir activity.	66377	5.4	28.0	1990	15
4	LjSGA_092567.1	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, cytoplasm, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	18467	7.8	61.4	1884	9
5	chr5.CM0328.690.nd	Nucleotide binding, ATP binding, ATP biosynthetic process, hydrogen-exporting ATPase activity, phosphorylative mechanism, ATP synthesis coupled proton transport, integral to membrane, proton-transporting two-sector ATPase complex, nucleoside-triphosphatase activity, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	59990	5.8	45.0	1552	23
6	chr1.CM0027.160.nc	Protein disulfide isomerase activity, endoplasmic reticulum, isomerase activity, cell redox homeostasis.	56636	4.8	48.2	1443	25
7	chr1.CM0295.260.nd	Nutrient reservoir activity.	54140	6.3	35.6	1189	20
8	chr5.CM0357.550.nc	Nutrient reservoir activity.	65051	5.8	33.6	1136	18
9	LjSGA_084876.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	37516	6.7	29.7	918	12
9	LjSGA_124257.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	35627	8.1	29.5	914	11
9	LjSGA_134471.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	22087	6.1	29.5	644	8
9	LjSGA_149364.1	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-biphosphate carboxylase activity.	18183	6.6	31.1	640	7
9	LjSGA_113307.1	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle.	22513	9.7	14.9	509	4
9	LjSGA_105267.1	Chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-biphosphate carboxylase activity.	22804	6.5	12.7	460	3
9	LjSGA_136714.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	31823	7.2	14.4	304	4

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
9	LjSGA_040977.3	Chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-bisphosphate carboxylase activity.	11439	9.2	32.4	217	5
9	LjSGA_106428.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-bisphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	14633	4.8	11.3	70	2
9	chr5.CM0019.360.nc	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-bisphosphate carboxylase activity, reductive pentose-phosphate cycle.	4597	10.0	20.0	61	2
9	LjSGA_117887.1	Chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-bisphosphate carboxylase activity.	9041	4.7	8.4	45	1
10	chr3.CM0115.240.nc	Iron ion binding, electron transport, lipoygenase activity, metal ion binding.	96342	5.8	31.5	866	23
10	chr3.CM0115.260.nc	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoygenase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, metal ion binding.	94760	6.0	5.2	137	4
10	chr3.CM0115.140.nd	Iron ion binding, electron transport, lipoygenase activity, metal ion binding.	79540	6.9	3.3	101	2
11	chr4.CM0126.1570.nc	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-bisphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	52775	6.3	16.5	841	8
11	chr3.CM0106.360.nd	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-bisphosphate carboxylase activity, reductive pentose-phosphate cycle.	6187	5.1	19.6	115	1
11	LjSGA_096321.1	Chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-bisphosphate carboxylase activity.	9488	8.9	12.9	115	1
11	LjSGA_102132.1	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-bisphosphate carboxylase activity, reductive pentose-phosphate cycle.	10749	4.5	9.3	48	1
12	LjSGA_043185.1	No GO annotations found.	21821	8.7	62.0	821	14
13	LjT41N19.20.nd	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, methyltransferase activity, zinc ion binding, amino acid biosynthetic process, methionine biosynthetic process, transferase activity, metal ion binding.	84017	6.2	28.0	791	19
13	chr5.CM0341.20.nc	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, zinc ion binding, amino acid biosynthetic process, methionine biosynthetic process.	10121	8.8	11.5	49	1
13	LjSGA_056527.2	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, zinc ion binding, amino acid biosynthetic process, methionine biosynthetic process.	9257	5.7	12.2	49	1

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
13	LjSGA_094289.1	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, methyltransferase activity, zinc ion binding, amino acid biosynthetic process, methionine biosynthetic process, transferase activity, metal ion binding.	23716	5.3	11.2	45	2
14	LjT17C10.10.nd	Protein binding, ATP binding.	41689	5.2	26.8	781	13
14	LjSGA_019708.2	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	14022	5.4	40.5	326	7
15	LjT29P04.130.nd	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	36687	6.3	12.4	750	5
16	LjSGA_086307.1	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	15950	6.6	37.3	697	4
17	LjB12N13.20.nc	Acetyl-CoA C-acyltransferase activity, L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, acyltransferase activity, oxidoreductase activity, malate dehydrogenase activity, transferase activity, L-malate dehydrogenase activity.	35558	6.1	42.2	658	13
17	chr5.CM0071.650.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	33340	6.1	27.2	352	7
17	LjSGA_070021.1	Acetyl-CoA C-acyltransferase activity, L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, acyltransferase activity, oxidoreductase activity, malate dehydrogenase activity, transferase activity, L-malate dehydrogenase activity.	18208	4.7	23.4	228	3
18	LjSGA_116237.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	37179	7.3	39.6	648	12
18	LjSGA_141109.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	29246	6.1	37.8	462	7
18	LjSGA_138404.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	22218	7.6	35.3	373	4
19	chr3.LjT44N20.60.nd	Nucleotide binding, protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	61745	5.4	19.3	635	10
20	chr4.CM0007.1000.nc	Photosynthesis, light harvesting, membrane.	28098	5.1	25.4	616	6
20	LjSGA_017687.2	Photosynthesis, light harvesting, membrane.	28108	5.3	20.1	191	4
20	LjSGA_061139.1	Photosynthesis, light harvesting, membrane.	28156	5.5	20.1	191	4
21	LjSGA_030216.1	Nutrient reservoir activity.	33723	8.0	40.1	605	12
22	chr3.CM0152.120.nc	Polysaccharide catabolic process, catalytic activity, carbohydrate metabolic process, metabolic process, beta-amylase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds, cation binding.	56164	5.1	33.9	596	15
23	LjSGA_018057.1	Transport, lipid transport, lipid binding.	11719	8.9	43.7	557	6

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
24	chr1.CM0378.190.nd	Phosphopyruvate hydratase complex, magnesium ion binding, acetyl-CoA C-acyltransferase activity, phosphopyruvate hydratase activity, glycolysis, acyltransferase activity, transferase activity, lyase activity.	47754	5.5	35.6	537	12
25	chr3.CM0452.230.nd	Nucleotide binding, ATP binding.	71584	5.4	20.6	514	12
25	chr4.CM0179.510.nd	ATP binding.	37113	7.6	25.7	419	7
25	LjSGA_025770.1	Nucleotide binding, ATP binding, endoplasmic reticulum.	45169	5.8	6.8	287	3
25	LjSGA_069657.1	Nucleotide binding, ATP binding.	24794	7.0	7.6	233	2
25	chr1.LjT14113.160.nd	ATP binding.	32488	6.7	5.5	152	1
25	chr6.CM0118.670.nc	ATP binding.	67618	5.9	3.5	110	2
25	chr6.CM0118.650.nc	ATP binding.	11409	6.8	13.0	95	1
25	LjSGA_050585.1	Nucleotide binding, ATP binding.	7109	4.7	16.4	93	1
25	LjSGA_042820.1	ATP binding.	58460	5.8	2.8	77	1
25	LjSGA_024670.1	ATP binding.	61011	5.5	2.7	77	1
25	chr1.LjT16O03.90.nd	ATP binding.	68642	8.9	2.0	50	1
25	LjSGA_089217.1	Nucleotide binding, ATP binding.	41142	8.0	3.3	50	1
25	chr1.LjT23O20.220.nd	ATP binding.	47049	7.6	1.7	41	1
26	LjSGA_031559.1	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	18038	8.6	57.3	512	10
26	LjSGA_090105.1	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	18473	8.3	16.9	115	5
27	LjT36L22.20.nd	Nucleotide binding, protein binding, ATP binding, protein folding, chloroplast, cellular protein metabolic process, unfolded protein binding.	72781	7.4	27.4	512	18
27	LjSGA_075236.1	Nucleotide binding, protein binding, ATP binding, protein folding, chloroplast, cellular protein metabolic process, unfolded protein binding.	21196	9.5	28.3	125	4
28	chr3.CM0282.370.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	35846	8.5	27.6	500	9
28	chr3.CM0282.420.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	14077	5.6	17.8	182	3
28	chr3.CM0282.440.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	4702	5.2	20.9	48	1
29	chr1.LjT16O03.100.nd	Legumain activity, cysteine-type endopeptidase activity, proteolysis.	51253	6.3	17.1	490	9
30	chr6.LjT23A02.60.nc	Inositol-3-phosphate synthase activity, inositol biosynthetic process, phospholipid biosynthetic process.	56434	5.3	22.5	450	11
30	chr4.CM0307.90.nc	Inositol-3-phosphate synthase activity, inositol biosynthetic process, phospholipid biosynthetic process.	56546	5.3	9.4	219	4
31	LjSGA_133863.1	No GO annotations found.	16617	8.8	46.8	450	9
32	chr1.CM0001.670.nc	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	49254	9.1	20.4	449	10
32	chr2.LjT12G08.20.nc	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	49389	9.1	18.6	449	9
32	chr5.CM0909.50.nc	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	49363	9.2	14.1	407	7
32	chr1.CM0192.320.nd	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	24416	8.8	18.0	271	5
32	LjSGA_022872.2	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	15585	6.2	7.1	105	1

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
32	LjSGA_053227.1	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	13254	9.6	8.8	105	1
32	LjSGA_132154.1	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	9315	9.9	12.5	105	1
33	LjSGA_082137.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	41349	5.2	26.1	443	9
33	LjSGA_135295.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	30567	5.5	30.6	432	8
33	LjB15P09.140.nc	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	55293	5.6	8.7	216	5
33	LjSGA_067288.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	30513	9.4	12.0	190	4
33	LjSGA_081554.1	Nucleotide binding, ATP binding, ATP biosynthetic process, hydrogen-exporting ATPase activity, phosphorylative mechanism, ATP synthesis coupled proton transport, integral to membrane, proton-transporting two-sector ATPase complex, nucleoside-triphosphatase activity, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	22269	5.5	12.9	146	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
33	LjSGA_114982.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	32256	4.9	8.8	146	2
33	LjSGA_129516.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	30254	4.9	9.5	146	2
34	chr2.CM0373.1010.nd	Protein binding, ATP binding.	41644	5.3	24.1	427	11
34	chr6.CM0314.690.nc	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	41592	5.3	20.7	427	10
34	chr1.LjT23O20.150.nd	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	41714	5.2	19.9	361	10
34	LjSGA_131797.1	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	17406	5.2	17.1	131	3
34	LjSGA_146200.1	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	13105	4.7	13.7	96	1
35	LjSGA_043401.1	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	22396	8.4	37.6	419	8
36	chr1.CM0231.140.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	18130	7.7	45.3	414	6
37	LjSGA_042035.1	Catalytic activity, metabolic process, amino acid biosynthetic process, dihydrodipicolinate synthase activity, lysine biosynthetic process, chloroplast, lyase activity, diaminopimelate biosynthetic process.	28943	5.7	20.5	404	7
38	chr3.LjT05P05.90.nd	Peroxidase activity, response to oxidative stress, metal ion binding.	27783	6.0	45.5	397	9
39	chr3.CM0091.630.nd	Nucleotide binding, nucleic acid binding.	16053	5.6	48.5	395	6
40	chr2.CM0210.60.nc	Nucleotide binding, ATP binding, protein folding, unfolded protein binding.	80087	5.0	21.6	378	15
40	LjT02J13.90.nc	Nucleotide binding, ATP binding, protein folding, unfolded protein binding.	80378	5.0	7.2	211	5
40	LjSGA_033246.1	ATP binding, protein folding, unfolded protein binding.	20342	10.1	10.6	163	2
40	CM1324.20.nd	Calcium ion binding, ATP binding, endoplasmic reticulum, protein folding, unfolded protein binding.	21455	6.0	6.2	153	1
41	CM1729.90.nc	Adenosine kinase activity, purine ribonucleoside salvage, kinase activity.	37530	5.2	22.0	376	5
41	chr1.CM0033.1040.nc	Adenosine kinase activity, purine ribonucleoside salvage, kinase activity.	37946	8.8	5.3	115	1
42	LjSGA_038906.1	Nucleotide binding, ATP binding.	20725	5.9	40.3	372	8
42	LjSGA_076792.1	Nucleotide binding, ATP binding.	19729	6.7	23.0	235	4
43	chr5.CM0052.430.nd	Response to stress.	25607	5.3	46.1	371	8
44	chr1.CM0222.50.nc	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	42687	8.1	24.9	365	9

Continues...

Supplemental Table S2.1: (*green_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
45	LjSGA_147202.1	ATP binding.	13786	9.2	52.8	357	7
46	LjSGA_131247.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	22874	8.6	39.4	346	8
46	LjSGA_143694.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	20350	7.8	38.0	318	7
46	chr4.CM0126.1530.nc	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	47411	5.4	12.6	229	6
46	LjSGA_096734.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	15550	8.9	41.5	207	5
46	LjSGA_077431.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	6567	6.0	37.1	78	2
47	LjSGA_011421.2	Protein binding, ATP binding.	27381	5.0	24.4	341	8

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
48	LjT35D18.30.nc	Nucleotide binding, magnesium ion binding, methionine adenosyltransferase activity, ATP binding, one-carbon compound metabolic process, transferase activity, potassium ion binding, metal ion binding.	42976	5.6	20.7	337	7
48	LjSGA_030253.1	Nucleotide binding, magnesium ion binding, methionine adenosyltransferase activity, ATP binding, one-carbon compound metabolic process, transferase activity, potassium ion binding, metal ion binding, cobalt ion binding.	34979	6.7	7.5	181	2
48	LjSGA_140570.1	Nucleotide binding, magnesium ion binding, methionine adenosyltransferase activity, ATP binding, one-carbon compound metabolic process, transferase activity, potassium ion binding, metal ion binding, cobalt ion binding.	23951	5.1	3.7	75	1
49	chr5.CM0260.320.nc	Isomerase activity.	23933	5.8	34.4	337	6
50	LjSGA_077045.1	Nucleotide binding, ATP binding, endoplasmic reticulum.	31964	5.4	37.0	335	11
51	chr2.CM1731.130.nc	Iron ion binding, electron transport, transport, chloroplast, photosystem II, thylakoid, response to herbicide, photosynthesis, membrane, integral to membrane, photosynthesis, light reaction, light-harvesting complex, plasma membrane light-harvesting complex, electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity, metal ion binding.	38973	5.2	6.8	329	2
51	chr4.CM0126.1600.nc	Iron ion binding, electron transport, transport, chloroplast, photosystem II, thylakoid, response to herbicide, photosynthesis, membrane, integral to membrane, photosynthesis, light reaction, light-harvesting complex, plasma membrane light-harvesting complex, electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity, metal ion binding.	38996	5.2	3.1	44	1
51	LjSGA_137513.1	Electron transport, chloroplast, membrane, photosynthesis, light reaction, light-harvesting complex, plasma membrane light-harvesting complex, electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity.	8217	5.4	14.5	44	1
52	LjSGA_007175.1	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	20102	5.3	29.9	321	4
52	chr4.CM0399.240.nd	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	19050	5.6	20.5	176	3
52	chr1.CM0033.1170.nc	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	13520	9.4	7.5	67	1
53	chr1.CM0033.1130.nc	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	89398	5.2	19.8	318	13
53	LjSGA_044103.1	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	36149	5.0	28.0	270	7
53	LjSGA_042412.1	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	26226	5.6	31.1	198	6
53	chr1.CM0171.740.nd	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	67009	4.9	11.9	159	6
53	chr3.LjT44N20.100.nd	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	27363	5.2	12.1	76	2
54	LjT37C05.70.nd	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	63424	5.2	24.5	312	11
55	chr6.CM1829.160.nc	Catalytic activity, metabolic process, lyase activity.	65882	7.6	17.1	310	8
56	chr6.CM0013.290.nc	Sucrose metabolic process, biosynthetic process, sucrose synthase activity, transferase activity, transferase activity, transferring glycosyl groups, sucrose-phosphate synthase activity.	92671	5.8	18.9	310	15

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
56	LjSGA_128664.1	Sucrose metabolic process, biosynthetic process, sucrose synthase activity, transferase activity, transferase activity, transferring glycosyl groups.	22184	5.5	12.9	62	2
57	chr4.CM0194.140.nc	Calcium ion binding, chloroplast, photosystem II, thylakoid, oxygen evolving complex, photosynthesis, membrane, extrinsic to membrane, manganese ion binding, photosystem II stabilization.	34962	5.8	32.1	308	9
57	LjSGA_048614.2	Calcium ion binding, oxygen evolving complex, photosynthesis, extrinsic to membrane, photosystem II stabilization.	15888	9.6	36.9	80	5
57	LjSGA_118676.1	Calcium ion binding, chloroplast, photosystem II, thylakoid, oxygen evolving complex, photosynthesis, membrane, extrinsic to membrane, manganese ion binding, photosystem II stabilization.	12386	5.3	21.9	74	2
57	LjSGA_066867.1	Calcium ion binding, chloroplast, photosystem II, thylakoid, oxygen evolving complex, photosynthesis, membrane, extrinsic to membrane, manganese ion binding, photosystem II stabilization.	10606	7.9	12.0	66	1
58	LjSGA_031182.1	Enzyme inhibitor activity, cell wall, pectinesterase activity, cell wall modification.	24364	8.4	17.2	305	3
59	LjSGA_091355.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	19276	9.2	57.4	304	8
59	LjSGA_135941.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	10299	6.1	57.7	109	4
59	LjSGA_098067.1	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, integral to membrane, proton-transporting two-sector ATPase complex, hydrolase activity, nucleoside-triphosphatase activity, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	8025	7.9	59.5	81	3
60	LjSGA_052805.1	Nucleotide binding, ATP binding.	54416	10.1	10.5	302	6
61	chr2.CM0002.140.nc	Binding, protein binding, protein complex assembly, intracellular protein transport, vesicle-mediated transport, transferase activity, clathrin vesicle coat, clathrin coat of trans-Golgi network vesicle, clathrin coat of coated pit.	192321	5.3	10.9	302	17
61	LjSGA_147823.1	Protein binding, intracellular protein transport, vesicle-mediated transport.	18689	6.6	6.8	66	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
61	LjSGA_067209.1	Binding, protein binding, coated pit, protein complex assembly, intracellular protein transport, vesicle-mediated transport, clathrin vesicle coat, clathrin coat of trans-Golgi network vesicle, clathrin coat of coated pit.	37399	9.3	3.4	46	1
62	LjSGA_000862.1	Nucleotide binding, ATP binding, mitochondrion, ATP biosynthetic process, transport, ion transport, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, proton-transporting two-sector ATPase complex, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	26234	5.2	30.2	299	7
63	chr3.CM0112.180.nd	Nucleic acid binding, DNA binding, RNA binding, regulation of transcription, DNA-dependent, zinc ion binding, metal ion binding.	19214	5.9	22.2	297	3
64	chr2.CM0323.140.nc	Calcium ion binding, chloroplast, photosystem II, thylakoid, oxygen evolving complex, photosynthesis, membrane, extrinsic to membrane, manganese ion binding, photosystem II stabilization.	34999	5.6	19.3	290	6
65	chr1.CM0122.480.nc	GTP binding, intracellular, small GTPase mediated signal transduction.	20883	6.1	31.7	288	8
65	chr2.CM0008.210.nc	GTP binding, intracellular, small GTPase mediated signal transduction.	21815	6.9	30.4	288	8
65	LjSGA_037475.1	Nucleotide binding, GTP binding, intracellular, transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	14500	5.4	26.2	187	5
65	chr2.CM0250.220.nd	Nucleotide binding, GTP binding, intracellular, transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	5721	10.1	21.2	113	2
65	LjSGA_070137.1	GTP binding, intracellular, small GTPase mediated signal transduction.	7464	5.5	22.6	53	1
66	LjT05F15.160.nd	Transporter activity, binding, mitochondrial inner membrane, transport, membrane, integral to membrane.	40777	9.8	19.7	288	9
66	LjSGA_104961.1	Transporter activity, binding, mitochondrial inner membrane, transport, membrane, integral to membrane.	10234	10.0	23.7	117	3
67	chr5.CM0328.790.nd	Catalytic activity, fructose-bisphosphate aldolase activity, glycolysis, metabolic process, lyase activity.	36834	6.1	19.8	287	4
68	chr3.CM0160.510.nc	Transporter activity, binding, mitochondrial inner membrane, transport, membrane, integral to membrane.	39506	9.8	20.2	280	9
69	chr4.CM0006.600.nc	Sucrose metabolic process, biosynthetic process, nodulation, sucrose synthase activity, transferase activity, transferase activity, transferring glycosyl groups.	95907	5.8	15.1	278	12
69	LjT48H14.80.nd	Sucrose metabolic process, biosynthetic process, sucrose synthase activity, transferase activity, transferase activity, transferring glycosyl groups.	13932	6.3	14.8	78	2
69	LjSGA_038745.1	Sucrose metabolic process, biosynthetic process, nodulation, sucrose synthase activity, transferase activity, transferase activity, transferring glycosyl groups.	16517	4.6	15.9	42	3
70	chr2.CM0191.170.nc	Photosynthesis, light harvesting, membrane.	28625	5.5	14.7	275	5
71	chr2.CM0056.380.nc	Defense response, response to biotic stimulus.	16951	4.9	56.9	274	7
72	chr2.CM0304.350.nc	Iron ion binding, oxidoreductase activity.	40211	5.6	24.2	267	6

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
73	LjSGA_000588.1	Nucleotide binding, ATP binding, mitochondrion, ATP biosynthetic process, transport, ion transport, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, proton-transporting two-sector ATPase complex, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	46892	8.5	15.8	266	6
73	LjSGA_000590.1	Nucleotide binding, ATP binding, mitochondrion, ATP biosynthetic process, transport, ion transport, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, proton-transporting two-sector ATPase complex, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	18729	7.9	15.2	126	2
74	LjSGA_057408.1	Nucleotide binding, ATP binding, endoplasmic reticulum.	27465	9.2	15.1	262	4
75	chr4.LjT30K03.110.nc	Metabolic process, oxidoreductase activity.	54420	5.4	24.9	260	10
76	LjSGA_014613.2	Phosphoglycerate kinase activity, glycolysis, kinase activity.	7278	4.8	37.0	251	2
76	LjSGA_047542.1	Phosphoglycerate kinase activity, glycolysis, kinase activity.	10715	5.1	16.2	236	1
77	chr1.CM0032.460.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	26346	10.2	26.9	251	5
78	chr5.CM0077.110.nd	Catalytic activity, cellular metabolic process, coenzyme binding.	38166	6.3	16.8	251	5
79	LjT22I05.20.nd	Catalytic activity, aspartate transaminase activity, amino acid metabolic process, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, pyridoxal phosphate binding.	45430	8.8	20.1	245	6
79	LjSGA_110862.1	Catalytic activity, aspartate transaminase activity, amino acid metabolic process, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, pyridoxal phosphate binding.	17178	9.2	16.8	74	2
80	chr3.CM0282.260.nc	Catalytic activity, tricarboxylic acid cycle, phosphoenolpyruvate carboxylase activity, carbon utilization by fixation of carbon dioxide, lyase activity.	110503	5.6	12.7	245	10
80	LjSGA_016084.1	Catalytic activity, tricarboxylic acid cycle, phosphoenolpyruvate carboxylase activity, carbon utilization by fixation of carbon dioxide, lyase activity.	63160	6.2	9.4	57	4
81	LjSGA_045033.1	No GO annotations found.	16687	5.0	18.1	244	3
82	chr1.CM0122.340.nc	Nucleotide binding, magnesium ion binding, methionine adenosyltransferase activity, ATP binding, one-carbon compound metabolic process, transferase activity, potassium ion binding, metal ion binding.	43042	5.5	13.5	241	5
83	LjT41B11.100.nd	Nucleotide binding, ATP binding.	74373	5.5	9.8	237	8
84	LjSGA_009509.2	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	17797	9.0	36.1	236	5
85	LjSGA_027059.1	Ketol-acid reductoisomerase activity, branched chain family amino acid biosynthetic process, oxidoreductase activity, coenzyme binding.	28627	9.3	15.7	233	5
86	LjSGA_066441.1	ATP binding.	47090	7.1	6.4	233	4
86	LjSGA_077967.1	ATP binding.	43502	8.4	6.6	152	3
87	chr1.LjT36P09.130.nd	Nucleotide binding, ATP binding.	23248	8.5	8.1	233	2
88	chr3.CM0115.330.nc	Iron ion binding, electron transport, lipoxygenase activity, metal ion binding.	97350	6.0	12.8	232	10

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Supplemental Table S2.1: (*green_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
88	chr3.LjT02L14.10.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylipin biosynthetic process, metal ion binding.	97160	6.0	1.3	81	1
88	LjT30L14.30.nd	Iron ion binding, electron transport, lipoxxygenase activity, metal ion binding.	38459	6.1	3.0	52	1
89	LjSGA_020408.2	ATP binding.	61975	6.1	7.6	232	4
89	chr1.LjT14I13.240.nd	ATP binding.	67653	8.6	5.3	205	2
89	LjSGA_097163.1	ATP binding.	39517	8.5	4.5	90	1
89	chr2.CM0120.590.nd	ATP binding.	67142	8.2	2.6	90	1
90	chr3.CM0106.290.nc	Enzyme inhibitor activity, pectinesterase activity.	20382	5.5	7.4	230	1
91	chr1.CM0023.30.nc	Magnesium ion binding, isocitrate dehydrogenase (NADP+) activity, glyoxylate cycle, tricarboxylic acid cycle, isocitrate metabolic process, metabolic process, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, manganese ion binding, metal ion binding.	45978	6.0	14.3	229	5
92	chr4.CM0337.850.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process.	83765	7.5	7.6	225	5
93	chr3.CM0091.670.nd	Nucleotide binding, nucleic acid binding.	9784	4.6	41.8	225	4
94	chr3.LjT02L14.80.nd	Nucleotide binding, nucleic acid binding, RNA binding, translation initiation factor activity, helicase activity, ATP binding, translation, ATP-dependent helicase activity, hydrolase activity.	46693	5.4	27.8	223	10
94	LjSGA_011343.1	Nucleotide binding, nucleic acid binding, translation initiation factor activity, helicase activity, ATP binding, ATP-dependent helicase activity, hydrolase activity.	34511	6.6	33.3	177	9
94	chr6.LjT10I04.10.nd	Nucleotide binding, nucleic acid binding, helicase activity, ATP binding, ATP-dependent helicase activity, hydrolase activity.	56308	6.1	15.2	159	7
95	chr1.CM0113.740.nd	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	48139	6.8	14.3	223	7
96	LjSGA_042776.1.2	Chloroplast, photosystem, photosynthetic electron transport, photosynthetic electron transport in photosystem II, membrane, chlorophyll binding, photosynthesis, light reaction, light-harvesting complex, electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity.	7571	10.5	23.9	221	1
97	chr6.CM0302.70.nc	Binding, protein binding, protein complex assembly, intracellular protein transport, vesicle-mediated transport, transferase activity, clathrin vesicle coat, clathrin coat of trans-Golgi network vesicle, clathrin coat of coated pit.	193031	5.3	10.3	220	16
98	chr1.CM0078.20.nc	Zinc ion binding, oxidoreductase activity, metal ion binding.	40989	7.5	18.9	219	8
99	chr1.CM0206.650.nd	Nucleotide binding, magnesium ion binding, methionine adenosyltransferase activity, ATP binding, one-carbon compound metabolic process, transferase activity, potassium ion binding, metal ion binding.	36905	5.3	13.5	219	4
100	LjSGA_008893.1	Calcium ion binding, cytoplasm.	18920	4.4	38.7	216	7
100	chr5.CM0299.300.nc	Cytoplasm.	19063	4.5	11.4	55	3
101	LjT09K03.140.nd	Aldehyde dehydrogenase (NAD) activity, metabolic process, oxidoreductase activity.	46087	6.4	18.9	208	7
102	LjSGA_039603.1	Calcium ion binding, chloroplast, photosystem II, thylakoid, oxygen evolving complex, photosynthesis, membrane, extrinsic to membrane.	10413	5.0	46.2	208	4
102	chr2.LjT36E17.90.nd	Calcium ion binding, chloroplast, photosystem II, thylakoid, oxygen evolving complex, photosynthesis, membrane, extrinsic to membrane.	28204	7.6	8.1	133	2
103	LjSGA_037126.2	Phosphoglycerate kinase activity, glycolysis, kinase activity.	14881	11.6	20.4	206	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
104	chr1.CM1409.60.nd	Calcium ion binding.	16821	4.1	22.1	206	2
104	LjSGA_007638.2	Calcium ion binding.	4463	3.8	43.6	92	1
104	LjSGA_007639.1	Calcium ion binding.	5758	4.1	33.3	92	1
104	LjSGA_007640.1	Calcium ion binding.	3933	3.8	50.0	92	1
105	chr3.CM0111.290.nc	Catalytic activity, tricarboxylic acid cycle, phosphoenolpyruvate carboxylase activity, carbon utilization by fixation of carbon dioxide, lyase activity.	110361	5.8	10.4	206	8
106	LjSGA_009490.3	ATP binding.	57986	8.5	8.0	205	3
106	LjSGA_030928.1	ATP binding.	33953	8.4	8.8	90	2
107	chr4.CM0119.240.nc	No GO annotations found.	41227	5.8	27.3	204	10
107	LjSGA_025931.2	Iron ion binding, oxidoreductase activity.	29758	4.9	29.8	156	8
108	LjSGA_117475.1	Chloroplast, photosystem, photosystem II, thylakoid, photosynthetic electron transport, photosynthesis, membrane, integral to membrane, chlorophyll binding, protein-chromophore linkage, photosynthesis, light reaction.	26277	6.1	17.6	202	3
108	LjSGA_122035.1	Chloroplast, photosystem, photosystem II, thylakoid, photosynthetic electron transport, photosynthesis, membrane, integral to membrane, chlorophyll binding, protein-chromophore linkage, photosynthesis, light reaction.	31116	6.2	14.7	202	3
108	LjSGA_123451.1	Chloroplast, photosystem, photosystem II, thylakoid, photosynthetic electron transport, photosynthesis, membrane, integral to membrane, chlorophyll binding, protein-chromophore linkage, photosynthesis, light reaction.	35039	6.7	12.9	202	3
108	LjSGA_114943.1	Chloroplast, photosystem, photosystem II, thylakoid, photosynthetic electron transport, photosynthesis, membrane, integral to membrane, chlorophyll binding, protein-chromophore linkage, photosynthesis, light reaction.	23562	8.7	5.3	113	1
109	chr3.LjT36L08.60.nc	Transketolase activity.	79704	6.3	13.8	199	8
110	chr3.LjT44N20.110.nd	Nucleotide binding, ATP binding, hydrolase activity, nucleoside-triphosphatase activity.	31212	5.1	25.6	198	6
111	chr2.LjT43N03.40.nd	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-bisphosphate carboxylase activity.	20037	9.2	16.9	196	4
111	chr1.LjT23D08.110.nc	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-bisphosphate carboxylase activity.	20329	9.0	4.4	51	1
111	chr1.LjT23D08.120.nc	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-bisphosphate carboxylase activity.	20317	9.2	4.4	51	1
111	LjSGA_030971.1	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-bisphosphate carboxylase activity.	13968	8.4	6.7	51	1
111	LjSGA_080821.1	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-bisphosphate carboxylase activity.	13955	8.4	6.7	51	1
112	chr4.CM0558.210.nc	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	50030	4.8	12.8	192	5
112	LjSGA_119221.2	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	15546	4.8	12.9	127	1
112	LjSGA_050733.1	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	31610	9.0	9.5	97	3

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
113	chr4.CM0007.1330.nd	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	49957	4.8	16.7	191	6
113	chr5.CM0148.400.nd	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	50368	4.7	16.5	191	6
113	chr6.CM0437.270.nc	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	50157	4.8	16.6	191	6
113	LjSGA_012413.2	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	50082	4.8	16.6	191	6
113	chr1.CM0269.190.nc	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	50574	4.8	12.7	188	5
113	LjSGA_034231.2	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	30999	6.1	15.5	129	3
113	LjSGA_045028.1	Nucleotide binding, GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	35751	4.7	12.4	99	4
113	LjSGA_112910.1	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	25481	4.8	9.6	43	2
114	LjSGA_030747.1	Nucleotide binding, ATP binding.	60978	8.5	10.3	191	5
115	LjSGA_012865.1	ATP binding.	54588	6.4	8.3	191	4
116	LjSGA_061979.1	Enzyme inhibitor activity, cell wall, pectinesterase activity, cell wall modification.	32507	7.7	22.2	189	6
117	chr4.CM0179.140.nc	Aminopeptidase activity, leucyl aminopeptidase activity, intracellular, cytoplasm, proteolysis, protein metabolic process, manganese ion binding.	59662	7.6	7.2	188	3
117	LjT06N06.10.nd	Aminopeptidase activity, leucyl aminopeptidase activity, intracellular, cytoplasm, proteolysis, protein metabolic process, manganese ion binding.	60335	8.1	7.2	188	3
118	chr5.CM0200.1290.nc	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, metabolic process, hydrolase activity, hydrolase activity, acting on glycosyl bonds, cation binding, xylan catabolic process.	62823	6.7	3.6	187	3
119	chr4.CM0042.2380.nc	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	49880	4.8	11.0	186	4
120	LjT24E19.100.nc	Nucleotide binding, catalytic activity, ATP binding, protein modification process, ubiquitin cycle, small protein activating enzyme activity, ligase activity.	126086	5.2	9.1	186	9
121	chr4.CM0006.280.nc	ATP binding, protein folding.	26812	8.9	28.0	185	5
122	chr6.CM0420.60.nd	ATP binding, protein folding.	29859	9.2	29.6	184	6
123	chr4.CM0042.1650.nc	Regulation of progression through cell cycle, binding, cytosol, protein complex.	108879	5.2	4.4	183	3
124	LjSGA_048339.1	Nucleotide binding, ATP binding, protein folding, unfolded protein binding.	57950	5.3	15.3	182	8
125	chr1.CM0544.400.nd	Pepsin A activity, proteolysis.	18881	8.7	22.5	181	3
126	LjSGA_039892.1	Electron transport, oxidoreductase activity, monodehydroascorbate reductase (NADH) activity, FAD binding.	17202	5.6	9.7	180	1

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
127	chr1.CM0378.40.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	28895	10.4	19.8	179	4
127	chr2.LjT09A11.20.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	30326	10.4	18.7	179	4
127	chr4.CM0042.1380.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	30215	10.4	18.9	179	4
127	LjSGA_025794.2	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	29818	10.3	19.1	179	4
127	chr2.CM0803.780.nd	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	10459	10.8	13.7	84	1
128	chr1.CM0206.500.nd	Catalytic activity, carbohydrate metabolic process, cation binding.	46672	5.8	18.1	179	6
129	chr2.CM0191.240.nc	ATP binding, protein folding, unfolded protein binding.	90455	5.2	3.3	175	2
130	chr6.CM0037.640.nd	Aminopeptidase activity, leucyl aminopeptidase activity, intracellular, cytoplasm, proteolysis, protein metabolic process, manganese ion binding.	60227	5.8	7.8	174	3
131	chr1.CM0544.80.nc	Superoxide dismutase activity, copper, zinc superoxide dismutase activity, copper ion binding, superoxide metabolic process, zinc ion binding, oxidoreductase activity, metal ion binding.	15314	6.3	23.0	172	3
132	chr5.CM0260.80.nd	Transketolase activity.	74962	6.2	7.8	170	5
133	chr1.CM0029.350.nd	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	17491	10.2	34.2	166	5
133	LjSGA_013603.1	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	9107	9.8	54.8	166	4
134	LjSGA_088368.2	Structural constituent of ribosome, intracellular, ribosome, translation.	40318	10.3	16.8	166	5
134	LjSGA_044287.1	Structural constituent of ribosome, intracellular, ribosome, translation.	27876	10.5	19.1	140	4
134	LjSGA_029445.1	Structural constituent of ribosome, intracellular, ribosome, translation.	42140	10.9	12.9	129	4
134	LjSGA_055825.1	Structural constituent of ribosome, intracellular, ribosome, translation.	16108	11.9	9.3	54	1
135	chr4.CM0042.2090.nc	No GO annotations found.	35674	7.6	33.0	164	8
136	chr1.CM0051.30.nc	Mitochondrial outer membrane, transport, ion transport, anion transport, voltage-gated ion-selective channel activity, porin activity, membrane, integral to membrane, outer membrane.	29522	8.6	25.7	163	6
136	chr2.CM0225.90.nc	Catalytic activity, plastid, chloroplast fission, cellular metabolic process, coenzyme binding.	6010	6.7	22.6	74	1
137	LjSGA_017053.1	DNA binding, ATP binding.	36329	6.7	7.9	161	2
138	chr4.CM0087.970.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	43394	8.1	11.2	161	3
139	chr3.CM0070.20.nc	Carboxypeptidase activity, serine carboxypeptidase activity, proteolysis.	56953	5.2	9.2	161	3
140	LjSGA_046206.1	Translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translational elongation.	52429	9.7	10.5	160	5
141	chr1.CM0017.210.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	26025	9.6	14.9	158	3
141	LjSGA_009417.2	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	18207	9.7	8.2	109	1
141	LjSGA_042121.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	9659	9.9	10.2	59	1
142	chr6.LjT21O06.20.nd	Acetyl-CoA C-acyltransferase activity, acyltransferase activity, transferase activity.	49210	8.0	13.2	157	5
143	LjSGA_100436.1	NADPH:quinone reductase activity, FMN binding, oxidoreductase activity.	19848	6.5	19.3	155	3
143	chr3.LjT01D08.20.nd	FMN binding, oxidoreductase activity, 2-hydroxy-1,4-benzoquinone reductase activity.	22203	6.9	12.3	132	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
144	chr2.LjT30P12.40.nc	Monolayer-surrounded lipid storage body.	20658	9.0	23.6	153	4
145	LjT04N09.110.nd	Photosynthesis, light harvesting, membrane.	16838	4.5	22.2	152	3
146	CM0319.40.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, rRNA binding, ribonucleoprotein complex.	20660	9.9	17.7	152	4
146	LjT43K05.240.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	19606	9.9	18.7	152	4
146	chr1.CM0133.1120.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, rRNA binding, ribonucleoprotein complex.	17857	10.0	9.0	110	1
147	chr3.CM0116.230.nc	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	27248	6.0	18.4	151	4
148	LjSGA_129817.1	ATP binding, protein folding, unfolded protein binding.	17910	4.4	14.0	150	2
149	chr2.CM0210.260.nc	Catalytic activity, fructose-bisphosphate aldolase activity, glycolysis, metabolic process, lyase activity.	38366	6.1	6.2	150	2
150	LjSGA_014826.1	No GO annotations found.	39252	8.9	3.8	150	3
151	chr5.LjT43D06.110.nd	Calcium ion binding, sugar binding, manganese ion binding, metal ion binding.	30790	5.7	10.4	150	2
152	chr5.CM0359.200.nc	Catalytic activity, fructose-bisphosphate aldolase activity, glycolysis, metabolic process, lyase activity.	38600	5.8	8.1	149	3
153	chr3.CM0142.570.nd	Catalytic activity, phospholipase D activity, calcium ion binding, metabolic process, membrane, lipid catabolic process, hydrolase activity, phosphatidylcholine metabolic process.	66538	5.9	7.3	149	3
154	chr5.CM0357.340.nc	No GO annotations found.	26210	4.8	34.1	149	5
155	chr1.CM0109.50.nd	Endopeptidase activity, threonine endopeptidase activity, nucleus, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	25562	5.5	27.2	147	6
155	LjSGA_070271.1	Endopeptidase activity, threonine endopeptidase activity, nucleus, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	5515	9.8	27.7	60	2
156	chr2.LjT07F03.120.nd	Nucleotide binding, catalytic activity, 6-phosphofructokinase activity, ATP binding, 6-phosphofructokinase complex, glycolysis, kinase activity, transferase activity, diphosphate-fructose-6-phosphate 1-phosphotransferase activity.	67251	7.2	10.8	146	5
156	chr1.CM0315.320.nc	6-phosphofructokinase activity, ATP binding, 6-phosphofructokinase complex, glycolysis, diphosphate-fructose-6-phosphate 1-phosphotransferase activity.	14160	7.9	9.2	54	1
156	chr2.LjT07F03.160.nd	Nucleotide binding, catalytic activity, 6-phosphofructokinase activity, ATP binding, 6-phosphofructokinase complex, glycolysis, kinase activity, transferase activity, diphosphate-fructose-6-phosphate 1-phosphotransferase activity.	7230	4.7	18.8	54	1
157	chr2.CM0608.590.nc	No GO annotations found.	31272	5.2	25.2	145	8
157	chr2.CM0608.600.nc	No GO annotations found.	31865	5.5	9.3	57	3
157	chr1.CM0123.430.nd	No GO annotations found.	31236	5.8	6.3	44	2
157	chr4.CM0170.300.nc	No GO annotations found.	31342	6.2	6.3	44	2
157	chr2.CM0225.110.nc	No GO annotations found.	31400	5.3	3.5	43	1
158	chr2.CM0373.850.nc	ATP binding.	69816	8.4	9.1	145	5
159	chr6.CM0139.590.nd	Oxidoreductase activity.	7016	4.5	43.1	145	2
160	chr4.CM0042.300.nc	Isomerase activity.	41205	5.9	9.8	143	3
161	chr5.CM0909.680.nc	Protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	59951	5.4	8.5	141	4

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
161	LjSGA_060796.1	Protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	20662	6.6	6.8	75	1
162	chr3.CM0634.370.nd	Catalytic activity, phosphoglycerate mutase activity, cytoplasm, glucose catabolic process, glycolysis, metabolic process, isomerase activity, manganese ion binding, metal ion binding.	60759	5.6	14.0	140	7
163	chr2.CM0168.100.nd	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	21439	9.4	11.8	139	2
163	LjSGA_019093.1	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	11179	9.1	8.8	51	1
164	CM0385.200.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, metabolic process, hydrolase activity, hydrolase activity, acting on glycosyl bonds, alpha-N-arabinofuranosidase activity.	42675	5.8	16.7	139	5
165	LjT19C19.50.nd	Aldehyde dehydrogenase (NAD) activity, metabolic process, oxidoreductase activity.	59155	8.0	8.1	139	3
166	LjSGA_011457.1	Transporter activity, binding, transport.	8493	4.2	37.5	139	2
167	chr1.CM0318.150.nd	Protein binding.	20026	8.6	6.1	138	1
168	LjSGA_015149.2	No GO annotations found.	41654	8.9	15.0	136	4
169	LjSGA_028864.1	ATP binding.	56236	5.0	8.5	136	5
170	chr1.CM0222.290.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	9362	9.3	45.2	135	3
171	LjSGA_085408.1	ATP binding.	15678	5.8	24.1	134	3
171	LjSGA_046788.2	Nucleotide binding, ATP binding.	27622	10.1	4.4	63	1
172	chr3.CM0106.300.nc	Ribokinase activity, D-ribose metabolic process, kinase activity.	35456	5.1	12.4	133	3
173	chr4.CM0042.1220.nc	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	17161	10.4	19.0	133	2
174	chr5.CM1574.170.nc	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	17092	10.4	19.2	130	2
175	LjSGA_021840.1	Structural constituent of ribosome, intracellular, ribosome, translational elongation.	11256	4.5	29.8	130	3
175	LjSGA_090516.1	Structural constituent of ribosome, intracellular, ribosome, translational elongation.	8856	5.2	36.2	130	3
176	chr3.CM0279.310.nc	Oxygen evolving complex, photosynthesis, thylakoid membrane.	14295	9.7	22.3	128	4
177	LjB14K02.60.nc	ATP binding, protein folding, unfolded protein binding.	75721	5.2	6.0	128	4
178	LjSGA_021837.1	Isocitrate dehydrogenase (NADP+) activity, glyoxylate cycle, isocitrate metabolic process, metabolic process, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, metal ion binding.	14843	7.8	9.5	127	1
179	chr6.LjT34E09.150.nc	Translation elongation factor activity, eukaryotic translation elongation factor 1 complex, translation, translational elongation.	25377	4.5	29.7	126	6
179	LjT39M07.170.nd	Translation elongation factor activity, eukaryotic translation elongation factor 1 complex, translation, translational elongation.	19251	8.7	4.0	42	1
180	chr3.LjT58I15.10.nd	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, proton-transporting two-sector ATPase complex, hydrolase activity, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	29590	8.7	12.8	126	3
181	chr2.CM0608.90.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process.	28217	8.1	25.8	126	6

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
182	LjSGA_021523.1	Catalytic activity, ATP binding, metabolic process.	25922	5.0	6.7	125	1
183	chr5.LjT43D06.20.nd	Calcium ion binding, sugar binding, manganese ion binding, metal ion binding.	23814	5.6	11.4	125	2
184	LjSGA_043096.1	Catalytic activity, metabolic process, amino acid biosynthetic process, dihydrodipicolinate synthase activity, lysine biosynthetic process, chloroplast, lyase activity, diaminopimelate biosynthetic process.	11819	5.6	29.2	125	4
185	chr4.CM0307.10.nc	Catalytic activity, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, 1-aminocyclopropane-1-carboxylate synthase activity, pyridoxal phosphate binding.	31263	7.7	9.4	125	2
185	chr6.LjT23A02.90.nc	Catalytic activity, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, 1-aminocyclopropane-1-carboxylate synthase activity, pyridoxal phosphate binding.	38236	6.6	4.3	82	1
186	LjSGA_119931.1	Translation elongation factor activity, GTPase activity, GTP binding.	30930	6.9	14.7	125	6
187	LjSGA_039295.1	Catalytic activity, transaldolase activity, cytoplasm, carbohydrate metabolic process, pentose-phosphate shunt, metabolic process.	18895	4.8	15.0	122	2
188	chr2.CM0008.290.nc	Structural constituent of ribosome, intracellular, ribosome, translation, protein modification process.	17640	9.9	17.4	120	3
188	LjT12A09.240.nd	Protein modification process.	13451	6.4	22.7	120	3
188	LjSGA_014576.1	Protein modification process.	11073	5.8	27.3	120	3
188	LjSGA_047101.1	Structural constituent of ribosome, intracellular, ribosome, translation, protein modification process.	14504	8.9	21.1	120	3
188	LjSGA_049093.1	Copper ion binding, mitochondrial intermembrane space, protein modification process, copper ion transport, copper chaperone activity.	12480	5.2	24.5	120	3
188	LjSGA_056269.1	Structural constituent of ribosome, intracellular, ribosome, translation, protein modification process.	17696	9.9	17.4	120	3
188	LjSGA_010124.3	Structural constituent of ribosome, intracellular, ribosome, translation, protein modification process.	18766	8.5	16.2	120	3
188	LjSGA_044371.1	Protein modification process.	26546	6.2	11.6	120	3
188	LjSGA_103437.1	Protein modification process.	24361	6.3	12.4	120	3
188	chr3.CM0292.520.nc	Protein modification process.	34171	6.9	8.9	120	3
188	LjT12A09.340.nd	Protein modification process.	34082	6.5	8.9	120	3
188	chr5.CM0956.190.nd	Protein modification process.	42673	7.0	7.1	120	3
188	LjSGA_029363.2	Structural constituent of ribosome, intracellular, ribosome, translation, protein modification process.	14299	8.1	14.5	120	2
188	LjSGA_063041.1	Structural constituent of ribosome, intracellular, ribosome, translation, protein modification process.	14299	8.1	14.5	120	2
189	LjT04M14.100.nd	Binding, protein binding, endoplasmic reticulum, Golgi-associated vesicle, protein complex assembly, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, protein transport, membrane, vesicle-mediated transport, COPI vesicle coat.	105755	5.6	3.7	119	3
190	chr2.CM0225.70.nc	Mitochondrial outer membrane, transport, ion transport, anion transport, voltage-gated ion-selective channel activity, porin activity, membrane, integral to membrane, outer membrane.	29696	8.6	18.8	118	5
191	chr5.CM0048.40.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, chloroplast, isomerase activity, peptide binding.	28628	9.0	8.0	117	2
192	LjSGA_029072.1	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization, cell division.	28525	5.8	5.6	117	1
193	chr4.CM0087.380.nc	Translation initiation factor activity, translational initiation.	17417	5.6	30.6	116	4
193	chr4.CM0179.120.nc	Translation initiation factor activity, translational initiation.	17517	5.5	5.0	57	1
193	LjT33K05.120.nd	Translation initiation factor activity, translational initiation.	9170	5.1	9.5	57	1

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
193	LjSGA_031436.1	Translation initiation factor activity, translational initiation.	12646	4.8	6.8	57	1
194	chr4.CM0165.150.nd	ATP binding, cytoplasm, ATP biosynthetic process, transport, ion transport, hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrogen ion transporter activity, ATP synthesis coupled proton transport, energy coupled proton transport, against electrochemical gradient, proton transport, proton-transporting two-sector ATPase complex, hydrolase activity, metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	42220	4.8	13.0	116	4
195	LjSGA_078699.1	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	22601	5.3	13.2	116	3
196	chr6.CM0014.300.nc	Catalytic activity, glutamate-ammonia ligase activity, glutamine biosynthetic process, nitrogen compound metabolic process, ligase activity.	39123	5.5	19.4	115	6
196	LjSGA_019428.1	Catalytic activity, glutamate-ammonia ligase activity, glutamine biosynthetic process, nitrogen compound metabolic process, nitrogen fixation, ligase activity.	12735	9.2	26.1	66	3
197	LjSGA_091217.1	Translation elongation factor activity, GTPase activity, GTP binding.	40722	8.7	11.2	115	4
197	LjSGA_018952.1	Translation elongation factor activity, GTPase activity, GTP binding.	38951	5.2	3.4	43	1
197	LjSGA_036784.1	Translation elongation factor activity, GTPase activity, GTP binding.	31098	5.0	4.3	43	1
198	chr3.LjT39G24.130.nd	Nucleotide binding, ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport, membrane.	23613	6.7	16.8	115	3
198	chr5.CM0180.240.nd	Nucleotide binding, ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport, membrane.	23761	6.6	16.7	115	3
198	chr1.LjT29L18.70.nd	Nucleotide binding, ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport, membrane.	22309	5.3	10.8	87	2
198	LjSGA_017346.1	ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport.	9063	9.4	27.2	87	2
198	LjSGA_013646.2	ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport.	13398	8.7	18.6	87	2
199	LjSGA_039694.1	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, alpha-galactosidase activity, carbohydrate metabolic process, metabolic process, hydrolase activity, hydrolase activity, acting on glycosyl bonds.	21709	8.9	6.8	115	1
200	LjT06B16.110.nc	Argininosuccinate synthase activity, ATP binding, arginine biosynthetic process.	52532	6.4	6.3	114	2
201	chr4.CM0007.620.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	18459	10.4	14.0	114	2
201	LjT35M05.50.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	17892	11.0	14.6	114	2
202	chr4.CM0617.490.nd	Malic enzyme activity, malate metabolic process, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, NAD binding.	65157	5.7	5.1	114	2
203	LjSGA_038270.1	Protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	15757	5.4	12.3	113	1
204	chr4.CM0173.280.nc	Cysteine-type endopeptidase activity, proteolysis, peptidase activity, cysteine-type peptidase activity, hydrolase activity.	39743	5.6	5.3	113	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
205	LjT42M11.210.nc	Endopeptidase activity, threonine endopeptidase activity, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process.	30257	4.8	17.8	113	4
206	chr4.CM0087.390.nc	Catalytic activity, fructose-bisphosphate aldolase activity, glycolysis, metabolic process, lyase activity.	43135	7.6	7.0	112	2
207	chr1.LjT14I13.60.nd	Argininosuccinate synthase activity, ATP binding, arginine biosynthetic process.	52561	6.8	6.3	112	2
208	LjSGA_019550.1	ATP binding.	74420	9.4	6.9	112	4
209	chr1.CM0147.760.nc	Catalytic activity, chloroplast, cellular metabolic process, coenzyme binding.	33881	9.0	19.5	111	5
210	chr4.CM0288.640.nc	No GO annotations found.	16393	4.1	15.3	111	2
211	LjSGA_011044.2	Phosphoglycerate dehydrogenase activity, L-serine biosynthetic process, metabolic process, amino acid binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, cofactor binding, NAD binding.	57872	6.3	11.2	110	4
212	LjSGA_010022.2	Transferase activity.	30099	9.2	13.3	109	3
213	LjT41B11.10.nd	Nucleotide binding, ATP binding.	104633	5.6	6.1	109	5
214	chr1.CM0133.1430.nc	Nucleotide binding, ATP binding.	55509	5.6	8.0	108	3
215	chr1.CM0033.430.nc	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	15111	10.3	8.1	108	1
216	chr4.CM1616.30.nc	Catalytic activity, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, pyridoxal phosphate binding.	35416	5.0	7.1	107	2
217	LjSGA_041684.1	Phosphopyruvate hydratase complex, magnesium ion binding, phosphopyruvate hydratase activity, glycolysis, lyase activity.	28535	7.4	9.3	106	2
218	LjSGA_122913.1	Biosynthetic process, chlorophyll biosynthetic process, magnesium chelatase activity.	27547	5.8	12.0	105	2
219	LjSGA_147294.1	Ketol-acid reductoisomerase activity, branched chain family amino acid biosynthetic process, oxidoreductase activity, coenzyme binding.	13711	5.2	9.8	105	1
220	chr1.CM0410.90.nc	Nucleotide binding, ATP binding, ATP biosynthetic process, transport, ion transport, chloroplast, thylakoid, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, membrane, proton-transporting two-sector ATPase complex, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, plasma membrane ATP synthesis coupled proton transport, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	13769	8.1	26.2	105	3
221	chr1.CM0016.120.nc	Protein domain specific binding.	29128	4.7	22.0	104	7
221	LjT06N06.430.nd	Protein domain specific binding.	19296	5.5	27.5	87	5
221	LjT09J10.70.nc	Protein domain specific binding.	12508	8.7	17.1	67	2
221	chr1.CM0982.360.nd	Protein domain specific binding.	5098	4.0	22.2	56	2
221	LjT46P06.260.nd	Protein domain specific binding.	22997	4.6	5.0	56	2
221	LjSGA_024472.2	Protein domain specific binding.	26859	5.2	4.1	56	2
221	LjSGA_087842.1	Protein domain specific binding.	6412	3.8	17.5	56	2
221	LjSGA_104179.1	Protein domain specific binding.	7430	4.2	15.2	56	2
222	chr1.CM0171.170.nc	Superoxide dismutase activity, copper, zinc superoxide dismutase activity, superoxide metabolic process, oxidoreductase activity, metal ion binding.	9276	4.7	41.8	104	3
222	chr3.CM0396.590.nc	Copper, zinc superoxide dismutase activity, copper ion binding, superoxide metabolic process, zinc ion binding, oxidoreductase activity, metal ion binding.	20424	6.2	19.2	104	3

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
222	chr1.CM0033.280.nc	Superoxide dismutase activity, copper, zinc superoxide dismutase activity, superoxide metabolic process, oxidoreductase activity, metal ion binding.	11008	5.7	22.1	79	2
223	LjSGA_013718.1	UTP:glucose-1-phosphate uridylyltransferase activity, metabolic process, transferase activity, nucleotidyltransferase activity.	20394	5.1	15.1	103	2
224	chr2.CM0191.630.nc	No GO annotations found.	41560	6.2	9.6	103	3
224	chr6.LjT17105.60.nd	Transferase activity.	5567	9.3	17.5	66	1
225	LjSGA_082478.1	Nucleotide binding, magnesium ion binding, nucleoside diphosphate kinase activity, ATP binding, GTP biosynthetic process, UTP biosynthetic process, CTP biosynthetic process, nucleotide metabolic process, pyrimidine ribonucleoside triphosphate biosynthetic process, kinase activity, transferase activity, metal ion binding.	13028	6.8	30.6	102	4
226	LjSGA_005533.1	Catalytic activity, metabolic process, amino acid biosynthetic process, dihydroadipic acid synthase activity, lysine biosynthetic process, chloroplast, lyase activity, diaminopimelate biosynthetic process.	38349	5.9	3.2	102	1
227	chr1.CM0591.260.nd	Endopeptidase activity, threonine endopeptidase activity, nucleus, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	22645	6.2	9.7	101	2
228	chr3.CM0116.300.nc	Binding, iron ion transport, iron ion homeostasis, ferric iron binding, oxidoreductase activity, transition metal ion binding.	29020	5.5	9.5	101	2
229	LjT24M21.140.nd	Photosynthesis, light harvesting, membrane.	31570	5.5	17.2	100	5
229	LjT24M21.110.nd	Photosynthesis, light harvesting, membrane.	13178	5.9	7.6	53	1
229	LjSGA_018808.1	Magnesium ion binding, chloroplast, photosystem I, photosystem II, chloroplast thylakoid membrane, thylakoid, photosynthesis, light harvesting, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding.	30476	5.7	3.3	48	1
230	chr4.LjT06107.80.nd	Structural constituent of ribosome, intracellular, ribosome, translational elongation, ribonucleoprotein complex.	12273	4.4	17.4	100	1
231	LjSGA_121474.1	Ribokinase activity, D-ribose metabolic process, kinase activity, transferase activity.	10993	5.0	23.7	99	2
231	LjSGA_131611.1	No GO annotations found.	6677	4.7	39.7	99	2
231	LjSGA_043018.2	No GO annotations found.	8017	5.4	15.5	99	1
232	chr6.CM0114.320.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	28148	10.7	12.5	99	2
232	LjT31M07.110.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	25393	11.0	14.0	99	2
233	LjSGA_064073.1	No GO annotations found.	19178	6.3	18.0	99	2
234	chr3.CM0106.120.nd	Proteolysis, caspase activity.	45954	5.0	11.3	98	3
235	chr2.CM0788.10.nc	Translation elongation factor activity, eukaryotic translation elongation factor 1 complex, translational elongation, transferase activity.	47910	5.7	10.2	97	4
235	chr4.CM0042.1550.nc	Translation elongation factor activity, eukaryotic translation elongation factor 1 complex, translational elongation, transferase activity.	47537	5.7	10.3	97	4
236	LjSGA_067100.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, rRNA binding, ribonucleoprotein complex.	19719	10.2	27.4	96	5
236	LjSGA_044802.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, rRNA binding, ribonucleoprotein complex.	16435	10.2	21.8	79	3
237	LjSGA_053319.1	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	16284	5.4	13.6	95	1
238	chr1.CM0800.280.nd	No GO annotations found.	17207	7.8	20.6	95	2
239	chr3.CM0080.50.nd	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	71754	8.4	1.8	95	1
240	LjSGA_077260.1	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	36123	4.8	3.5	95	1
241	LjT41F16.210.nd	No GO annotations found.	34280	8.7	4.0	95	1

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
242	chr3.CM0136.230.nd	Mitochondrion, endoplasmic reticulum, response to oxidative stress, isomerase activity, cell redox homeostasis.	63438	4.5	10.1	95	5
243	chr6.CM0037.760.nc	Catalytic activity, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, pyridoxal phosphate binding.	49846	7.0	5.2	94	2
243	chr4.CM1616.50.nc	Catalytic activity, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, pyridoxal phosphate binding.	14342	9.4	9.0	56	1
244	LjSGA_070717.1	Mitochondrial outer membrane, anion transport, voltage-gated ion-selective channel activity.	22430	5.8	12.6	94	2
245	LjSGA_074884.1	Translation elongation factor activity, GTPase activity, GTP binding.	44733	5.5	9.8	94	3
246	chr4.CM0026.460.nc	Lactoylglutathione lyase activity, carbohydrate metabolic process, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen.	31415	5.7	12.9	93	3
247	LjSGA_100703.1.1	Iron ion binding, electron transport, transport, electron carrier activity, chloroplast, thylakoid, photosynthesis, membrane, integral to membrane, oxidoreductase activity, heme binding, metal ion binding.	24519	8.9	11.5	93	2
247	LjSGA_106942.1.1	Iron ion binding, electron transport, transport, electron carrier activity, chloroplast, thylakoid, photosynthesis, membrane, integral to membrane, oxidoreductase activity, heme binding, metal ion binding.	24283	7.6	11.6	93	2
247	LjSGA_103041.1	Iron ion binding, electron transport, transport, electron carrier activity, chloroplast, thylakoid, photosynthesis, membrane, integral to membrane, oxidoreductase activity, heme binding, metal ion binding.	4885	4.4	31.7	90	1
248	chr4.CM1616.360.nc	Catalytic activity, cellular metabolic process, coenzyme binding.	36862	6.6	7.7	92	2
249	LjSGA_071976.1.1	Structural constituent of ribosome, intracellular, ribosome, translation.	16370	9.5	16.1	92	2
250	LjT08D05.60.nd	Magnesium ion binding, catalytic activity, pyruvate kinase activity, glycolysis, kinase activity, potassium ion binding.	51916	6.7	2.5	91	1
251	chr5.CM0299.350.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	13956	9.6	26.6	91	3
251	chr5.LjT38I13.150.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	13559	9.5	27.7	91	3
252	LjSGA_126077.1	Glycerol ether metabolic process, electron carrier activity, chloroplast, protein disulfide oxidoreductase activity, cell redox homeostasis.	11431	6.8	11.8	91	1
253	chr5.CM0357.630.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	29725	9.9	18.4	91	3
253	LjSGA_038721.1	Structural constituent of ribosome, intracellular, ribosome, translation.	15159	9.2	10.6	47	1
254	chr4.CM0042.1960.nc	Nucleotide binding, protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	57559	6.8	5.1	91	2
254	chr4.CM0432.120.nd	Nucleotide binding, protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	57318	6.8	5.1	91	2
255	chr3.CM0216.760.nc	Catalytic activity, fructose-bisphosphate aldolase activity, glycolysis, metabolic process, lyase activity.	43115	7.6	6.5	91	2
256	LjSGA_025401.2	No GO annotations found.	32237	7.6	10.9	91	3
257	chr1.LjT14I13.210.nd	ATP binding.	69367	5.7	4.2	90	2
258	LjSGA_000267.1	Magnesium ion binding, monooxygenase activity, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, oxidoreductase activity, lyase activity, ribulose-bisphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	31302	7.7	5.8	89	3
259	chr1.CM0248.160.nc	Superoxide dismutase activity, superoxide metabolic process, oxidoreductase activity, metal ion binding.	26890	7.2	7.7	89	2
260	chr4.CM0044.530.nc	Hydrolase activity, hydrolyzing O-glycosyl compounds, cell wall, carbohydrate metabolic process, glucan metabolic process, metabolic process, xyloglucan:xyloglucosyl transferase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds, apoplast.	32241	9.3	8.9	89	2
261	LjSGA_021575.2	Argininosuccinate synthase activity, ATP binding, arginine biosynthetic process.	20092	7.0	17.6	89	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
262	chr1.CM0378.320.nd	Nucleus, nucleotide-excision repair, protein modification process.	34720	4.7	4.7	89	1
263	chr1.CM0098.210.nc	L-arabinose metabolic process, alpha-N-arabinofuranosidase activity.	59097	5.4	6.1	88	3
264	LjT18K22.30.nc	Peroxidase activity, antioxidant activity, oxidoreductase activity.	29224	6.4	20.3	88	4
265	chr6.CM0114.310.nc	No GO annotations found.	28475	5.3	5.0	88	1
266	LjSGA_015672.1	Catalytic activity, triose-phosphate isomerase activity, metabolic process, isomerase activity.	14547	5.1	9.0	87	1
267	LjSGA_016889.1	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	55657	8.3	4.6	87	2
267	chr2.CM0783.60.nd	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	80918	8.7	1.6	60	1
268	chr1.CM0023.150.nc	Protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	56910	5.5	8.0	87	3
269	LjSGA_026224.1	Nucleus, methyltransferase activity, chloroplast, transferase activity, [ribulose-bisphosphate carboxylase]-lysine N-methyltransferase activity.	34169	4.8	3.7	87	1
270	chr5.CM0040.320.nc	Nucleic acid binding, aminoacyl-tRNA ligase activity, aspartate-tRNA ligase activity, ATP binding, cytoplasm, tRNA aminoacylation for protein translation, aspartyl-tRNA aminoacylation.	60270	6.0	4.4	86	2
271	LjSGA_117719.1	Catalytic activity, cellular metabolic process, coenzyme binding.	10764	9.5	14.4	86	1
272	chr2.CM0608.160.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, metabolic process, xylan 1,4-beta-xylosidase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds.	19922	6.2	5.6	86	1
273	chr1.CM0442.310.nd	GTPase activity, protein binding, GTP binding, intracellular protein transport, nucleocytoplasmic transport, signal transduction, small GTPase mediated signal transduction.	25130	6.4	9.5	86	2
273	chr1.CM0442.350.nd	GTPase activity, protein binding, GTP binding, intracellular protein transport, nucleocytoplasmic transport, signal transduction, small GTPase mediated signal transduction.	25073	6.4	9.5	86	2
273	LjSGA_031947.1	GTPase activity, protein binding, GTP binding, intracellular protein transport, nucleocytoplasmic transport, signal transduction, small GTPase mediated signal transduction.	24934	6.7	9.6	86	2
274	chr2.CM0021.160.nc	Catalytic activity, branched-chain-amino-acid transaminase activity, metabolic process, transaminase activity, branched chain family amino acid metabolic process, transferase activity.	44836	6.6	3.9	84	1
275	chr5.CM0077.680.nc	Nucleotide binding, ATP binding, nucleus, cytoplasm, cytosol, membrane, hydrolase activity, nucleoside-triphosphatase activity, protein catabolic process, protein complex.	44528	8.5	8.8	83	3
276	chr4.CM0182.340.nd	Cytoplasm, fatty acid biosynthetic process, hydro-lyase activity.	24371	9.2	16.1	83	3
276	chr4.CM0182.40.nc	Cytoplasm, fatty acid biosynthetic process, hydro-lyase activity.	24371	9.2	16.1	83	3
277	chr3.CM0070.370.nc	Nucleosome, DNA binding, nucleus, chromosome, nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota).	15644	10.1	18.2	83	2
277	chr3.LjT39G24.210.nd	Nucleosome, DNA binding, nucleus, chromosome, nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota).	16298	10.1	17.4	83	2
277	chr3.LjT39G24.30.nd	Nucleosome, DNA binding, nucleus, chromosome, nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota).	15742	10.1	18.1	83	2
277	LjSGA_022700.1	Nucleosome, DNA binding, nucleus, nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota).	15629	10.1	18.3	83	2
278	chr1.CM0150.640.nd	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, cation binding.	49406	4.9	6.0	83	2
279	LjSGA_033928.1	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, calcium ion binding, carbohydrate metabolic process, cation binding.	12698	5.1	11.5	83	1
280	chr5.CM0239.440.nd	Endoplasmic reticulum, isomerase activity, cell redox homeostasis.	39247	5.5	7.8	82	2
281	chr5.CM0335.10.nc	Copper ion binding, oxidoreductase activity.	35553	6.4	4.0	81	1

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
282	LjSGA_023994.2	No GO annotations found.	32598	5.6	3.7	81	1
282	LjSGA_045237.1	No GO annotations found.	34034	5.8	3.5	81	1
283	LjSGA_046369.1	Nucleotide binding, ATP binding.	44402	8.9	5.3	81	2
284	LjSGA_094099.1	Acyltransferase activity, transferase activity.	35299	9.1	7.0	81	2
285	chr2.CM0031.300.nc	No GO annotations found.	103310	8.8	4.7	80	4
286	LjSGA_075461.1	No GO annotations found.	15315	9.4	9.4	80	1
287	chr1.CM0318.110.nd	Protein binding.	15168	9.2	14.6	80	2
288	LjSGA_006403.1	Catalytic activity, metabolic process, lyase activity.	32547	6.4	4.6	79	1
289	chr3.CM0091.440.nd	Dolichyl-diphosphooligosaccharide-protein glycotransferase activity, endoplasmic reticulum membrane, cellulose and pectin-containing cell wall, transferase activity, protein amino acid N-linked glycosylation via asparagine.	48152	5.8	8.3	79	3
290	chr6.LjT02P05.170.nd	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	23133	7.0	10.9	77	2
291	LjSGA_017763.1	Catalytic activity, 3-hydroxyacyl-CoA dehydrogenase activity, dodecenoyl-CoA delta-isomerase activity, enoyl-CoA hydratase activity, lipid metabolic process, fatty acid metabolic process, fatty acid beta-oxidation, metabolic process, 3-hydroxybutyryl-CoA epimerase activity, glyoxysome, oxidoreductase activity, lyase activity, isomerase activity, 3-hydroxyacyl-CoA dehydratase activity, coenzyme binding.	36498	8.6	4.6	77	1
292	LjSGA_063269.1	Defense response, response to biotic stimulus.	16769	5.0	30.4	77	4
293	LjSGA_001057.3	Mitochondrion, mitochondrial electron transport, NADH to ubiquinone, NADH dehydrogenase (ubiquinone) activity.	22580	6.9	5.3	77	1
293	LjSGA_008141.1	Mitochondrion, mitochondrial electron transport, NADH to ubiquinone, NADH dehydrogenase (ubiquinone) activity.	26496	7.8	4.5	77	1
294	LjT16G18.110.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity, peptide binding.	8512	7.8	22.8	76	2
295	chr6.CM0314.590.nc	Methylenetetrahydrofolate reductase (NADPH) activity, methionine metabolic process.	39120	5.8	14.6	76	4
296	chr6.CM0037.810.nc	Metabolic process, glyceraldehyde-3-phosphate dehydrogenase (NADP+) activity, oxidoreductase activity.	54221	8.4	6.2	76	3
297	chr1.LjT43O05.80.nd	Alcohol dehydrogenase activity, zinc ion binding, oxidoreductase activity, metal ion binding.	25600	6.1	12.9	76	3
298	chr1.CM0050.40.nc	Adenine phosphoribosyltransferase activity, purine ribonucleoside salvage, adenine salvage, nucleoside metabolic process, transferase activity, transferase activity, transferring glycosyl groups.	19477	5.3	8.4	76	1
298	chr1.LjT45O14.130.nd	Adenine phosphoribosyltransferase activity, purine ribonucleoside salvage, adenine salvage, nucleoside metabolic process, transferase activity, transferase activity, transferring glycosyl groups.	19477	5.3	8.4	76	1
299	LjB01J01.10.nc	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	18534	9.0	32.6	75	4
300	LjSGA_048933.1	No GO annotations found.	13532	9.5	24.6	75	2
300	chr4.CM0501.190.nd	No GO annotations found.	22345	9.8	7.5	69	1
301	LjSGA_077870.1	Nucleotide binding, ATP binding, endoplasmic reticulum.	23702	4.8	5.3	75	1
302	chr1.LjT48M07.70.nc	Catalytic activity, cysteine synthase activity, cysteine biosynthetic process from serine, metabolic process, pyridoxal phosphate binding.	30536	6.8	4.4	75	1
303	chr4.CM0617.300.nd	Actin binding, cytoskeleton organization and biogenesis, actin cytoskeleton, actin cytoskeleton organization and biogenesis.	14063	4.6	24.4	75	4
303	chr2.CM0783.270.nd	Actin binding, cytoskeleton organization and biogenesis, actin cytoskeleton, actin cytoskeleton organization and biogenesis.	14077	4.6	16.8	75	3

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
304	chr4.CM0025.300.nc	Nucleotide binding, nucleoside diphosphate kinase activity, ATP binding, GTP biosynthetic process, UTP biosynthetic process, CTP biosynthetic process, kinase activity, transferase activity.	25346	9.4	15.3	74	4
304	chr2.CM0060.440.nc	Nucleotide binding, nucleoside diphosphate kinase activity, ATP binding, GTP biosynthetic process, UTP biosynthetic process, CTP biosynthetic process, kinase activity, transferase activity.	25712	9.1	8.0	61	3
305	LjSGA_085597.1	Phosphopyruvate hydratase complex, magnesium ion binding, phosphopyruvate hydratase activity, glycolysis, lyase activity.	20960	8.7	9.3	74	2
306	LjT22I05.200.nd	Catalytic activity, aspartate transaminase activity, amino acid metabolic process, transaminase activity, biosynthetic process, transferase activity, transferase activity, transferring nitrogenous groups, pyridoxal phosphate binding.	20944	10.4	19.6	74	3
307	chr5.CM0077.700.nc	Catalytic activity, beta-galactosidase activity, carbohydrate metabolic process, metabolic process, beta-galactosidase complex, hydrolase activity, hydrolase activity, acting on glycosyl bonds, cation binding.	62938	8.0	4.6	74	2
308	CM0319.130.nd	Nucleic acid binding, DNA binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, DNA integration.	89579	9.8	1.2	74	1
309	chr3.CM0792.20.nd	Response to stress, response to cold.	18063	5.0	7.3	73	1
310	LjB03P03.140.nd	Catalytic activity, fumarylacetoacetase activity, metabolic process, aromatic amino acid family metabolic process.	46069	5.7	5.9	73	2
311	chr2.CM0695.320.nd	No GO annotations found.	45629	4.7	3.3	73	1
312	LjSGA_019091.2	3-oxoacyl-[acyl-carrier-protein] reductase activity, fatty acid biosynthetic process, metabolic process, lipid biosynthetic process, chloroplast, oxidoreductase activity, NAD binding.	18773	9.2	7.5	73	1
313	LjSGA_039741.1	Protein binding, endoplasmic reticulum, Golgi-associated vesicle, protein complex assembly, intracellular protein transport, ER to Golgi vesicle-mediated transport, protein transporter activity, vesicle-mediated transport, COPI vesicle coat.	63345	9.6	5.6	72	3
314	LjSGA_114323.1	Oxidoreductase activity.	10327	5.4	14.1	72	1
315	LjT16G18.150.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity, peptide binding.	13844	7.2	9.2	72	1
316	chr6.CM0679.170.nd	Adenosylhomocysteinase activity, one-carbon compound metabolic process, hydrolase activity.	29601	8.2	13.0	72	4
317	chr1.CM0064.390.nc	Catalytic activity, metabolic process, ligase activity.	57658	7.9	2.8	72	1
318	LjSGA_088248.1	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, intracellular, translation, translational elongation, chloroplast.	19807	9.3	22.0	71	3
319	chr1.CM0371.130.nc	GTPase activity, structural molecule activity, GTP binding, microtubule, microtubule-based process, microtubule-based movement, protein complex, protein polymerization.	49715	4.9	7.8	71	3
320	chr2.CM0168.320.nc	Mitochondrial outer membrane, anion transport, voltage-gated ion-selective channel activity.	29121	9.1	18.8	71	5
321	LjSGA_145133.1	No GO annotations found.	8477	5.5	19.2	71	1
322	chr1.CM0012.470.nc	Nucleotide binding, ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport, membrane.	22804	6.0	5.3	71	1
323	LjSGA_038243.1	Intracellular.	21496	10.0	15.3	71	2
323	LjSGA_040678.1	Intracellular, ribonucleoprotein complex.	14911	10.5	11.6	53	1
324	LjSGA_054553.2.1	Mitochondrial outer membrane, anion transport, voltage-gated ion-selective channel activity.	4910	6.3	26.7	70	1
325	chr2.CM0608.40.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process.	15996	9.1	9.0	70	1

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
326	LjSGA_038169.1	Iron ion binding, electron transport, lipoxygenase activity, metal ion binding.	24323	6.4	11.2	70	2
327	chr6.CM0055.10.nd	Nucleotide binding, ATP binding, mitochondrion, protein folding, unfolded protein binding.	73119	5.6	2.7	69	2
328	chr6.CM0679.120.nd	Catalytic activity, carbohydrate metabolic process, racemase and epimerase activity, acting on carbohydrates and derivatives, cellular metabolic process, coenzyme binding.	47932	9.3	2.7	69	1
329	LjSGA_019672.2	Catalytic activity, 2-isopropylmalate synthase activity, metabolic process, leucine biosynthetic process, transferase activity, lyase activity, carboxylic acid metabolic process, transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer.	44241	6.6	10.4	69	3
330	LjSGA_081530.1	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, intracellular, translation, translational elongation, chloroplast.	22067	9.7	5.8	69	1
331	chr6.CM0139.780.nd	Nucleotide binding, nucleic acid binding.	44868	6.2	2.5	68	1
332	chr4.CM0119.50.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	28116	10.6	8.8	68	3
332	LjSGA_122226.1	Structural constituent of ribosome, intracellular, ribosome, translation.	28070	10.6	8.8	68	3
332	LjT17O07.90.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	28117	10.7	4.2	57	2
332	LjT48K17.180.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	16658	10.3	7.0	57	2
332	LjT48K17.130.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	24079	9.9	5.5	49	1
333	LjT43D04.90.nc	Chloroplast inner membrane, membrane.	34473	7.7	4.4	68	1
334	LjT13C08.100.nc	Transport, lipid transport, lipid binding.	11419	9.3	27.0	68	3
335	LjSGA_041825.1.1	Calcium ion binding, calcium-dependent phospholipid binding.	26982	8.5	10.5	68	2
336	chr2.CM0783.340.nd	Actin binding, cytoskeleton organization and biogenesis, actin cytoskeleton, actin cytoskeleton organization and biogenesis.	14210	5.1	16.5	67	3
337	LjSGA_017574.2	Mitochondrion, endoplasmic reticulum, response to oxidative stress, isomerase activity, cell redox homeostasis.	32289	4.5	7.7	67	1
338	LjSGA_085428.1	Catalytic activity, ATP binding, fatty acid biosynthetic process, metabolic process, lipid biosynthetic process, biotin binding, ligase activity.	19695	9.1	6.9	67	1
339	chr1.CM0206.150.nd	Nucleotide binding, GTP binding, intracellular, endoplasmic reticulum, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	21957	6.4	5.7	66	1
339	chr4.CM0429.130.nd	Nucleotide binding, GTP binding, intracellular, endoplasmic reticulum, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	22053	6.1	5.7	66	1
339	CM0385.100.nd	Nucleotide binding, GTP binding, intracellular, endoplasmic reticulum, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	24855	6.2	5.1	66	1
340	LjT07P16.160.nd	Translation initiation factor activity, translation, translational initiation.	17316	5.6	18.9	66	3
341	chr5.LjT02I10.300.nd	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	31807	9.3	13.9	66	4
342	LjSGA_071971.1	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, methyltransferase activity, zinc ion binding, amino acid biosynthetic process, methionine biosynthetic process, transferase activity, metal ion binding.	27972	5.7	12.5	66	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
343	LjSGA_068268.1	Nucleotide binding, magnesium ion binding, ATP binding, endoplasmic reticulum, transport, ER to Golgi vesicle-mediated transport, protein transport, hydrolase activity, nucleoside-triphosphatase activity, metal ion binding.	19392	8.4	7.4	66	1
344	LjT30M06.90.nd	Ubiquitin thiolesterase activity, ubiquitin-dependent protein catabolic process.	36023	5.2	7.1	66	2
344	chr2.CM0545.290.nc	Ubiquitin thiolesterase activity, ubiquitin-dependent protein catabolic process, peptidase activity.	131315	5.4	0.9	56	1
345	chr1.LjT01D01.60.nd	No GO annotations found.	14181	6.9	9.6	66	1
345	LjSGA_079444.1	No GO annotations found.	9969	7.3	13.3	66	1
346	chr4.CM0173.30.nd	Nucleotide binding, nucleic acid binding, RNA binding, mRNA processing, chloroplast, ribonucleoprotein complex.	33353	4.7	7.8	66	2
347	LjT04E07.20.nc	Peroxidase activity, antioxidant activity, oxidoreductase activity.	28619	6.1	20.8	65	4
348	chr1.CM0433.180.nd	Nucleotide binding, protein binding, ATP binding, nucleoside-triphosphatase activity, protein metabolic process.	67931	5.5	1.3	65	1
349	chr4.CM0680.130.nc	Protein binding, photosystem I, photosynthesis, thylakoid membrane.	17133	8.9	6.3	65	1
350	chr1.CM0233.110.nc	Malic enzyme activity, malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, malate metabolic process, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, metal ion binding, NAD binding.	70069	6.3	4.4	65	2
350	LjSGA_137596.1	Malic enzyme activity, malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, malate metabolic process, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, metal ion binding, NAD binding.	15869	6.3	8.8	59	1
351	LjSGA_012802.2	No GO annotations found.	25752	6.3	5.2	65	1
353	chr1.CM0206.230.nc	Protein binding.	18495	6.8	25.7	64	3
354	LjSGA_005489.3	No GO annotations found.	34024	9.7	3.5	64	1
355	LjSGA_060719.2	Structural constituent of ribosome, intracellular, ribosome, translation.	9499	6.6	11.1	64	1
356	chr2.CM0102.150.nd	Nucleotide binding, homoserine kinase activity, ATP binding, threonine metabolic process, amino acid biosynthetic process, threonine biosynthetic process, kinase activity, phosphorylation, transferase activity.	39223	7.1	3.2	63	1
357	chr4.CM0617.240.nd	Metalloendopeptidase activity, mitochondrial processing peptidase activity, mitochondrion, mitochondrial respiratory chain, electron transport, proteolysis, transport, ubiquinol-cytochrome-c reductase activity, peptidase activity, metallopeptidase activity, oxidoreductase activity, hydrolase activity.	23358	6.3	7.0	63	1
358	LjSGA_016231.2	No GO annotations found.	29916	7.9	3.6	63	1
359	LjSGA_034228.1	ATP binding.	16697	4.7	19.9	63	3
360	chr1.CM0122.460.nc	Regulation of nitrogen utilization, enzyme regulator activity.	21471	9.7	5.6	62	1
361	chr4.CM0042.1530.nc	Aspartate-semialdehyde dehydrogenase activity, cytoplasm, mitochondrion, amino acid metabolic process, amino acid biosynthetic process, methionine biosynthetic process, threonine biosynthetic process, oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor, protein dimerization activity, NADP binding, NAD binding.	41232	6.0	2.9	62	1
362	LjSGA_056310.1	Outer membrane.	14417	7.9	7.4	62	1
363	LjSGA_051623.1	Nucleic acid binding, peptidase activity, zinc ion binding.	12305	10.1	6.5	62	1
364	LjT48C16.170.nd	Catalytic activity, cellular metabolic process, coenzyme binding.	18236	6.4	15.3	62	2
365	chr6.CM0066.640.nc	Aspartic-type endopeptidase activity, pepsin A activity, proteolysis.	45127	8.7	10.1	62	3
365	chr3.CM0127.710.nc	Pepsin A activity, proteolysis.	39127	9.5	3.7	54	1

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
366	LjSGA_052954.1	Magnesium ion binding, iron ion binding, electron transport, transport, electron carrier activity, chloroplast, photosystem I, thylakoid, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding, iron-sulfur cluster binding, 4 iron, 4 sulfur cluster binding.	31065	6.8	4.3	61	1
366	LjSGA_090599.1	Magnesium ion binding, iron ion binding, electron transport, transport, electron carrier activity, chloroplast, photosystem I, thylakoid, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding, iron-sulfur cluster binding, 4 iron, 4 sulfur cluster binding.	35567	7.4	3.8	61	1
366	LjSGA_102170.1	Magnesium ion binding, iron ion binding, electron transport, transport, electron carrier activity, chloroplast, photosystem I, thylakoid, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding, iron-sulfur cluster binding, 4 iron, 4 sulfur cluster binding.	26616	7.3	5.1	61	1
367	chr5.CM0077.20.nd	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	30434	5.3	8.6	61	2
368	LjSGA_030023.1.2	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	25077	10.1	6.4	61	1
368	LjSGA_039485.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	25434	10.2	6.5	61	1
368	LjSGA_040951.0.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	19970	10.2	8.0	61	1
368	LjSGA_041952.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	21510	10.3	7.4	61	1
368	LjSGA_055307.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	23077	10.0	7.0	61	1
368	LjSGA_059014.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	25177	10.5	6.5	61	1
368	LjSGA_080429.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	25003	10.2	6.5	61	1
368	LjSGA_091127.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	24944	10.2	6.4	61	1
368	LjSGA_094940.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	13998	10.4	11.5	61	1
368	LjSGA_103684.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	13801	10.2	11.6	61	1
368	LjSGA_107226.0.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	17223	10.2	9.4	61	1

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
368	LjSGA_112701.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	25655	10.1	6.2	61	1
368	LjSGA_116308.2	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	18649	10.1	8.6	61	1
368	LjSGA_118901.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	26633	10.1	6.0	61	1
368	LjSGA_128247.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	25077	10.1	6.4	61	1
369	LjSGA_035136.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, chloroplast, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	24960	10.2	6.5	61	1
370	chr1.CM0017.490.nc	Catalytic activity, porphyrin biosynthetic process, transaminase activity, chloroplast, chlorophyll biosynthetic process, isomerase activity, pyridoxal phosphate binding, tetrapyrrole biosynthetic process, glutamate-1-semialdehyde 2,1-aminomutase activity.	50238	7.1	6.6	61	2
371	chr4.CM0126.670.nc	Catalytic activity, cellular metabolic process, coenzyme binding.	33464	6.4	6.6	61	2
372	LjSGA_038659.1	Protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	39475	9.4	3.2	61	1
373	chr1.CM0593.380.nc	Acyltransferase activity, biosynthetic process, transferase activity, transferring groups other than amino-acyl groups.	42767	6.2	5.1	60	2
374	chr3.CM0091.660.nd	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	80852	9.3	3.2	60	2
375	chr1.CM0284.440.nc	Catalytic activity, phosphomannomutase activity, cytoplasm, metabolic process, isomerase activity, mannose biosynthetic process.	27862	5.7	10.5	60	2
376	chr4.CM0042.1600.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	16961	10.3	6.6	60	1
377	chr1.CM0147.900.nc	Steroid metabolic process.	52207	5.0	3.0	60	1
378	chr6.LjT30N23.130.nd	DNA binding, nucleus, DNA replication, regulation of DNA replication, DNA polymerase processivity factor activity, PCNA complex.	29506	4.7	4.5	60	1
379	chr2.LjT01H08.60.nc	Catalytic activity, glutamate-ammonia ligase activity, glutamine biosynthetic process, nitrogen compound metabolic process.	39034	5.4	5.9	59	2
381	chr1.CM0105.1320.nd	No GO annotations found.	39458	5.5	3.0	59	1
382	LjSGA_041906.1	Nucleotide binding, ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport, membrane.	4904	11.0	48.8	58	2
383	LjSGA_009908.1	L-lactate dehydrogenase activity, cytoplasm, glycolysis, tricarboxylic acid cycle intermediate metabolic process, oxidoreductase activity, anaerobic glycolysis.	37804	5.9	3.4	58	1
384	LjT32D02.120.nc	Catalytic activity, glutamate-ammonia ligase activity, glutamine biosynthetic process, nitrogen compound metabolic process, ligase activity.	47568	6.5	6.7	58	2
385	chr5.CM0052.420.nd	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation.	17393	10.3	6.0	57	1
385	LjSGA_085279.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation.	13202	9.6	7.8	57	1
386	chr3.CM0111.260.nc	Protein domain specific binding.	30027	4.7	6.8	56	3
387	chr1.LjB18K24.40.nd	Signal peptidase complex, signal peptide processing, signal peptidase activity, integral to membrane.	16087	8.7	6.4	56	1
387	chr1.CM0544.600.nd	Signal peptidase complex, signal peptide processing, signal peptidase activity, integral to membrane.	12541	8.3	8.0	56	1

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
387	chr5.CM0089.680.nd	Signal peptidase complex, signal peptide processing, signal peptidase activity, integral to membrane.	19048	9.0	5.4	56	1
388	LjT35C01.110.nd	Structural constituent of ribosome, intracellular, ribosome, translation, large ribosomal subunit, ribonucleoprotein complex.	20323	11.2	5.6	56	1
389	LjT30L14.20.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylipin biosynthetic process, metal ion binding.	55309	5.4	3.8	56	2
390	chr1.CM0171.780.nd	No GO annotations found.	25758	7.7	3.4	56	1
391	chr4.CM0119.370.nc	Ferredoxin-NADP+ reductase activity, electron transport, oxidoreductase activity, thylakoid membrane, FAD binding, NADP binding.	40605	8.8	3.9	56	1
392	chr6.CM0302.80.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	24675	9.8	5.1	56	1
393	LjT01G11.120.nd	Structural constituent of ribosome, intracellular, ribosome, translational elongation.	11279	4.3	10.7	56	1
394	chr5.LjT24B10.140.nc	Monoxygenase activity, iron ion binding, electron transport, membrane, oxidoreductase activity, heme binding, metal ion binding.	60458	8.5	1.9	56	1
395	LjSGA_054224.1	ATP binding, ATP biosynthetic process, chloroplast, ATP synthesis coupled proton transport, proton-transporting two-sector ATPase complex, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	9848	9.5	9.1	56	1
396	LjSGA_018602.1	Aldehyde dehydrogenase (NAD) activity, metabolic process, oxidoreductase activity.	19704	5.9	8.6	56	1
397	chr2.CM0124.90.nc	Nucleotide binding, ATP binding, mitochondrion, protein folding, unfolded protein binding.	89141	5.0	2.9	56	2
398	chr4.LjT13D08.30.nd	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	15444	8.7	8.2	56	1
399	LjB01J01.30.nc	Endopeptidase activity, threonine endopeptidase activity, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process.	8342	4.6	13.5	55	1
400	chr2.CM0695.90.nd	RNA binding, aconitate hydratase activity, metabolic process, lyase activity, hydro-lyase activity, 4 iron, 4 sulfur cluster binding.	98063	6.0	2.9	55	2
401	chr3.CM0792.110.nd	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	23672	6.2	11.1	55	2
401	LjSGA_058377.2	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	7304	5.7	17.2	48	1
402	chr1.CM0094.310.nc	Nucleic acid binding, nuclease activity.	108660	6.1	2.6	55	2
402	chr1.CM0094.340.nc	Nucleic acid binding, nuclease activity.	108664	6.3	2.6	55	2
402	chr1.CM0094.360.nc	Nucleic acid binding, nuclease activity.	108564	6.1	2.6	55	2
403	chr1.CM0109.360.nc	Catalytic activity, aromatic compound metabolic process, hydrolase activity.	36218	5.6	9.4	55	3
404	chr2.CM0272.170.nc	Catalytic activity, L-serine biosynthetic process, metabolic process, transaminase activity, transferase activity, pyridoxal phosphate binding.	46909	8.3	3.3	55	1
405	chr1.LjT14I13.300.nd	Aminoacyl-tRNA ligase activity, leucine-tRNA ligase activity, ATP binding, cytoplasm, translation, tRNA aminoacylation for protein translation.	60646	6.2	2.0	55	1
405	LjSGA_031174.2.1	Aminoacyl-tRNA ligase activity, leucine-tRNA ligase activity, ATP binding, cytoplasm, translation, tRNA aminoacylation for protein translation.	12398	9.4	10.3	55	1
406	LjSGA_036172.1	Structural constituent of ribosome, intracellular, ribosome, translation.	7535	11.2	18.5	55	1

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
407	LjSGA_003098.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	7292	5.8	20.0	55	1
407	LjSGA_118471.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	10924	5.0	13.1	55	1
408	LjSGA_129660.2	Nucleic acid binding, DNA binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, DNA integration.	27216	9.4	2.9	55	1
409	LjSGA_108878.1	Oxidoreductase activity.	10789	8.5	10.3	55	1
410	LjSGA_037888.1	UDP-glucose:glycoprotein glucosyltransferase activity, protein amino acid glycosylation, transferase activity.	26610	5.0	5.0	55	1
411	chr6.CM0041.320.nd	No GO annotations found.	19435	8.0	6.7	55	1
412	chr5.LjT41L03.150.nd	Glycogen (starch) synthase activity, starch synthase activity, biosynthetic process, glucan biosynthetic process, transferase activity, transferase activity, transferring glycosyl groups.	394269	8.8	5.6	54	3
413	chr4.CM0007.860.nd	Catalytic activity, fatty acid biosynthetic process, transferase activity.	49944	8.5	2.8	54	1
414	chr1.CM0544.500.nd	Metabolic process, oxidoreductase activity.	37876	6.7	7.9	54	2
414	LjSGA_029600.1	Metabolic process, oxidoreductase activity.	22054	9.1	13.9	54	2
415	LjSGA_036526.1.1	Binding, intracellular, RNA processing, transferase activity.	13139	3.6	10.3	54	1
416	LjSGA_017485.1	Carbohydrate metabolic process, xylose isomerase activity, isomerase activity.	30872	8.9	6.3	54	1
417	LjSGA_062145.1	Nucleotide binding, ATP binding, mitochondrion, protein folding, unfolded protein binding.	30366	9.2	6.4	54	2
418	LjSGA_093090.1	Nucleotide binding, RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, rRNA binding, ribonucleoprotein complex.	2832	6.6	50.0	54	1
419	chr3.CM0711.10.nd	Iron ion binding, electron transport, transport, ubiquinol-cytochrome-c reductase activity, plastoquinol-plastocyanin reductase activity, chloroplast, thylakoid, membrane, integral to membrane, oxidoreductase activity, ubiquinol-cytochrome-c reductase complex, metal ion binding, iron-sulfur cluster binding, 2 iron, 2 sulfur cluster binding.	23992	8.8	5.3	54	1
420	chr6.CM0066.230.nc	Actin binding, intracellular.	15681	5.5	8.8	53	1
421	chr6.CM0057.310.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	21254	10.3	12.4	53	2
421	LjT35M05.20.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	20461	10.4	12.8	53	2
422	LjSGA_034891.1	Endoplasmic reticulum.	20817	9.3	5.9	53	1
423	CM0385.180.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process.	17327	9.4	6.9	53	1
424	chr2.CM0008.650.nc	Magnesium ion binding, ribose phosphate diphosphokinase activity, mitochondrion, nucleoside metabolic process, nucleotide biosynthetic process, kinase activity, transferase activity, metal ion binding.	45822	8.1	2.6	53	1
425	LjT30N04.290.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	15458	10.2	22.2	53	2
426	chr5.CM0019.20.nd	Catalytic activity, glycine dehydrogenase (decarboxylating) activity, mitochondrion, glycine dehydrogenase complex (decarboxylating), glycine metabolic process, oxidoreductase activity, pyridoxal phosphate binding.	114302	6.7	2.7	53	2
427	CM1729.60.nc	Cytoplasm, L-phenylalanine catabolic process, biosynthetic process, ammonia ligase activity, lyase activity, ammonia-lyase activity.	79358	5.9	2.9	53	2
428	LjSGA_014026.1	Intracellular.	21523	10.0	7.9	53	1
429	chr5.CM0200.440.nc	Phosphoglycerate dehydrogenase activity, mitochondrion, L-serine biosynthetic process, metabolic process, oxidoreductase activity, amino acid binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, cofactor binding, NAD binding.	63089	6.8	5.7	53	3
430	chr5.CM0052.270.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	44494	9.9	3.6	53	1

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
430	chr5.CM0052.280.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	44318	10.3	3.6	53	1
431	LjSGA_124612.1	Electron transport, chloroplast, photosystem I, thylakoid, photosynthesis, integral to membrane, metal ion binding.	15879	9.9	5.7	53	1
431	LjSGA_125379.2	Magnesium ion binding, iron ion binding, electron transport, transport, electron carrier activity, chloroplast, photosystem I, thylakoid, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding, iron-sulfur cluster binding, 4 iron, 4 sulfur cluster binding.	30980	9.0	2.8	53	1
431	LjSGA_127553.2	Magnesium ion binding, iron ion binding, electron transport, transport, electron carrier activity, chloroplast, photosystem I, thylakoid, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding, iron-sulfur cluster binding, 4 iron, 4 sulfur cluster binding.	27906	9.5	3.1	53	1
431	LjSGA_128526.2	Magnesium ion binding, iron ion binding, electron transport, transport, electron carrier activity, chloroplast, photosystem I, thylakoid, photosynthesis, membrane, integral to membrane, protein-chromophore linkage, metal ion binding, iron-sulfur cluster binding, 4 iron, 4 sulfur cluster binding.	21631	8.7	4.1	53	1
433	chr5.CM0211.170.nc	Chloroplast thylakoid membrane.	32205	8.5	5.7	52	1
434	chr4.CM0739.260.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	14360	11.5	6.9	52	1
434	LjT32D02.180.nc	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	14792	9.8	6.9	52	1
435	chr6.CM0679.70.nc	Selenium binding.	53656	5.7	2.3	52	1
436	LjSGA_022701.1	Structural molecule activity.	20739	7.9	12.0	52	2
437	LjSGA_029241.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	20758	10.2	10.8	52	2
438	chr6.CM0118.520.nd	ATP binding.	25528	9.3	5.7	52	1
439	LjSGA_148679.1	Polygalacturonase activity, carbohydrate metabolic process, hydrolase activity.	12083	6.8	12.7	52	1
440	chr3.LjT02L14.180.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylin biosynthetic process, metal ion binding.	40123	5.5	5.0	52	2
442	chr5.LjT08O17.200.nd	Metal ion transport, metal ion binding.	13212	4.5	20.8	52	2
443	chr1.LjT43O05.70.nd	Alcohol dehydrogenase activity, zinc ion binding, oxidoreductase activity, metal ion binding.	18653	5.9	13.6	52	2
444	LjSGA_030247.1	Catalytic activity, glutamate-ammonia ligase activity, glutamine biosynthetic process, nitrogen compound metabolic process, ligase activity.	10952	5.2	11.1	52	1
445	chr1.CM0016.130.nc	Cytochrome-c oxidase activity, mitochondrion, electron transport.	19818	4.4	12.0	52	2
446	LjSGA_017894.1.1	Electron transport, electron carrier activity, oxidoreductase activity, acting on NADH or NADPH, iron-sulfur cluster binding.	14543	8.9	9.5	52	1
447	LjSGA_015801.1	Nutrient reservoir activity.	38154	6.2	4.5	52	1
447	LjSGA_115896.1	Nutrient reservoir activity.	23447	6.7	7.4	52	1
448	chr4.CM0307.70.nc	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, cation binding.	57676	6.1	4.9	52	2
449	LjSGA_116769.1	No GO annotations found.	39112	9.4	3.3	51	1
450	chr3.LjT03D10.60.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	19170	9.4	10.7	51	2
450	LjSGA_071678.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	9775	9.1	21.2	51	2

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Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
450	chr3.CM0160.930.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	18910	9.4	10.8	51	2
451	LjT31F05.60.nd	Catalytic activity, UDP-rhamnose biosynthetic process, oxidoreductase activity, lyase activity, cellular metabolic process, UDP-glucose 4,6-dehydratase activity, coenzyme binding.	56684	6.6	8.6	51	3
452	LjT33L17.40.nc	Oxidoreductase activity.	17443	5.3	5.6	51	1
453	LjSGA_091288.1	Nutrient reservoir activity.	32648	6.2	8.0	51	2
454	chr1.CM0192.420.nd	Hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, cellulose and pectin-containing cell wall.	59484	6.7	3.1	51	2
455	LjSGA_068738.1	Actin binding, cytoskeleton organization and biogenesis.	17763	5.2	9.4	51	1
455	LjSGA_146350.1	Actin binding, calcium ion binding, cytoskeleton, cytoskeleton organization and biogenesis, barbed-end actin filament capping.	7862	11.4	19.7	51	1
456	LjSGA_082502.1	Structural constituent of ribosome, intracellular, ribosome, translation.	10159	8.6	13.5	50	2
457	LjSGA_031155.1	Binding, transport, membrane, integral to membrane.	22792	9.1	13.7	50	3
458	LjSGA_008384.1	Calcium ion binding, sugar binding, endoplasmic reticulum, protein folding, unfolded protein binding.	44725	4.4	2.6	50	1
459	chr1.CM0150.610.nd	Binding, protein binding, Golgi-associated vesicle, protein complex assembly, intracellular protein transport, vesicle-mediated transport, COPI vesicle coat.	98652	8.3	2.7	50	2
459	LjSGA_026406.2	Binding, protein binding, Golgi-associated vesicle, protein complex assembly, intracellular protein transport, vesicle-mediated transport, COPI vesicle coat.	44118	7.1	3.0	46	1
461	chr1.CM0029.40.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	18624	10.7	15.2	50	3
462	LjSGA_026492.1	ATP binding, mitochondrion, protein folding.	10577	8.0	36.1	50	3
463	LjSGA_051144.1	ATP binding.	53553	5.3	6.0	50	3
464	LjSGA_087577.1	Nucleotide binding, structural molecule activity, protein binding, ATP binding, cytoskeleton.	15502	6.2	17.0	50	3
465	chr1.LjT29N14.160.nd	DNA binding, DNA integration, transferase activity.	42025	10.2	2.2	49	2
466	chr3.CM0590.750.nc	Photosynthesis, light harvesting, membrane.	29007	5.1	3.7	49	1
466	LjSGA_009322.1	Photosynthesis, light harvesting, membrane.	24360	5.2	4.4	49	1
467	chr2.CM0153.150.nd	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	62501	8.8	1.6	49	1
467	LjSGA_042867.1	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	26840	5.5	3.6	49	1
467	LjSGA_134435.1	Subtilase activity, proteolysis, peptidase activity, identical protein binding, negative regulation of enzyme activity.	32244	8.2	3.1	49	1
468	LjT39N06.220.nd	No GO annotations found.	132076	9.4	0.6	49	1
469	chr5.CM0040.270.nc	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, alpha-galactosidase activity, carbohydrate metabolic process, metabolic process, hydrolase activity, hydrolase activity, acting on glycosyl bonds.	46577	6.7	5.0	49	2
469	LjSGA_047213.1	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, alpha-galactosidase activity, carbohydrate metabolic process, metabolic process, hydrolase activity, hydrolase activity, acting on glycosyl bonds.	18567	4.9	6.6	49	1
470	LjSGA_031900.1	Protein domain specific binding.	23907	5.3	24.3	49	5
471	chr3.CM0160.1010.nc	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	23635	5.5	5.2	48	1
471	LjT39G17.10.nc	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	24253	5.6	5.0	48	1
471	LjSGA_036175.1.1	Nucleotide binding, GTP binding, small GTPase mediated signal transduction, protein transport, membrane.	8275	5.3	14.9	48	1

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Supplemental Table S2.1: (*green_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
472	LjSGA_032513.2	Nucleotide binding, ATP binding, GTP binding, intracellular, regulation of transcription, DNA-dependent, small GTPase mediated signal transduction, transcription factor binding, protein transport, membrane.	15356	8.0	7.8	48	1
473	chr1.CM0098.40.nd	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, protein complex.	14569	8.4	10.9	48	1
474	LjSGA_120105.0.1	RNA binding, endoribonuclease activity.	17946	5.7	10.7	48	2
475	LjSGA_018437.1	Calcium ion binding, kinase activity.	16519	4.7	15.6	48	2
476	LjSGA_008385.1	Calcium ion binding, sugar binding, endoplasmic reticulum, protein folding, unfolded protein binding.	25844	5.4	8.3	48	2
478	LjSGA_014341.1	Nucleic acid binding, zinc ion binding.	116872	9.1	3.0	47	4
479	chr6.LjT28D11.70.nc	No GO annotations found.	103174	8.8	1.1	47	1
480	chr3.CM0460.50.nc	Aminoacyl-tRNA ligase activity, isoleucine-tRNA ligase activity, ATP binding, tRNA aminoacylation for protein translation, isoleucyl-tRNA aminoacylation, ligase activity.	134417	5.9	0.8	47	1
481	LjSGA_066832.1	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	7184	4.6	16.4	47	1
482	LjSGA_038377.1.1	DNA binding, DNA integration.	21019	4.5	5.4	47	1
482	LjSGA_097533.1	DNA binding, DNA integration.	41298	9.3	2.8	47	1
483	chr3.CM0261.320.nd	Metabolic process, methyltransferase activity, transferase activity.	36139	9.0	3.2	47	2
484	LjSGA_013606.1	Catalytic activity, metabolic process, ligase activity.	41723	5.7	3.6	47	1
485	LjSGA_026337.1	Structural constituent of ribosome, intracellular, ribosome, translation.	14363	9.9	14.2	47	2
486	chr2.CM0021.670.nc	Glycine cleavage complex, glycine catabolic process.	17850	4.9	5.4	47	1
487	LjSGA_086102.1	Catalytic activity, succinate-CoA ligase (ADP-forming) activity, metabolic process, ligase activity.	8056	9.7	15.4	47	1
488	LjSGA_013409.1	Catalytic activity, methylenetetrahydrofolate dehydrogenase (NADP+) activity, folic acid and derivative biosynthetic process, oxidoreductase activity, hydrolase activity.	31386	7.7	4.8	47	1
488	LjSGA_094337.1	Catalytic activity, methylenetetrahydrofolate dehydrogenase (NADP+) activity, folic acid and derivative biosynthetic process, oxidoreductase activity, hydrolase activity.	7393	9.4	20.0	47	1
489	chr1.CM0378.170.nd	Peroxidase activity, protein binding, chloroplast, antioxidant activity, oxidoreductase activity, peroxiredoxin activity.	23192	8.8	5.0	47	1
490	LjSGA_044439.1	RNA binding, nucleus, rRNA processing.	5366	8.2	22.4	47	1
491	LjSGA_011958.1	Aminopeptidase activity, membrane alanyl aminopeptidase activity, proteolysis, metallopeptidase activity, zinc ion binding.	40023	5.2	3.1	47	1
492	LjSGA_065625.1	Phosphogluconate dehydrogenase (decarboxylating) activity, pentose-phosphate shunt, oxidoreductase activity, NADP binding, coenzyme binding.	21107	9.4	8.1	46	1
493	chr5.LjT39E05.230.nd	Protein binding, endoplasmic reticulum, protein complex assembly, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, protein transport, membrane, vesicle-mediated transport, clathrin vesicle coat.	35843	7.1	2.8	46	1
494	chr6.CM0066.70.nd	Transport, integral to membrane, vesicle-mediated transport.	26090	8.8	4.7	46	1
495	LjSGA_046433.1	Magnesium ion binding, phosphoglucomutase activity, carbohydrate metabolic process, glucose metabolic process, isomerase activity, intramolecular transferase activity, phosphotransferases, metal ion binding.	14784	4.9	11.1	46	1
497	chr4.CM0234.330.nd	No GO annotations found.	15529	9.4	6.6	46	1
498	chr1.CM0147.490.nc	ATP binding.	72818	8.6	3.8	46	3

Continues...

Supplemental Table S2.1: (green_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
499	LjT09O11.20.nd	Nucleotide binding, nucleic acid binding, intracellular, transport.	56404	5.1	2.3	46	1
500	chr4.CM0006.640.nd	ARF guanyl-nucleotide exchange factor activity, intracellular, regulation of ARF protein signal transduction.	195169	5.5	1.9	46	3
501	chr1.CM0318.590.nd	Adenylosuccinate synthase activity, GTP binding, purine nucleotide biosynthetic process.	52966	7.2	4.5	46	2
502	chr5.CM0260.200.nc	Formate-tetrahydrofolate ligase activity, ATP binding, folic acid and derivative biosynthetic process, ligase activity.	29962	6.3	3.5	46	1
503	chr4.CM0429.360.nc	Monooxygenase activity, iron ion binding, electron transport, oxidoreductase activity, heme binding, metal ion binding.	57333	8.2	2.0	46	1
504	LjSGA_015992.1	Biosynthetic process, chlorophyll biosynthetic process, magnesium chelatase activity.	82992	5.1	3.3	46	2
505	LjSGA_014973.1	Nucleic acid binding, DNA binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, DNA integration.	42403	11.8	1.9	46	1
506	chr5.CM0095.260.nd	No GO annotations found.	53560	9.4	3.6	46	2
507	LjSGA_007953.1	Protein domain specific binding.	29768	4.7	12.5	46	5
507	chr2.CM0120.430.nc	Protein domain specific binding.	29725	4.8	9.6	46	4
507	chr4.CM0229.540.nc	Protein domain specific binding.	29767	4.8	6.9	46	3
508	LjSGA_065280.2	No GO annotations found.	23114	5.1	6.0	46	1
509	LjSGA_121030.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, RNA-dependent DNA replication, transport, zinc ion binding.	36674	9.1	2.5	46	1
510	LjSGA_038851.1	Carbohydrate metabolic process, hydrolase activity, phosphoric ester hydrolase activity.	18250	5.1	7.2	46	1
511	chr3.CM0396.200.nc	Catalytic activity, cellular metabolic process, coenzyme binding.	43460	5.8	6.7	45	2
511	LjSGA_006242.1	Catalytic activity, cellular metabolic process, coenzyme binding.	18363	6.0	5.6	41	1
512	chr6.CM0055.1140.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	12014	6.6	19.6	45	2
512	chr6.CM0055.920.nc	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	12014	6.6	19.6	45	2
513	chr1.CM0318.10.nd	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	13661	9.6	9.8	45	1
513	chr6.CM0037.1210.nd	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	13625	9.5	9.8	45	1
514	LjSGA_102150.1	No GO annotations found.	15007	5.8	11.2	45	1
515	LjSGA_016798.1	Regulation of progression through cell cycle, cytosol, protein complex.	32551	8.2	8.0	45	2
516	LjSGA_053764.1	No GO annotations found.	13854	8.0	8.4	45	1
517	LjSGA_148099.1	Phosphopyruvate hydratase complex, phosphopyruvate hydratase activity, glycolysis, lyase activity.	4545	9.8	14.6	45	1
519	chr2.CM0323.110.nc	Nucleic acid binding, DNA binding, zinc ion binding, DNA integration, transferase activity.	77046	9.4	1.5	45	1
519	chr6.CM0836.570.nd	No GO annotations found.	64600	10.4	1.8	45	1
519	LjSGA_143024.1	DNA binding, DNA integration, transferase activity.	29211	9.1	3.9	45	1
520	chr6.CM0037.1610.nc	No GO annotations found.	26850	6.1	7.0	44	1
521	LjSGA_013043.2	Protein serine/threonine kinase activity, kinase activity.	13756	11.8	8.3	44	3
522	LjSGA_010753.1	Nucleic acid binding, exonuclease activity, intracellular.	51497	10.0	2.5	44	1
523	LjSGA_024368.1	No GO annotations found.	19761	8.0	8.2	44	1
525	LjSGA_024132.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation.	19793	10.1	12.3	44	2
526	chr1.CM0133.1010.nc	Transcription factor activity, nucleus, regulation of transcription, DNA-dependent.	26767	5.2	3.8	43	1
526	chr2.CM0018.340.nd	Transcription factor activity, nucleus, regulation of transcription, DNA-dependent.	20286	5.9	4.8	43	1
526	chr2.CM0018.470.nd	Transcription factor activity, nucleus, regulation of transcription, DNA-dependent.	20956	5.9	4.7	43	1

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Supplemental Table S2.1: (*green_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
526	chr2.CM0018.610.nd	Transcription factor activity, nucleus, regulation of transcription, DNA-dependent.	22490	4.8	4.4	43	1
526	chr5.CM0040.1050.nd	Transcription factor activity, nucleus, regulation of transcription, DNA-dependent.	28409	4.4	3.5	43	1
527	LjT46P06.210.nd	Binding.	67670	8.8	1.6	43	1
528	chr5.LjT48O19.170.nd	Peptidyl-prolyl cis-trans isomerase activity, endoplasmic reticulum, protein folding, isomerase activity.	10085	8.0	14.0	43	1
529	chr5.CM0260.520.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	14143	11.0	10.7	43	1
530	chr6.CM0885.50.nc	Iron ion binding, electron transport, transport, electron carrier activity, metal ion binding, iron-sulfur cluster binding, 2 iron, 2 sulfur cluster binding.	15052	4.4	10.5	43	2
531	LjSGA_040309.1	Steroid binding, nucleus, lipid binding, heme binding, transition metal ion binding.	10920	6.2	8.0	43	1
532	chr1.CM0094.150.nc	Nucleotide binding, protein binding, ATP binding, protein folding, chloroplast, nucleoside-triphosphatase activity, protein metabolic process.	104990	8.6	1.1	43	1
532	LjSGA_033557.1	Nucleotide binding, DNA binding, nuclease activity, protein binding, ATP binding, nucleotide-excision repair, protein folding, chloroplast, nucleoside-triphosphatase activity, protein metabolic process.	25977	5.4	4.7	43	1
532	chr4.CM0175.340.nc	Nucleotide binding, DNA binding, nuclease activity, protein binding, ATP binding, nucleotide-excision repair, protein folding, chloroplast, nucleoside-triphosphatase activity, protein metabolic process.	102520	6.3	1.2	43	1
533	chr4.CM0042.940.nc	Protein binding.	5120	9.7	36.2	42	1
534	chr2.CM0249.1110.nc	Regulation of nitrogen utilization, transcriptional repressor activity.	33960	5.3	3.9	42	1
535	LjT25G12.90.nc	Endopeptidase activity, threonine endopeptidase activity, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, protein complex.	24601	6.4	4.0	42	1
536	chr3.CM0574.200.nd	Mitochondrion, ATP biosynthetic process, transport, ion transport, hydrogen ion transporter activity, ATP synthesis coupled proton transport, proton transport, proton-transporting two-sector ATPase complex, hydrolase activity, proton-transporting ATP synthase complex, catalytic core F(1), metal ion binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	10173	10.4	9.7	42	1
537	LjSGA_020183.1	Transferase activity.	5801	6.1	23.1	42	1
537	LjSGA_054228.1	No GO annotations found.	12866	5.4	10.8	42	1
538	LjSGA_024816.2	Catalytic activity, acetyl-CoA carboxylase activity, ATP binding, metabolic process, biotin binding, ligase activity.	43771	7.9	2.6	42	1
539	chr1.LjT04O06.30.nc	No GO annotations found.	41855	6.2	3.0	42	1
540	LjSGA_025007.1	Catalytic activity, cellular metabolic process, coenzyme binding.	14929	9.7	5.2	42	1
541	LjSGA_104128.1	RNA binding, RNA-directed DNA polymerase activity, aspartic-type endopeptidase activity, RNA-dependent DNA replication, proteolysis.	25922	9.4	5.3	42	1
542	chr3.CM0127.200.nc	No GO annotations found.	31953	9.7	4.2	42	1
543	LjSGA_074342.1	Protein folding, zinc ion binding, heat shock protein binding, metal ion binding, unfolded protein binding.	12756	4.5	7.1	42	1
544	LjSGA_025475.1.1	Extracellular region, cellulose and pectin-containing cell wall organization and biogenesis.	17995	9.4	5.6	42	1
545	chr1.CM0012.430.nc	Catalytic activity, triose-phosphate isomerase activity, metabolic process, chloroplast, isomerase activity, reductive pentose-phosphate cycle.	4692	5.1	23.3	42	1
546	LjSGA_138374.1	Catalytic activity, cellular metabolic process, coenzyme binding.	18896	8.5	4.9	42	1
547	chr1.CM0001.430.nc	Lipid metabolic process, cellulose and pectin-containing cell wall, hydrolase activity, acting on ester bonds.	42605	6.7	2.9	42	1

Continues...

Supplemental Table S2.1: (*green_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
548	LjSGA_038689.1	Golgi apparatus, cellulose and pectin-containing cell wall, cellulose biosynthetic process, alpha-1,4-glucan-protein synthase (UDP-forming) activity.	15631	5.9	7.2	42	1
549	chr3.CM0005.500.nc	Cysteine protease inhibitor activity.	26636	5.8	11.0	41	2
550	LjSGA_036265.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	9796	10.8	9.9	41	1
550	LjSGA_092476.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	9710	11.0	9.9	41	1

Supplemental Table S2.2: The 14 peaks identified in the “green_LotusNT” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table [S2.12](#).

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	chr6.CM0679.100.nd	No GO annotations found.	6909	4.1	23.9	118	1
2	LjSGA_039741.1	No GO annotations found.	62457	5.8	5.1	102	2
3	LjSGA_057408.1	No GO annotations found.	27020	8.5	9.4	93	2
4	LjSGA_031454.1	No GO annotations found.	17997	6.5	8.0	92	2
5	chr3.CM0164.170.nd	No GO annotations found.	64973	9.4	2.0	90	1
6	LjSGA_013193.1	No GO annotations found.	13545	4.7	14.6	89	1
7	chr4.CM0500.250.nd	No GO annotations found.	16109	3.8	10.7	87	1
8	chr1.CM0012.440.nc	No GO annotations found.	11141	9.2	12.8	76	1
9	LjSGA_059009.1	No GO annotations found.	9600	6.8	26.7	74	2
10	LjSGA_011073.1	No GO annotations found.	26867	9.2	5.6	71	1
11	LjSGA_111606.1	No GO annotations found.	18773	4.4	7.6	67	1
12	LjT32C22.20.nd	No GO annotations found.	60319	6.7	2.1	65	1
13	LjSGA_020590.0.1	No GO annotations found.	13825	6.8	7.5	54	1
14	LjSGA_066691.0.1	No GO annotations found.	9153	9.9	13.3	47	1

Supplemental Table S2.3: The 29 peaks identified in the “green_NCBInr” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.13.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	gi 1076373	No GO annotations found.	1434	9.7	92.9	189	2
2	gi 11023055	No GO annotations found.	54401	6.2	4.3	141	2
2	gi 37721488	No GO annotations found.	54674	6.2	4.2	141	2
3	gi 7230391	No GO annotations found.	49241	9.0	4.5	99	2
3	gi 48527431	No GO annotations found.	49293	9.2	4.5	99	2
3	gi 89275337	No GO annotations found.	26795	7.2	8.2	99	2
4	gi 22330456	No GO annotations found.	41445	5.5	4.2	95	2
4	gi 23476263	No GO annotations found.	40164	5.4	4.3	95	2
4	gi 51535181	No GO annotations found.	43428	6.0	3.9	95	2
4	gi 113595266	No GO annotations found.	46906	7.1	3.7	95	2
5	Unknown/dead	No GO annotations found.	1393	5.8	91.7	88	1
6	gi 5924375	No GO annotations found.	41083	6.0	5.2	76	1
6	gi 51039637	No GO annotations found.	42646	5.6	5.1	76	1
6	gi 51556895	No GO annotations found.	42800	5.8	5.1	76	1
7	gi 20146556	No GO annotations found.	42894	6.0	5.5	76	1
7	gi 20146600	No GO annotations found.	42866	6.2	5.5	76	1
8	gi 16588840	No GO annotations found.	21765	6.1	6.5	74	1
9	gi 51039632	No GO annotations found.	15641	4.6	10.9	67	1
10	gi 62183962	No GO annotations found.	54763	6.1	3.8	60	1
10	gi 86156419	No GO annotations found.	25914	5.2	7.9	60	1
10	Unknown/dead	No GO annotations found.	54334	5.3	3.8	60	1
10	gi 113205159	No GO annotations found.	59709	5.4	3.5	60	1
11	gi 2708324	No GO annotations found.	11133	8.4	23.1	58	1
12	gi 6911142	No GO annotations found.	14154	8.7	10.9	52	1
12	gi 6911146	No GO annotations found.	16255	7.8	9.4	52	1
13	gi 113565257	No GO annotations found.	20006	7.8	7.8	51	1
15	gi 20146580	No GO annotations found.	42560	6.2	5.5	47	1
16	gi 27461579	No GO annotations found.	44470	5.7	5.3	45	1
17	gi 14334219	No GO annotations found.	12899	9.6	13.9	44	1

Supplemental Table S2.4: The 46 peaks identified in the “green_SPROT” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.14.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	METE_ARATH	CIMS, At5g17920, MPI7.9: 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase.	84304	6.1	2.7	107	1
1	METE_MESCR	METE: 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase.	84769	5.9	2.7	107	1
2	TBA_DAUCA	TBA: Tubulin alpha chain.	49609	4.9	3.1	106	1
2	TBA_PRUDU	TUBA: Tubulin alpha chain.	49495	4.9	3.1	106	1
2	TBA_WHEAT	TUBA: Tubulin alpha chain.	49711	4.9	3.1	106	1
2	TBA1_ANEPH	TUBA1: Tubulin alpha-1 chain.	49754	5.0	3.1	106	1
2	TBA1_ELEIN	TUBA1, TUA1: Tubulin alpha-1 chain.	49699	4.9	3.1	106	1
2	TBA1_GOSHI	Tubulin alpha-1 chain.	49706	4.9	3.1	106	1
2	TBA1_MAIZE	TUBA1, TUA1: Tubulin alpha-1 chain.	49699	4.9	3.1	106	1
2	TBA1_PEA	TUBA1: Tubulin alpha-1 chain.	49621	4.9	3.1	106	1
2	TBA2_ARATH	TUBA2, TUA2, At1g50010, F2J10.11, TUBA4, TUA4, At1g04820, F13M7.19: Tubulin alpha-2/alpha-4 chain.	49509	4.9	3.1	106	1
2	TBA2_GOSHI	Tubulin alpha-2 chain.	49509	4.9	3.1	106	1
2	TBA2_HORVU	TUBA2, ATUB2: Tubulin alpha-2 chain.	49669	4.9	3.1	106	1
2	TBA2_MAIZE	TUBA2, TUA2: Tubulin alpha-2 chain.	49699	4.9	3.1	106	1
2	TBA2_ORYSA	No GO annotations found.	49705	4.8	3.1	106	1
2	TBA3_HORVU	TUBA3, ATUB3: Tubulin alpha-3 chain.	49697	4.9	3.1	106	1
2	TBA3_MAIZE	TUBA3, TUA3: Tubulin alpha-3 chain.	49529	5.1	3.1	106	1
2	TBA4_GOSHI	Tubulin alpha-4 chain.	49539	4.9	3.1	106	1
2	TBA6_ARATH	TUBA6, TUA6, At4g14960, dl3520c: Tubulin alpha-6 chain.	49506	4.9	3.1	106	1
3	ATPB_SCHSP	AtpB: ATP synthase subunit beta.	53610	5.3	4.2	75	1
4	MDAR_PEA	Monodehydroascorbate reductase.	47279	5.8	3.0	74	1
5	PSA6_ORYSA	No GO annotations found.	27556	6.2	12.2	71	2
6	PSAE_SPIOL	PSAE-1, PSAE-2: Photosystem I reaction center subunit IV, chloroplast precursor.	13359	10.0	16.0	59	1
7	EFTU_ARATH	TUFA, At4g20360, F9F13.10: Elongation factor Tu, chloroplast precursor.	51598	5.8	3.4	56	1
7	EFTU1_SOYBN	TUFA: Elongation factor Tu, chloroplast precursor.	52063	6.2	3.3	56	1
7	EFTU2_SOYBN	TUFB1: Elongation factor Tu, chloroplast precursor.	52476	6.3	3.3	56	1
8	TBA_CHLVU	TUBA, TUA1: Tubulin alpha chain.	49680	4.9	3.1	50	1
8	TBA1_CHLRE	TUBA1: Tubulin alpha-1 chain.	49555	5.0	3.1	50	1
8	TBA1_VOLCA	TUBA1, TUBA2: Tubulin alpha-1/alpha-2 chain.	49525	5.0	3.1	50	1
8	TBA2_CHLRE	TUBA2: Tubulin alpha-2 chain.	49554	5.0	3.1	50	1
9	RL40_BRARA	60S ribosomal protein L40.	6118	10.7	21.2	50	1
9	RL40_NICSY	UBICEP52-7, RPL40: 60S ribosomal protein L40.	6190	10.6	21.2	50	1
10	EF1A_MAIZE	EF1A: Elongation factor 1-alpha.	49202	9.2	5.4	50	1
11	MDARS_CUCSA	Monodehydroascorbate reductase, seedling isozyme.	47387	5.3	3.2	48	1
11	MDAR_SOLLC	AFRR: Monodehydroascorbate reductase.	47006	5.8	3.2	48	1
12	SUCA2_ARATH	At5g23250, MKD15.11: Succinyl-CoA ligase [GDP-forming] subunit alpha-2, mitochondrial precursor.	35294	8.8	6.2	44	1
13	UGPA_HORVU	UTP-glucose-1-phosphate uridylyltransferase.	51612	5.2	3.2	42	1
14	BADH_ARATH	No GO annotations found.	54397	5.2	2.4	41	1
15	TKTC_CRAPL	TKT3: Transketolase, chloroplast (Fragment).	56152	5.8	2.9	37	1
16	CB2A_SPIOL	Chlorophyll a-b binding protein, chloroplast precursor.	28406	5.3	13.1	37	1
16	CB2G_SOLLC	CAB3C: Chlorophyll a-b binding protein 3C, chloroplast precursor.	28307	5.5	13.1	37	1
16	CB21_MAIZE	CAB1: Chlorophyll a-b binding protein 1, chloroplast precursor.	27798	5.1	13.4	37	1

Continues...

Supplemental Table S2.4: (*green_SPROT GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
16	CB22_ORYSA	No GO annotations found.	27535	5.3	13.4	37	1
16	CB22_PEA	AB80: Chlorophyll a-b binding protein AB80, chloroplast precursor.	28635	5.5	13.0	37	1
16	CB28_PEA	CAB8, LHCB1: Chlorophyll a-b binding protein 8, chloroplast precursor.	28508	5.2	13.1	37	1
18	ALF2_PEA	Fructose-bisphosphate aldolase, cytoplasmic isozyme 2.	38467	6.8	5.6	32	1

Supplemental Table S2.5: The 80 peaks identified in the “green_lotusEST_TIGR” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.15.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	TC9431	No GO annotations found.	52558	5.6	4.1	567	1
2	TC14090	Chloroplast, mesoderm development, lyase activity, pentose-phosphate shunt, striated muscle contraction, cytoplasm, glycolysis, fructose metabolism, cellular_component unknown, fructose-bisphosphate aldolase activity.	53341	8.0	23.2	531	8
3	TC19114	No GO annotations found.	25906	5.9	20.9	482	3
4	TC18091	No GO annotations found.	24315	7.8	6.8	394	1
5	TC8325	Alpha-galactosidase activity.	51989	8.5	11.3	328	4
6	TC14411	Phospholipase inhibitor activity, calcium ion binding, biological_process unknown, calcium-dependent phospholipid binding, cellular_component unknown.	48453	7.4	15.9	306	6
7	TC7865	One-carbon compound metabolism, porphyrin biosynthesis, adenosyl-homocysteine activity, cytoplasm, methionine metabolism, selenocysteine metabolism, hydroxymethylbilane synthase activity, DNA methylation, L-serine biosynthesis, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, mitochondrion, hydrolase activity, cellular_component unknown, S-adenosylhomocysteine catabolism.	67254	6.3	9.2	227	5
8	TC8215	ATP binding, hydrogen-transporting ATP synthase activity, rotational mechanism, proton transport.	55783	-	14.0	221	5
9	TC8009	Phosphoglycerate kinase activity, glycolysis.	60404	8.4	21.8	213	9
10	TC16258	No GO annotations found.	21896	6.4	15.0	190	3
11	TC7926	Phosphoglycerate kinase activity, glycolysis.	65219	8.5	14.7	188	7
12	TC14283	Ubiquitin-dependent protein catabolism, proteasome core complex (sensu Eukarya), endopeptidase activity, peptidase activity, cytosol.	39389	5.1	11.1	178	3
13	TC8165	Lactoylglutathione lyase activity, carbohydrate metabolism, aromatic amino acid family metabolism, 4-hydroxyphenylpyruvate dioxygenase activity, cellular_component unknown.	42760	5.6	8.1	173	2
14	TC8727	No GO annotations found.	49829	9.6	8.3	165	3
15	TC8258	Translational elongation, translation elongation factor activity, guanyl-nucleotide exchange factor activity, cytosol, eukaryotic translation elongation factor 1 complex.	35906	4.6	6.5	159	2
16	TC10840	Negative regulation of cell cycle, response to hydrogen peroxide, cytoplasm, mitochondrion, cytosol, cellular_component unknown, transferase activity, mitochondrial intermembrane space, negative regulation of cell proliferation, induction of apoptosis, microtubule, transcription factor activity, pyrimidine base metabolism, CTP biosynthesis, kinase activity, nucleoside-diphosphate kinase activity, UTP biosynthesis, purine nucleotide biosynthesis, RNA metabolism, ATP binding, GTP biosynthesis, nucleoside metabolism, nucleotide metabolism, regulation of transcription, DNA-dependent, nucleotide kinase activity, nucleus, DNA metabolism.	18886	8.6	12.8	150	2
17	TC9761	No GO annotations found.	20817	6.2	15.1	133	3
18	TC14102	Mature ribosome assembly, laminin receptor activity, ribosomal small subunit assembly and maintenance, intracellular, structural constituent of ribosome, cell adhesion, cytoplasm, cytosolic small ribosomal subunit (sensu Eukarya), small ribosomal subunit, protein biosynthesis.	43893	5.5	2.9	129	1
19	CN825001	No GO annotations found.	24434	9.2	23.9	124	5

Continues...

Supplemental Table S2.5: (*green_lotusEST_TIGR GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
20	TC9795	Endoplasmic reticulum.	36068	8.6	7.6	115	3
21	TC9755	ATP-binding and phosphorylation-dependent chloride channel activity, proton-transporting ATP synthase complex (sensu Eukarya), proton-transporting ATP synthase, catalytic core (sensu Eukarya), spermatid development, proton transport, mitochondrion, hydrolase activity, ATP synthesis coupled proton transport, ATP biosynthesis, ATP binding, proton-transporting two-sector ATPase complex, hydrogen ion transporter activity, hydrogen-transporting ATP synthase activity, rotational mechanism, transporter activity.	72981	6.6	6.6	113	3
22	TC8048	Ubiquitin-dependent protein catabolism, proteasome core complex (sensu Eukarya), endopeptidase activity, peptidase activity, RNA binding, cytosol.	38398	6.6	16.2	105	4
23	TC16731	Response to reactive oxygen species, high affinity iron ion transport, copper chaperone activity, copper ion homeostasis, aging.	18127	8.8	15.2	104	2
24	TC9709	No GO annotations found.	21055	8.4	11.5	102	2
25	TC14129	Photosynthetic water oxidation, oxygen evolving complex, extrinsic to membrane, thylakoid (sensu Viridiplantae), photosystem II (sensu Viridiplantae), thylakoid lumen (sensu Viridiplantae), molecular_function unknown.	37177	8.7	9.8	96	2
26	CN825207	No GO annotations found.	25323	7.0	7.1	90	1
27	TC14826	Ribosomal large subunit assembly and maintenance, structural constituent of ribosome, intracellular, ribosome, cytosolic large ribosomal subunit (sensu Eukarya), RNA binding, protein biosynthesis.	41446	9.9	7.8	88	2
28	TC14233	SRP-dependent cotranslational membrane targeting, translocation, regulation of cell cycle, heat shock protein activity, protein-mitochondrial targeting, vesicle-mediated transport, ATPase activity, coupled, protein folding, vacuolar membrane (sensu Fungi), cytoplasm, neurotransmitter secretion, spermatid development, response to heat, cellular_component unknown, cytosol, anti-apoptosis, apoptosis inhibitor activity, response to stress, non-chaperonin molecular chaperone ATPase activity, cell wall (sensu Fungi), reproduction, inhibition of caspase activation, mRNA catabolism, male meiosis, protein binding, embryonic development, ATP binding, protein-nucleus import, translocation, ATPase activity, intracellular, chaperone activity, nucleus.	58203	5.1	2.5	87	1
28	TC14234	SRP-dependent cotranslational membrane targeting, translocation, regulation of cell cycle, heat shock protein activity, protein-mitochondrial targeting, vesicle-mediated transport, ATPase activity, coupled, protein folding, vacuolar membrane (sensu Fungi), cytoplasm, neurotransmitter secretion, spermatid development, response to heat, cellular_component unknown, cytosol, anti-apoptosis, apoptosis inhibitor activity, response to stress, non-chaperonin molecular chaperone ATPase activity, cell wall (sensu Fungi), reproduction, inhibition of caspase activation, mRNA catabolism, male meiosis, protein binding, ATP binding, embryonic development, protein-nucleus import, translocation, ATPase activity, intracellular, chaperone activity, nucleus.	56477	5.7	2.6	87	1
29	TC14860	Triose-phosphate isomerase activity, metabolism, cytosol.	32494	9.0	7.9	83	2
30	TC16128	Electron transport, molecular_function unknown, photosystem I reaction center.	21636	9.4	6.5	83	1
31	TC8046	Phosphate transporter activity, adenine phosphoribosyltransferase activity, pyrimidine nucleotide biosynthesis, nucleoside metabolism, orotate phosphoribosyltransferase activity, adenine salvage, cellular_component unknown, cytosol.	45585	9.1	4.2	82	2
32	TC11167	Biological_process unknown, molecular_function unknown, cellular_component unknown.	30270	4.9	5.1	82	1

Continues...

Supplemental Table S2.5: (*green_lotusEST_TIGR GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
33	TC14170	Response to oxidative stress, photosystem II.	42117	9.2	8.5	82	2
34	TC14768	No GO annotations found.	38111	6.9	4.3	80	2
35	TC14111	No GO annotations found.	23302	8.2	6.5	80	1
36	TC14758	Nucleic acid binding, biological_process unknown, circadian rhythm, mitochondrion, nucleus, RNA binding.	24265	5.5	8.3	80	1
37	TC18990	No GO annotations found.	12590	9.6	24.6	78	2
38	TC8324	Transport, energy pathways, integral to plasma membrane, symporter activity, mitochondrial inner membrane, phosphate carrier activity, mitochondrion, binding.	57548	9.2	3.4	73	1
39	TC16164	No GO annotations found.	21081	6.2	14.3	73	2
40	TC10602	Ribosome biogenesis, structural constituent of ribosome, ribosome, protein biosynthesis, molecular_function unknown.	17111	9.6	7.1	73	1
40	TC11545	Ribosome biogenesis, structural constituent of ribosome, ribosome, protein biosynthesis, molecular_function unknown.	16403	9.0	7.6	73	1
41	TC14070	Response to sucrose stimulus, cytoplasm, glyceraldehyde-3-phosphate dehydrogenase activity, response to heat, cytosol, cellular_component unknown, response to oxidative stress, glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, oxidoreductase activity, response to stress, gluconeogenesis, lipid particle, cell wall (sensu Fungi), glycolysis.	50234	7.3	3.0	72	1
42	TC8011	Cytoplasm, cytosol, chloroplast, reductive pentose-phosphate cycle, gluconeogenesis, triose-phosphate isomerase activity, metabolism, glycolysis.	46308	9.1	6.7	71	2
43	TC14938	Biological_process unknown, endomembrane system.	56069	6.4	2.9	71	1
44	TC8718	Molecular_function unknown.	38162	8.4	4.3	68	1
45	TC14174	No GO annotations found.	126210	-	2.4	68	2
46	TC16511	Intracellular, structural constituent of ribosome, ribosome, cytosolic small ribosomal subunit (sensu Eukarya), RNA binding, protein biosynthesis.	32087	9.3	3.7	66	1
46	TC16742	Intracellular, structural constituent of ribosome, ribosome, cytosolic small ribosomal subunit (sensu Eukarya), RNA binding, protein biosynthesis.	34207	9.9	3.5	66	1
47	TC8440	No GO annotations found.	23573	9.0	6.0	65	1
48	TC8596	Biological_process unknown, peroxisomal membrane, peroxisome division, endomembrane system, molecular_function unknown, cellular_component unknown.	41138	9.7	3.2	62	1
49	TC16605	Biological_process unknown, cellular_component unknown.	22535	5.5	7.1	62	1
50	TC14545	No GO annotations found.	40417	5.2	5.6	62	2
51	TC13498	Ubiquitin-dependent protein catabolism, proteasome core complex (sensu Eukarya), endopeptidase activity, peptidase activity, proteasome complex (sensu Eukarya).	21043	7.9	6.6	61	1
52	TC16034	Isomerase activity, endoplasmic reticulum membrane, endoplasmic reticulum, biological_process unknown, protein folding, thylakoid lumen (sensu Viridiplantae), FK506 binding, peptidyl-prolyl cis-trans isomerase activity.	21048	6.5	7.7	61	1
53	TC16259	Catalytic activity, metabolism, carnitine racemase activity, cellular_component unknown.	33327	8.8	5.0	61	1
54	BP043716	No GO annotations found.	19814	8.9	9.5	60	1
55	TC9804	No GO annotations found.	23498	7.1	5.5	59	1
56	TC9618	Mitochondrial inner membrane presequence translocase complex, protein translocase activity, protein transport.	27162	8.0	4.3	58	1
57	TC9100	Biological_process unknown, mitochondrion.	26557	5.3	5.9	58	1
57	BP055887	No GO annotations found.	18299	6.2	8.3	58	1

Continues...

Supplemental Table S2.5: (green_lotusEST_TIGR GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
58	TC9294	No GO annotations found.	37353	6.8	3.7	58	1
59	TC16914	Reproduction, ribosome, cytosolic large ribosomal subunit (sensu Eukarya), RNA binding, protein biosynthesis, embryonic development, structural constituent of ribosome, intracellular, large ribosomal subunit.	28177	9.0	6.5	57	1
60	AV776844	No GO annotations found.	13229	5.0	11.7	55	1
61	TC14220	Oxidoreductase activity, acting on NADH or NADPH.	49334	7.6	8.0	54	3
62	TC9107	Alanine-glyoxylate transaminase activity.	49744	7.4	2.8	53	1
63	TC7901	Biological_process unknown, cell wall biosynthesis (sensu Magnoliophyta), cellulose synthase (UDP-forming) activity, Golgi stack, molecular_function unknown, cellular_component unknown, membrane, Golgi trans cisterna.	50054	6.3	3.1	53	1
64	TC17673	No GO annotations found.	21389	9.4	6.8	51	1
65	TC10225	Arsenate reductase (glutaredoxin) activity, electron transport, thiol-disulfide exchange intermediate activity.	26080	8.3	5.0	49	1
66	TC8223	Mitochondrial outer membrane, anion transport, biological_process unknown, voltage-dependent ion-selective channel activity, molecular_function unknown, cellular_component unknown.	45102	8.2	2.6	47	1
67	TC14632	Structural constituent of ribosome, ribosome, DASH complex, cytosolic large ribosomal subunit (sensu Eukarya), cytoplasm, protein biosynthesis.	29190	9.8	3.9	46	1
68	TC8417	Galactose biosynthesis, UDP-glucose 4-epimerase activity.	29345	7.3	3.8	46	1
69	TC8618	No GO annotations found.	18178	7.2	9.6	44	1
70	TC8712	Dihydrolipoyl dehydrogenase activity, mitochondrial matrix, response to light.	43665	6.2	5.1	43	2
71	TC12003	Actin cortical patch (sensu Fungi), regulation of transcription from Pol II promoter, heart development, protein secretion, muscle development, sperm individualization, establishment of cell polarity (sensu Saccharomyces), vesicle transport along actin filament, structural constituent of cytoskeleton, actin cytoskeleton organization and biogenesis, cell cycle-dependent actin filament reorganization, cytoskeleton, cytokinesis, histone acetylation, actin cortical patch (sensu Saccharomyces), cytoskeleton organization and biogenesis, actin filament, mitochondrion inheritance, response to osmotic stress, vacuole inheritance, reproduction, exocytosis, mitotic spindle orientation (sensu Fungi), endocytosis, apical bud growth, sporulation (sensu Saccharomyces), isotropic bud growth, histone acetyltransferase complex, cell wall organization and biogenesis, embryonic development, actin cable (sensu Saccharomyces), actin cable (sensu Fungi), contractile ring (sensu Saccharomyces).	22363	5.5	5.4	43	1
72	BP070882	No GO annotations found.	17883	8.6	8.5	43	1
73	TC8611	No GO annotations found.	20181	8.3	7.2	42	1
74	TC10826	Ribosome, cytosolic large ribosomal subunit (sensu Eukarya), RNA binding, protein biosynthesis, ribosome biogenesis, ribosomal large subunit assembly and maintenance, rRNA binding, cytosolic large ribosomal subunit (sensu Bacteria), intracellular, structural constituent of ribosome.	27612	10.3	4.8	41	1
75	TC14770	Potassium channel activity, potassium ion transport.	41533	6.3	3.9	41	1
77	TC20208	Biological_process unknown, cellular_component unknown.	15594	6.6	10.1	40	1

Supplemental Table S2.6: The 242 peaks identified in the “mature_LotusAA” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.16.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	chr5.CM0357.530.nc	Nutrient reservoir activity.	64823	6.3	44.2	16306	23
2	chr5.LjT15N12.90.nc	Nutrient reservoir activity.	66377	5.4	35.3	10387	18
3	chr5.LjT15N12.80.nc	Nutrient reservoir activity.	66257	5.4	32.3	10067	16
4	chr1.CM0295.260.nd	Nutrient reservoir activity.	54140	6.3	48.6	7228	23
5	chr5.CM0357.550.nc	Nutrient reservoir activity.	65051	5.8	47.1	5238	26
6	LjSGA_030216.1	Nutrient reservoir activity.	33723	8.0	64.3	4289	16
7	LjSGA_133863.1	No GO annotations found.	16617	8.8	66.7	2033	16
8	LjSGA_052214.1	No GO annotations found.	36907	6.0	33.0	1504	10
9	LjT46P06.60.nd	No GO annotations found.	75202	6.1	21.3	1296	11
10	chr2.LjT30P12.40.nc	Monolayer-surrounded lipid storage body.	20658	9.0	41.5	904	10
11	LjT03L06.120.nd	Defense response, response to biotic stimulus.	15480	5.1	65.3	827	7
12	chr4.CM0126.1570.nc	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	52775	6.3	13.3	665	6
12	LjSGA_084876.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	37516	6.7	12.8	408	4
12	LjSGA_124257.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	35627	8.1	11.4	408	3
12	LjSGA_141109.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	29246	6.1	17.2	370	4
12	LjSGA_116237.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	37179	7.3	13.5	370	4
12	LjSGA_138404.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	22218	7.6	16.4	350	3
12	LjSGA_105267.1	Chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-biphosphate carboxylase activity.	22804	6.5	8.8	329	2

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
12	LjSGA_134471.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	22087	6.1	9.0	329	2
12	LjSGA_149364.1	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-biphosphate carboxylase activity.	18183	6.6	6.6	329	1
12	LjSGA_113307.1	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle.	22513	9.7	5.6	329	1
12	chr3.CM0106.360.nd	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle.	6187	5.1	19.6	202	1
12	LjSGA_096321.1	Chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-biphosphate carboxylase activity.	9488	8.9	12.9	202	1
12	LjSGA_102132.1	Monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle.	10749	4.5	9.3	121	1
12	LjSGA_136714.1	Magnesium ion binding, monooxygenase activity, chloroplast, chloroplast ribulose biphosphate carboxylase complex, photorespiration, carbon utilization by fixation of carbon dioxide, photosynthesis, oxidoreductase activity, lyase activity, ribulose-biphosphate carboxylase activity, reductive pentose-phosphate cycle, metal ion binding.	31823	7.2	8.8	112	2
13	chr5.CM0357.340.nc	No GO annotations found.	26210	4.8	58.5	652	12
14	chr6.CM0114.310.nc	No GO annotations found.	28475	5.3	28.6	628	10
15	chr1.CM0544.400.nd	Pepsin A activity, proteolysis.	18881	8.7	14.5	610	2
16	LjSGA_015149.2	No GO annotations found.	41654	8.9	21.8	599	7
17	chr5.LjT43D06.110.nd	Calcium ion binding, sugar binding, manganese ion binding, metal ion binding.	30790	5.7	27.1	566	5
18	LjSGA_034221.1	Monolayer-surrounded lipid storage body.	19499	6.6	27.2	543	5
19	LjSGA_091288.1	Nutrient reservoir activity.	32648	6.2	14.2	537	3
20	chr5.LjT43D06.20.nd	Calcium ion binding, sugar binding, manganese ion binding, metal ion binding.	23814	5.6	26.9	482	5
21	chr1.LjT38A19.110.nc	Embryonic development.	14256	9.6	31.7	393	4
21	chr5.LjT10N02.50.nd	Embryonic development.	17794	6.6	6.4	197	1
22	LjSGA_145133.1	No GO annotations found.	8477	5.5	53.8	390	6
23	chr3.LjT02L14.180.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxxygenase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylipin biosynthetic process, metal ion binding.	40123	5.5	10.9	351	3
23	LjT30L14.20.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxxygenase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylipin biosynthetic process, metal ion binding.	55309	5.4	7.9	351	3

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
23	chr3.CM0115.370.nc	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, metal ion binding.	89847	5.4	1.4	61	1
23	LjSGA_052903.1	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylipin biosynthetic process, metal ion binding.	30422	5.2	4.1	61	1
24	chr3.CM0246.60.nd	Nutrient reservoir activity.	55035	5.2	22.2	341	11
25	LjSGA_025401.2	No GO annotations found.	32237	7.6	37.6	301	12
26	chr3.LjT02L14.10.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, oxylipin biosynthetic process, metal ion binding.	97160	6.0	10.6	293	8
26	chr3.CM0115.330.nc	Iron ion binding, electron transport, lipoxxygenase activity, metal ion binding.	97350	6.0	2.5	69	2
27	chr1.CM0544.500.nd	Metabolic process, oxidoreductase activity.	37876	6.7	23.0	289	6
27	LjSGA_029600.1	Metabolic process, oxidoreductase activity.	22054	9.1	18.6	150	3
27	LjSGA_014692.1	Ribokinase activity, D-ribose metabolic process, kinase activity, transferase activity.	31568	4.7	8.3	137	2
28	chr1.CM0032.460.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	26346	10.2	19.7	282	3
29	LjSGA_092567.1	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, cytoplasm, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	18467	7.8	33.9	251	4
29	LjSGA_086307.1	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	15950	6.6	19.3	143	2
29	LjT29P04.130.nd	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	36687	6.3	4.1	140	1
30	chr3.CM0110.130.nc	Defense response, response to biotic stimulus.	17494	5.9	65.6	238	10
30	chr3.CM0110.30.nc	Defense response, response to biotic stimulus.	17416	5.8	8.6	50	1
31	LjSGA_014613.2	Phosphoglycerate kinase activity, glycolysis, kinase activity.	7278	4.8	37.0	189	2
31	LjSGA_047542.1	Phosphoglycerate kinase activity, glycolysis, kinase activity.	10715	5.1	16.2	155	1
32	chr2.LjT43N03.40.nd	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, ribulose-biphosphate carboxylase activity.	20037	9.2	22.0	186	4
32	chr1.LjT23D08.110.nc	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-biphosphate carboxylase activity.	20329	9.0	4.4	75	1
32	chr1.LjT23D08.120.nc	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-biphosphate carboxylase activity.	20317	9.2	4.4	75	1
32	LjSGA_030971.1	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-biphosphate carboxylase activity.	13968	8.4	6.7	75	1
32	LjSGA_080821.1	Chloroplast ribulose biphosphate carboxylase complex, carbon utilization by fixation of carbon dioxide, lyase activity, ribulose-biphosphate carboxylase activity.	13955	8.4	6.7	75	1
33	chr5.CM0260.650.nd	Oxidoreductase activity, glutathione dehydrogenase (ascorbate) activity.	20024	5.8	25.7	179	4

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
34	chr1.CM0248.160.nc	Superoxide dismutase activity, superoxide metabolic process, oxidoreductase activity, metal ion binding.	26890	7.2	10.6	168	2
35	LjSGA_082478.1	Nucleotide binding, magnesium ion binding, nucleoside diphosphate kinase activity, ATP binding, GTP biosynthetic process, UTP biosynthetic process, CTP biosynthetic process, nucleotide metabolic process, pyrimidine ribonucleoside triphosphate biosynthetic process, kinase activity, transferase activity, metal ion binding.	13028	6.8	23.1	163	3
36	LjSGA_031559.1	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	18038	8.6	21.6	156	3
36	chr1.CM0231.140.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	18130	7.7	16.9	149	2
36	LjSGA_090105.1	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity.	18473	8.3	4.7	46	1
37	chr1.CM0133.420.nc	No GO annotations found.	21063	6.2	21.7	135	4
38	LjT42M11.210.nc	Endopeptidase activity, threonine endopeptidase activity, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process.	30257	4.8	5.8	135	1
39	chr3.CM0282.370.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	35846	8.5	15.5	130	4
39	chr3.CM0282.420.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	14077	5.6	8.1	53	1
40	chr1.CM0027.160.nc	Protein disulfide isomerase activity, endoplasmic reticulum, isomerase activity, cell redox homeostasis.	56636	4.8	11.8	128	5
41	chr1.CM0051.30.nc	Mitochondrial outer membrane, transport, ion transport, anion transport, voltage-gated ion-selective channel activity, porin activity, membrane, integral to membrane, outer membrane.	29522	8.6	13.8	126	3
42	LjSGA_065420.1	Peroxidase activity, nucleus, antioxidant activity, oxidoreductase activity, peroxiredoxin activity.	18361	7.0	35.6	122	5
43	chr5.CM0328.690.nd	Nucleotide binding, ATP binding, ATP biosynthetic process, hydrogen-exporting ATPase activity, phosphorylative mechanism, ATP synthesis coupled proton transport, integral to membrane, proton-transporting two-sector ATPase complex, nucleoside-triphosphatase activity, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen ion transporting ATPase activity, rotational mechanism.	59990	5.8	8.8	120	4
44	LjSGA_071976.1.1	Structural constituent of ribosome, intracellular, ribosome, translation.	16370	9.5	22.4	113	2
45	chr3.CM0115.260.nc	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, metal ion binding.	94760	6.0	2.7	109	2
46	LjSGA_014026.1	Intracellular.	21523	10.0	15.7	109	2
47	LjSGA_038243.1	Intracellular.	21496	10.0	15.8	109	2
47	LjSGA_040678.1	Intracellular, ribonucleoprotein complex.	14911	10.5	23.3	109	2
48	LjT36L22.20.nd	Nucleotide binding, protein binding, ATP binding, protein folding, chloroplast, cellular protein metabolic process, unfolded protein binding.	72781	7.4	1.6	109	1
48	LjSGA_075236.1	Nucleotide binding, protein binding, ATP binding, protein folding, chloroplast, cellular protein metabolic process, unfolded protein binding.	21196	9.5	5.8	109	1

Continues...

Supplemental Table S2.6: (mature_LotusAA GeLC-MS/MS Peaks continued)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
49	chr1.CM0378.70.nc	No GO annotations found.	16170	5.0	23.8	106	3
50	chr3.CM0116.300.nc	Binding, iron ion transport, iron ion homeostasis, ferric iron binding, oxidoreductase activity, transition metal ion binding.	29020	5.5	16.4	106	3
51	chr3.CM0091.670.nd	Nucleotide binding, nucleic acid binding.	9784	4.6	41.8	99	3
52	chr6.CM0420.60.nd	ATP binding, protein folding.	29859	9.2	16.1	96	3
52	chr4.CM0006.280.nc	ATP binding, protein folding.	26812	8.9	4.7	95	1
53	chr1.CM0113.140.nc	Response to stress, response to water.	16034	8.0	7.8	96	1
54	chr4.CM0558.260.nc	Peroxidase activity, glutathione peroxidase activity, response to oxidative stress, oxidoreductase activity.	26153	8.8	14.0	95	2
55	chr3.LjT44N20.60.nd	Nucleotide binding, protein binding, ATP binding, protein folding, cellular protein metabolic process, unfolded protein binding.	61745	5.4	6.5	95	3
56	CM1729.90.nc	Adenosine kinase activity, purine ribonucleoside salvage, kinase activity.	37530	5.2	6.2	94	1
57	LjSGA_067203.1	Nutrient reservoir activity.	21682	6.5	8.3	93	1
58	LjSGA_008893.1	Calcium ion binding, cytoplasm.	18920	4.4	20.8	92	3
58	chr5.CM0299.300.nc	Cytoplasm.	19063	4.5	5.4	63	1
59	LjSGA_059392.1	Endopeptidase inhibitor activity.	23816	5.0	8.6	90	1
60	chr2.CM0210.60.nc	Nucleotide binding, ATP binding, protein folding, unfolded protein binding.	80087	5.0	3.4	86	2
60	LjSGA_048339.1	Nucleotide binding, ATP binding, protein folding, unfolded protein binding.	57950	5.3	2.8	68	1
61	chr6.CM1829.160.nc	Catalytic activity, metabolic process, lyase activity.	65882	7.6	2.6	86	1
62	LjT16G18.150.nd	Peptidyl-prolyl cis-trans isomerase activity, protein folding, isomerase activity, peptide binding.	13844	7.2	9.2	82	1
63	LjT04E07.20.nc	Peroxidase activity, antioxidant activity, oxidoreductase activity.	28619	6.1	6.5	82	1
63	LjT18K22.30.nc	Peroxidase activity, antioxidant activity, oxidoreductase activity.	29224	6.4	6.4	82	1
64	LjT33L17.40.nc	Oxidoreductase activity.	17443	5.3	6.2	80	2
65	chr1.CM0442.310.nd	GTPase activity, protein binding, GTP binding, intracellular protein transport, nucleocytoplasmic transport, signal transduction, small GTPase mediated signal transduction.	25130	6.4	9.5	80	2
65	chr1.CM0442.350.nd	GTPase activity, protein binding, GTP binding, intracellular protein transport, nucleocytoplasmic transport, signal transduction, small GTPase mediated signal transduction.	25073	6.4	9.5	80	2
65	LjSGA_031947.1	GTPase activity, protein binding, GTP binding, intracellular protein transport, nucleocytoplasmic transport, signal transduction, small GTPase mediated signal transduction.	24934	6.7	9.6	80	2
66	LjSGA_011457.1	Transporter activity, binding, transport.	8493	4.2	37.5	79	2
67	LjT32C22.170.nd	No GO annotations found.	12219	5.5	18.8	78	2
68	chr3.CM0996.130.nd	No GO annotations found.	8061	5.0	21.8	78	1
69	chr5.CM0148.90.nd	Heme binding, transition metal ion binding.	17015	4.5	12.9	78	1
70	LjSGA_037505.1	No GO annotations found.	6162	9.6	20.7	78	1
71	chr1.CM0033.430.nc	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	15111	10.3	8.1	77	1
72	chr1.CM0001.670.nc	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	49254	9.1	4.3	77	2
72	chr1.CM0192.320.nd	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	24416	8.8	8.6	77	2
72	chr2.LjT12G08.20.nc	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	49389	9.1	4.3	77	2
72	chr5.CM0909.50.nc	Nucleotide binding, translation elongation factor activity, GTPase activity, GTP binding, cytoplasm, translation, translational elongation.	49363	9.2	4.3	77	2
73	chr5.CM0052.420.nd	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation.	17393	10.3	13.2	76	2
73	LjSGA_085279.1	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation.	13202	9.6	17.4	76	2

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Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
74	LjSGA_042082.1	Glutathione transferase activity, transferase activity.	7369	6.2	35.4	75	2
75	chr5.CM0260.520.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	14143	11.0	10.7	74	1
76	chr1.CM0105.500.nc	Structural constituent of ribosome, intracellular, ribosome, translational elongation.	11214	4.3	10.0	73	1
77	chr3.LjT03D10.60.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	19170	9.4	6.5	73	2
77	LjSGA_071678.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	9775	9.1	12.9	73	2
77	chr3.CM0160.930.nd	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	18910	9.4	6.6	73	2
78	chr1.CM0017.210.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	26025	9.6	8.9	72	2
78	LjSGA_009417.2	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	18207	9.7	13.2	72	2
79	chr1.LjT43O05.80.nd	Alcohol dehydrogenase activity, zinc ion binding, oxidoreductase activity, metal ion binding.	25600	6.1	4.1	72	1
80	chr4.CM0387.130.nc	Metabolic process, oxidoreductase activity.	34664	5.8	7.5	71	2
81	LjSGA_123620.1	Receptor activity, kinase activity.	7180	4.8	23.4	71	1
82	LjSGA_068070.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	12786	10.2	10.1	70	1
83	chr3.CM0005.500.nc	Cysteine protease inhibitor activity.	26636	5.8	11.0	68	2
84	LjSGA_093090.1	Nucleotide binding, RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, rRNA binding, ribonucleoprotein complex.	2832	6.6	50.0	66	1
85	LjSGA_036172.1	Structural constituent of ribosome, intracellular, ribosome, translation.	7535	11.2	18.5	66	1
86	chr4.CM0007.620.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	18459	10.4	14.0	66	2
86	LjT35M05.50.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	17892	11.0	14.6	66	2
87	LjSGA_046195.1	Response to desiccation.	8763	4.3	14.6	65	1
88	chr5.CM0096.480.nc	Nucleotide binding, structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	15717	10.6	10.9	65	1
88	LjSGA_118363.1	Nucleotide binding, structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	11630	10.4	14.9	65	1
89	chr1.CM0378.40.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	28895	10.4	5.7	65	1
89	chr2.LjT09A11.20.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	30326	10.4	5.4	65	1
89	chr4.CM0042.1380.nc	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	30215	10.4	5.5	65	1
89	LjSGA_025794.2	RNA binding, structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit.	29818	10.3	5.5	65	1
90	chr4.CM0179.510.nd	ATP binding.	37113	7.6	7.2	65	2
90	chr1.CM0133.1430.nc	Nucleotide binding, ATP binding.	55509	5.6	2.6	47	1
90	chr3.CM0452.230.nd	Nucleotide binding, ATP binding.	71584	5.4	2.0	47	1
90	chr6.CM0118.650.nc	ATP binding.	11409	6.8	13.0	47	1
90	chr6.CM0118.670.nc	ATP binding.	67618	5.9	2.2	47	1
90	LjSGA_038906.1	Nucleotide binding, ATP binding.	20725	5.9	6.8	47	1
91	LjSGA_085074.2	No GO annotations found.	21503	4.5	4.8	65	1
92	chr1.LjT01D01.60.nd	No GO annotations found.	14181	6.9	9.6	64	1
92	LjSGA_079444.1	No GO annotations found.	9969	7.3	13.3	64	1
93	chr2.CM0021.220.nc	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	18284	10.9	7.5	64	1
93	chr4.CM0175.570.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	17944	10.6	7.5	64	1

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
94	chr1.CM0109.50.nd	Endopeptidase activity, threonine endopeptidase activity, nucleus, cytosol, proteasome core complex (sensu Eukaryota), ubiquitin-dependent protein catabolic process, peptidase activity, hydrolase activity, protein complex.	25562	5.5	8.9	61	1
95	LjSGA_043401.1	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glucose metabolic process, glycolysis, glyceraldehyde-3-phosphate dehydrogenase activity, NAD binding.	22396	8.4	16.6	61	2
96	chr1.CM0029.40.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	18624	10.7	4.9	60	1
97	LjSGA_029241.1	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	20758	10.2	6.5	58	1
97	LjSGA_044797.1	Structural constituent of ribosome, intracellular, ribosome, translation.	20281	10.3	6.6	58	1
98	chr4.CM0501.190.nd	No GO annotations found.	22345	9.8	7.5	58	1
98	LjSGA_048933.1	No GO annotations found.	13532	9.5	13.2	58	1
99	chr1.CM0206.150.nd	Nucleotide binding, GTP binding, intracellular, endoplasmic reticulum, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	21957	6.4	5.7	58	1
99	chr4.CM0429.130.nd	Nucleotide binding, GTP binding, intracellular, endoplasmic reticulum, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	22053	6.1	5.7	58	1
99	CM0385.100.nd	Nucleotide binding, GTP binding, intracellular, endoplasmic reticulum, transport, intracellular protein transport, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport.	24855	6.2	5.1	58	1
100	chr4.CM0429.210.nc	No GO annotations found.	26196	5.2	13.5	58	3
101	LjSGA_051623.1	Nucleic acid binding, peptidase activity, zinc ion binding.	12305	10.1	6.5	57	1
102	chr2.CM0056.690.nd	Structural constituent of ribosome, intracellular, ribosome, translation, large ribosomal subunit, ribonucleoprotein complex.	18977	10.4	6.6	57	1
103	LjSGA_013905.2	No GO annotations found.	11425	10.6	17.3	57	2
103	chr1.CM0113.320.nd	No GO annotations found.	11729	10.7	9.4	57	1
103	chr3.CM0216.350.nc	No GO annotations found.	11870	10.8	9.3	57	1
104	chr4.LjT06I07.80.nd	Structural constituent of ribosome, intracellular, ribosome, translational elongation, ribonucleoprotein complex.	12273	4.4	17.4	57	1
105	chr4.CM0044.290.nd	Cysteine protease inhibitor activity.	14198	6.7	7.1	56	1
106	chr1.CM0105.70.nd	No GO annotations found.	111891	9.3	0.9	55	1
106	chr1.CM0982.190.nd	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	26518	8.2	3.8	55	1
106	chr1.CM1255.70.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	111894	8.9	0.9	55	1
106	chr1.CM1875.100.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	125661	9.1	0.8	55	1
106	chr2.CM0020.70.nd	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	112061	9.5	0.9	55	1
106	chr2.CM0695.40.nd	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	148813	9.3	0.7	55	1
106	chr6.CM0066.560.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	154062	9.2	0.7	55	1
106	LjT47D03.240.nd	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	124310	9.0	0.8	55	1

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
106	LjT13L03.70.nd	No GO annotations found.	93603	9.2	1.1	55	1
106	LjSGA_005191.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	70489	9.5	1.5	55	1
106	LjSGA_027221.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	78175	9.2	1.3	55	1
106	LjSGA_043425.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	51110	9.0	2.0	55	1
106	LjSGA_049007.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	56170	8.9	1.8	55	1
106	LjSGA_050485.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	48267	9.5	2.1	55	1
106	LjSGA_057788.2	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	52058	8.9	2.0	55	1
106	LjSGA_069294.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	46951	9.2	2.2	55	1
106	LjSGA_070239.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	42472	8.9	2.4	55	1
106	LjSGA_071661.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	47040	8.2	2.2	55	1
106	LjSGA_144027.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	28797	8.6	3.6	55	1
106	chr1.CM1956.240.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	183998	10.1	0.6	55	1
106	chr2.LjT12G08.70.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	79926	9.7	1.3	55	1
106	chr6.CM0037.630.nd	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	116653	9.1	0.9	55	1
106	LjSGA_024652.2	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	83824	9.6	1.2	55	1
106	LjT17C09.90.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	199411	9.6	0.5	55	1
107	chr5.CM0071.360.nd	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	104142	9.2	1.0	55	1
107	chr5.CM0357.500.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	210115	9.0	0.5	55	1
108	chr4.LjT08E06.90.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication.	144754	9.1	0.7	55	1
109	chr1.CM0033.150.nd	Glutathione transferase activity, cytoplasm, metabolic process, transferase activity.	30216	4.9	6.7	55	2
109	chr1.CM0033.160.nd	Glutathione transferase activity, cytoplasm, metabolic process, transferase activity.	25702	5.4	8.1	55	2
110	LjT46P06.210.nd	Binding.	67670	8.8	1.6	54	1

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
111	chr1.CM0029.350.nd	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	17491	10.2	8.2	54	1
111	LjSGA_013603.1	Structural constituent of ribosome, intracellular, ribosome, translation, small ribosomal subunit, ribonucleoprotein complex.	9107	9.8	15.5	54	1
112	chr2.CM0250.40.nc	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	204233	9.0	1.0	54	2
113	chr4.CM0042.770.nc	Structural constituent of ribosome, intracellular, ribosome, translation.	22037	9.8	14.7	53	3
114	chr4.CM0087.970.nc	L-lactate dehydrogenase activity, glycolysis, tricarboxylic acid cycle, tricarboxylic acid cycle intermediate metabolic process, malate metabolic process, oxidoreductase activity, malate dehydrogenase activity, L-malate dehydrogenase activity.	43394	8.1	5.6	53	2
115	chr2.LjT39I02.70.nc	Carbohydrate metabolic process, isomerase activity.	40762	9.6	4.3	52	1
116	chr6.CM0139.590.nd	Oxidoreductase activity.	7016	4.5	18.5	51	1
117	LjSGA_088290.1	Nucleic acid binding, DNA binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, DNA integration.	43229	9.9	3.8	51	2
118	chr2.CM0191.540.nc	Phosphoglycerate kinase activity, glycolysis, kinase activity, transferase activity.	4400	4.0	19.0	51	1
118	LjT16O05.90.nd	Phosphoglycerate kinase activity, glycolysis, kinase activity.	7538	5.8	12.1	51	1
118	LjSGA_086166.1	Phosphoglycerate kinase activity, glycolysis, kinase activity, transferase activity.	4016	4.0	21.1	51	1
119	LjSGA_016382.1	No GO annotations found.	18515	5.6	8.8	50	1
120	LjSGA_020557.1	Nucleic acid binding, RNA binding, RNA-directed DNA polymerase activity, ribonuclease H activity, RNA-dependent DNA replication, zinc ion binding.	88984	9.7	1.2	49	1
121	chr6.CM0679.70.nc	Selenium binding.	53656	5.7	2.3	48	1
122	chr4.CM0087.1060.nc	RNA binding, structural constituent of ribosome, intracellular, translation, small ribosomal subunit, rRNA binding, ribonucleoprotein complex.	23059	10.3	17.3	48	3
123	chr1.CM0544.80.nc	Superoxide dismutase activity, copper, zinc superoxide dismutase activity, copper ion binding, superoxide metabolic process, zinc ion binding, oxidoreductase activity, metal ion binding.	15314	6.3	7.9	48	1
124	LjSGA_063286.1	Catalytic activity, hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, cellulose and pectin-containing cell wall, glucosidase activity, cation binding.	22895	9.1	4.0	48	1
125	chr1.CM0145.90.nc	No GO annotations found.	17377	5.4	10.5	48	1
127	LjSGA_027840.1	No GO annotations found.	13353	6.1	13.4	47	1
128	LjB14K02.60.nc	ATP binding, protein folding, unfolded protein binding.	75721	5.2	2.3	47	1
128	LjSGA_129817.1	ATP binding, protein folding, unfolded protein binding.	17910	4.4	9.4	47	1
129	LjSGA_064891.1	Ferroxidase activity, binding, iron ion binding, iron ion transport, iron ion homeostasis, ferric iron binding, chloroplast, oxidoreductase activity, metal ion binding, transition metal ion binding.	12980	6.4	12.8	47	1
130	LjT41N19.20.nd	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, methyltransferase activity, zinc ion binding, amino acid biosynthetic process, methionine biosynthetic process, transferase activity, metal ion binding.	84017	6.2	3.1	46	2
131	LjSGA_059569.1	DNA binding, DNA integration.	50472	8.9	2.0	46	1
132	LjSGA_020081.2	No GO annotations found.	31887	10.0	2.8	46	1
133	chr5.CM0953.170.nc	Protein kinase activity, protein serine/threonine kinase activity, ATP binding, protein amino acid phosphorylation, carbohydrate biosynthetic process, transferase activity, transferring hexosyl groups.	41956	7.7	2.4	46	1
134	LjT07L17.10.nd	No GO annotations found.	60797	4.9	1.5	46	1

Continues...

Supplemental Table S2.6: (*mature_LotusAA GeLC-MS/MS Peaks continued*)

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
135	chr5.CM0357.40.nd	Iron ion binding, electron transport, fatty acid biosynthetic process, lipid biosynthetic process, lipoxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, metal ion binding.	80257	5.8	1.7	46	1
136	chr1.CM0222.290.nd	Structural constituent of ribosome, intracellular, ribosome, translation.	9362	9.3	15.5	46	1
138	LjSGA_106255.1	No GO annotations found.	37828	9.4	2.9	45	1
139	LjT11L09.120.nd	No GO annotations found.	77266	6.8	0.9	45	1
140	LjSGA_091805.2	No GO annotations found.	25502	10.8	3.2	45	1
141	chr2.CM0056.380.nc	Defense response, response to biotic stimulus.	16951	4.9	7.8	45	1
142	chr4.CM0429.60.nd	Mitochondrial inner membrane, protein transporter activity, protein transport.	18676	6.1	7.2	45	1
144	LjSGA_033282.0.1	Membrane.	7504	8.9	16.4	44	3
145	LjSGA_053764.1	No GO annotations found.	13854	8.0	8.4	44	1
146	LjSGA_079668.1	No GO annotations found.	43464	9.8	2.8	43	1
147	LjT48O01.60.nd	No GO annotations found.	49596	7.5	1.9	42	1
148	LjSGA_009509.2	Structural constituent of ribosome, intracellular, ribosome, translation, ribonucleoprotein complex.	17797	9.0	22.3	42	2
150	CM0458.170.nd	No GO annotations found.	172213	9.4	0.5	41	1
151	chr4.CM0128.40.nc	Nuclease activity, transferase activity, nucleotidyltransferase activity, hydrolase activity.	12873	8.5	7.0	41	1
153	LjSGA_016038.1	Response to stress.	13364	9.3	21.0	41	2
154	LjSGA_009196.2	Response to stress.	11990	9.1	10.3	41	1

Supplemental Table S2.7: The 18 peaks identified in the “mature_LotusEST_TIGR” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.17.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	TC9431	No GO annotations found.	52558	5.6	6.3	1095	2
2	CN825001	No GO annotations found.	24434	9.2	17.0	237	3
3	TC8009	Phosphoglycerate kinase activity, glycolysis.	60404	8.4	11.5	110	4
4	TC14860	Triose-phosphate isomerase activity, metabolism, cytosol.	32494	9.0	7.9	100	2
5	TC8554	Intracellular, ribosome, structural constituent of ribosome, cytosolic large ribosomal subunit (sensu Eukarya), large ribosomal subunit, RNA binding, protein biosynthesis.	29313	10.9	4.7	78	1
6	TC10602	Ribosome biogenesis, structural constituent of ribosome, ribosome, protein biosynthesis, molecular_function unknown.	17111	9.6	7.1	71	1
6	TC11545	Ribosome biogenesis, structural constituent of ribosome, ribosome, protein biosynthesis, molecular_function unknown.	16403	9.0	7.6	71	1
7	AV410268	No GO annotations found.	16124	9.1	14.8	67	1
8	TC14826	Ribosomal large subunit assembly and maintenance, structural constituent of ribosome, intracellular, ribosome, cytosolic large ribosomal subunit (sensu Eukarya), RNA binding, protein biosynthesis.	41446	9.9	3.8	64	1
9	TC14170	Response to oxidative stress, photosystem II.	42117	9.2	4.5	64	1
10	TC18990	No GO annotations found.	12590	9.6	15.3	59	1
11	TC9972	Ribosome biogenesis, structural constituent of ribosome, intracellular, ribosome, cytosolic large ribosomal subunit (sensu Eukarya), protein biosynthesis.	24084	10.2	5.2	58	1
13	TC16731	Response to reactive oxygen species, high affinity iron ion transport, copper chaperone activity, copper ion homeostasis, aging.	18127	8.8	8.2	50	1
14	TC8165	Lactoylglutathione lyase activity, carbohydrate metabolism, aromatic amino acid family metabolism, 4-hydroxyphenylpyruvate dioxygenase activity, cellular_component unknown.	42760	5.6	2.9	47	1
15	TC10840	Negative regulation of cell cycle, response to hydrogen peroxide, cytoplasm, mitochondrion, cytosol, cellular_component unknown, transferase activity, mitochondrial intermembrane space, negative regulation of cell proliferation, induction of apoptosis, microtubule, transcription factor activity, pyrimidine base metabolism, CTP biosynthesis, kinase activity, nucleoside-diphosphate kinase activity, UTP biosynthesis, purine nucleotide biosynthesis, RNA metabolism, ATP binding, GTP biosynthesis, nucleoside metabolism, nucleotide metabolism, regulation of transcription, DNA-dependent, nucleotide kinase activity, nucleus, DNA metabolism.	19769	8.6	5.0	43	1
16	TC8322	Biological_process unknown, mitochondrion.	40401	5.7	6.9	43	1
17	TC14090	Chloroplast, mesoderm development, lyase activity, pentose-phosphate shunt, striated muscle contraction, cytoplasm, glycolysis, fructose metabolism, cellular_component unknown, fructose-bisphosphate aldolase activity.	53341	8.0	2.2	41	1
18	TC8725	Ribosome biogenesis, structural constituent of ribosome, ribosome, protein biosynthesis.	24620	10.1	5.1	40	1

Supplemental Table S2.8: The 4 peaks identified in the “mature_LotusNT” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table [S2.18](#).

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	chr3.CM0164.170.nd	No GO annotations found.	64973	9.4	2.0	723	1
2	LjT03L06.120.nd	No GO annotations found.	15594	5.1	9.0	192	1
3	chr6.CM0679.100.nd	No GO annotations found.	6909	4.1	23.9	81	1
4	LjSGA_121732.1	No GO annotations found.	14404	9.3	8.8	48	1

Supplemental Table S2.9: The 10 peaks identified in the “mature_NCBInr” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.19.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	gi 7230391	No GO annotations found.	49241	9.0	4.5	66	1
1	gi 48527431	No GO annotations found.	49293	9.2	4.5	66	1
1	gi 89275337	No GO annotations found.	26795	7.2	8.2	66	1
2	Unknown/dead	No GO annotations found.	134613	9.4	1.5	54	2
3	gi 1297072	No GO annotations found.	52374	5.5	2.6	52	1
4	gi 4585271	No GO annotations found.	16678	5.2	7.2	48	1
5	gi 2462734	No GO annotations found.	72128	5.7	1.6	44	1
5	gi 15219744	No GO annotations found.	74550	6.1	1.5	44	1
5	gi 15219746	No GO annotations found.	32862	4.6	3.3	44	1
5	Unknown/dead	No GO annotations found.	72453	5.9	1.5	44	1

Supplemental Table S2.10: The 10 peaks identified in the “mature_SPROT” GeLC-MS/MS analysis. The hit number and identifier are shown in the two first columns. GO annotations, predicted molecular mass in dalton (D), predicted isoelectric point (pI), sequence coverage, MOWSE score, and number of matched peptides are shown in the next six columns. The complete list of peptides belonging to each peak is shown in Supplemental Table S2.20.

Hit no.	Identifier	GO Annotation	Predicted molecular mass	Predicted pI	Sequence coverage	MOWSE score	No. of matched peptides
1	EMB1_DAUCA	No GO annotations found.	9911	6.7	14.1	179	1
2	SEEP_RAPSA	Late seed maturation protein P8B6.	8975	6.6	15.7	174	1
2	EM6_ARATH	No GO annotations found.	9928	6.8	14.1	174	1
3	EMP1_ORYSA	No GO annotations found.	10159	5.6	13.7	121	1
3	EM2_WHEAT	EM: Em protein CS41.	9981	5.3	13.8	121	1
4	PSB5A_ARATH	PBE1, PRCE, At1g13060, F3F19.8: Proteasome subunit beta type-5-A precursor.	29648	6.0	6.9	81	1
4	PSB5B_ARATH	PBE2, At3g26340, F20C19.6: Proteasome subunit beta type-5-B precursor.	29466	5.8	7.0	81	1
5	EM1_ARATH	No GO annotations found.	16602	5.8	11.2	57	1
7	TIP31_ARATH	At1g73190, T18K17.14, TIP3-1: Aquaporin TIP3-1.	28290	7.2	4.1	46	1
7	TIP32_ARATH	TIP3-2, At1g17810, F2H15.4: Probable aquaporin TIP3-2.	28165	6.5	4.1	46	1

Supplemental Table S2.11: The complete list of the 2589 peptides identified in the “green_LotusAA” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.1. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	chr5.CM0357.530.nc	612.96	1223.90	1224.68	-0.78	2	216	226	R	AILTIVNPNDR	D	0	-	41.7
		637.37	1272.73	1272.64	0.09	2	329	339	K	ASQDQIQLSR	H	0	-	79.5
		756.42	1510.83	1511.79	-0.97	2	498	510	R	DDNVISQIERPVK	E	0	-	68.1
		679.43	1356.84	1356.75	0.09	2	385	396	R	DLIDLLSEAQIK	E	0	-	57.2
		922.53	1843.04	1842.91	0.13	2	313	328	R	EEQRGEQSQGVIVK	A	1	-	71.9
		866.42	1730.82	1731.89	-1.07	2	511	526	K	ELAFPGSAEEIESLIK	N	0	-	73.2
		851.88	1701.75	1701.64	0.11	2	125	140	R	ESEEEGSSSSSESSR	R	0	-	106.1
		819.44	1636.86	1636.75	0.11	2	155	167	R	FQTHFENEHGHVR	V	0	-	69.8
		507.46	1012.90	1013.55	-0.65	2	420	428	R	GELELVAQR	R	0	-	43.0
		651.38	1300.74	1300.66	0.08	2	317	328	R	GEQSQGEQGVIVK	A	0	-	81.6
		743.90	1485.79	1486.62	-0.83	2	434	445	R	GQEEEQEEQPR	I	0	-	79.6
		488.46	974.90	975.53	-0.62	2	372	379	K	LFETITPEK	N	0	-	58.4
		598.47	1194.93	1195.60	-0.67	2	178	186	K	LFENLQNYR	I	0	-	72.6
		954.98	1907.95	1907.81	0.14	2	530	546	R	NSCFASAQPQQGEEGR	S	0	Propionamide (C)	94.9
		415.74	829.47	829.42	0.05	2	71	76	R	RPSWER	K	0	-	20.9
		706.42	1410.82	1410.73	0.10	2	176	186	R	SKLFENLQNYR	I	1	-	71.4
		473.96	945.91	946.51	-0.60	2	360	368	R	SSKPISSNK	F	0	-	27.3
2	chr5.LjT15N12.80.nc	424.47	846.92	847.42	-0.50	2	414	420	R	ADLYNPR	A	0	-	52.9
		714.47	1426.93	1427.79	-0.86	2	534	547	R	ATPAVLNFAFGIR	Q	0	-	85.0
		834.36	1666.71	1666.56	0.15	2	317	329	R	EEDEDEDEDEER	Q	0	-	26.6
		951.39	1900.76	1901.90	-1.14	2	556	572	K	FSGNWGPLINPDNTQSR	S	0	-	116.4
		534.28	1066.55	1066.49	0.07	2	29	36	R	FSQCQLDR	I	0	Propionamide (C)	75.9
		1187.65	2373.29	2373.13	0.16	2	100	121	R	GALGIAIPGCPETYEPPQSQSR	Q	0	Propionamide (C)	32.5
		695.35	1388.69	1388.60	0.09	2	341	350	R	HFEREDEDEER	E	1	-	31.0
		617.96	1233.91	1234.65	-0.74	2	404	413	K	IHENINRPSR	A	0	-	30.8
		520.85	1039.69	1040.53	-0.83	2	37	45	R	INALEPDNR	V	0	-	61.0
		728.01	1454.00	1453.85	0.15	2	424	436	R	ISDINSLTLPILR	F	0	-	112.4
		853.51	1705.01	1704.83	0.19	2	476	490	R	IVNCQGGQAVFNDELK	K	0	-	27.6
		889.03	1776.05	1775.86	0.19	2	476	490	R	IVNCQGGQAVFNDELK	K	0	Propionamide (C)	99.3
		953.07	1904.12	1903.96	0.16	2	476	491	R	IVNCQGGQAVFNDELK	G	1	Propionamide (C)	75.4
		772.45	1542.88	1542.78	0.10	2	60	73	R	QSPQLQCAGVSVVR	C	0	Propionamide (C)	91.7
		1082.51	2163.01	2162.85	0.17	2	313	329	R	RPSREDEDEDEDEER	Q	1	-	68.2
		787.45	1572.88	1572.78	0.10	2	46	59	R	VESEAGLIETWSPR	Q	0	-	62.2
3	chr5.LjT15N12.90.nc	424.47	846.92	847.42	-0.50	2	415	421	R	ADLYNPR	A	0	-	52.9
		723.47	1444.92	1444.77	0.16	2	535	548	R	ATPAVLNFAFGIR	Q	0	-	78.8
		834.36	1666.71	1666.56	0.15	2	317	329	R	EEDEDEDEDEER	Q	0	-	26.6
		945.03	1888.05	1887.89	0.16	2	557	573	K	FSGNWGPLVNPNDNTQSR	S	0	-	73.6
		534.28	1066.55	1066.49	0.07	2	29	36	R	FSQCQLDR	I	0	Propionamide (C)	75.9
		1187.65	2373.29	2373.13	0.16	2	100	121	R	GALGIAIPGCPETYEPPQSQSR	Q	0	Propionamide (C)	32.5
		695.35	1388.69	1388.60	0.09	2	342	351	R	HFEREDEDEER	E	1	-	31.0
		617.96	1233.91	1234.65	-0.74	2	405	414	K	IHENINRPSR	A	0	-	30.8
		535.32	1068.62	1068.56	0.06	2	37	45	R	INVLEPDNR	V	0	-	56.1
		728.01	1454.00	1453.85	0.15	2	425	437	R	ISDINSLTLPILR	F	0	-	112.4
		853.51	1705.01	1704.83	0.19	2	477	491	R	IVNCQGGQAVFNDELK	K	0	-	27.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		889.03	1776.05	1775.86	0.19	2	477	491	R	IVNCQGGQAVFNDELRL	K	0	Propionamide (C)	99.3
		953.07	1904.12	1903.96	0.16	2	477	492	R	IVNCQGGQAVFNDELRLK	G	1	Propionamide (C)	75.4
		1082.51	2163.01	2162.85	0.17	2	313	329	R	RPSREDEDEDEDEER	Q	1	-	68.2
		1143.21	2284.41	2284.12	0.29	2	187	206	R	VFYLAGNPAIEHPETQQSQR	Q	0	-	74.4
4	LjSGA_092567.1	530.94	1059.87	1060.54	-0.67	2	102	111	K	AAIKEESEGEK	L	1	-	69.5
		717.41	1432.81	1433.75	-0.94	2	43	57	R	AASFNIIPSSSTGAAK	A	0	-	49.3
		454.94	907.87	908.46	-0.59	2	94	101	K	AATYDQIK	A	0	-	45.3
		580.93	1159.85	1160.62	-0.77	2	141	151	K	AGIALNDNFVK	L	0	-	69.9
		1016.40	2030.78	2031.12	-0.34	2	10	28	R	FGIVKGLMTTVHSITATQK	T	1	-	115.4
		1025.16	2048.31	2047.11	1.20	2	10	28	R	FGIVKGLMTTVHSITATQK	T	1	Oxidation (M)	84.0
		1093.65	2185.28	2185.02	0.26	2	114	133	K	GILGYTEDDVSTDFIGDNR	S	0	-	133.8
		406.49	810.97	810.50	0.47	2	62	69	K	VLPALNGK	L	0	-	26.3
		750.01	1498.01	1497.84	0.17	2	77	90	R	VPTVDVSVVDLTVR	L	0	-	107.1
5	chr5.CM0328.690.nd	846.35	1690.69	1691.78	-1.09	2	295	309	K	CALVYQGMNEPPGAR	A	0	Oxidation (M); Propionamide (C)	33.7
		838.95	1675.88	1675.78	0.10	2	295	309	K	CALVYQGMNEPPGAR	A	0	Propionamide (C)	65.6
		925.48	1848.94	1849.92	-0.98	2	325	340	R	DAEGQDVLFLVDNIFR	F	0	-	83.4
		1094.66	2187.30	2187.14	0.16	2	197	216	R	EAPSFVEQATEQQILVTGIK	V	0	-	31.6
		510.94	1019.86	1020.52	-0.66	2	277	285	R	EMIESGVIK	L	0	Oxidation (M)	22.2
		703.90	1405.79	1406.70	-0.91	2	516	528	K	ENITSFQGVLDGK	Y	0	-	61.1
		746.00	2234.97	2236.17	-1.20	3	103	122	R	FEGLPPIILTALEVLDTSR	L	0	-	72.0
		746.41	1490.80	1491.77	-0.97	2	341	354	R	FTQANSEVSALLGR	I	0	-	114.9
		487.97	973.92	974.55	-0.64	2	230	240	K	IGLFGGAGVGK	T	0	-	55.6
		679.00	1355.98	1356.70	-0.71	2	172	183	R	IMNVIGEPIDEK	G	0	-	56.0
		686.91	1371.81	1372.69	-0.88	2	172	183	R	IMNVIGEPIDEK	G	0	Oxidation (M)	55.9
		1101.65	2201.28	2201.13	0.15	2	355	375	R	IPSAVGYQPTLSTDLGGLQER	I	0	-	25.7
		431.45	860.88	861.44	-0.56	2	78	85	K	ITDEVTKG	G	0	-	47.9
		810.02	1618.02	1617.92	0.10	2	123	137	R	LVLEVAQHLGEGVVR	T	0	-	70.6
		615.25	1842.72	1843.91	-1.20	3	437	452	R	MLSPLILGEDHYETAR	G	0	-	48.5
		620.58	1858.71	1859.91	-1.20	3	437	452	R	MLSPLILGEDHYETAR	G	0	Oxidation (M)	43.1
		624.41	1246.81	1247.62	-0.81	2	138	149	R	TIAMDGTGEGVVR	G	0	-	76.0
		632.41	1262.80	1263.61	-0.81	2	138	149	R	TIAMDGTGEGVVR	G	0	Oxidation (M)	69.0
		728.94	1455.87	1456.83	-0.96	2	241	253	K	TVLIMELINNVAK	A	0	-	62.0
		736.95	1471.88	1472.83	-0.95	2	241	253	K	TVLIMELINNVAK	A	0	Oxidation (M)	63.7
		700.44	1398.86	1398.76	0.10	2	312	324	R	VGLTGTLVAEHFR	D	0	-	86.6
		705.04	1408.06	1408.80	-0.74	2	153	166	R	VLNTGSPITVPVGR	V	0	-	68.4
		603.92	1205.83	1206.61	-0.78	2	217	226	K	VVDMLAPYQR	G	0	Oxidation (M)	32.7
6	chr1.CM0027.160.nc	794.81	1587.60	1587.90	-0.29	2	74	89	K	AAAVLSSHDPPIVLAK	V	0	-	69.4
		481.45	960.89	961.49	-0.60	2	358	366	K	DGNVAPYVK	S	0	-	29.8
		866.87	865.87	866.38	-0.51	1	292	298	R	EAAEEYR	K	0	-	21.1
		561.44	1120.86	1121.56	-0.70	2	130	139	R	EADGIVDYLK	K	0	-	58.6
		625.45	1248.88	1249.66	-0.77	2	130	140	R	EADGIVDYLLK	Q	1	-	61.5
		681.92	1361.83	1362.68	-0.84	2	473	483	K	EDIIQFIENSR	D	0	-	46.5
		848.92	1695.83	1696.89	-1.06	2	323	337	K	EEDVPLIIQQTDGK	K	0	-	65.4
		539.44	1076.87	1077.53	-0.66	2	230	238	K	EFNVEALEK	F	0	-	49.0
		490.94	979.86	980.47	-0.62	2	264	271	K	FFNSQNP	A	0	-	35.3
		935.00	2801.96	2802.39	-0.42	3	239	263	K	FIEESSIPVTVFNNDPSNHPFVSK	F	0	-	37.0
		875.44	1748.86	1749.79	-0.93	2	173	187	K	FSGEEFDNFFALAEK	L	0	-	87.8
		536.94	1071.87	1072.55	-0.68	2	206	216	R	GESSVSGPVVR	L	0	-	64.4
		432.45	862.88	863.41	-0.53	2	463	470	K	ISPYDGGR	T	0	-	61.9
		486.01	970.00	970.62	-0.62	2	164	172	K	IVIVGVFPK	F	0	-	54.3
		550.02	1098.03	1098.72	-0.69	2	163	172	K	KIVIVGVFPK	F	1	-	60.9

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		580.22	1158.43	1158.62	-0.20	2	140	150	K	KQTGPASTEIK	S	1	-	20.4
		481.94	961.87	962.47	-0.60	2	66	73	K	NLAPEYEK	A	0	-	25.4
		515.95	1029.89	1030.53	-0.64	2	141	150	K	QTGPASTEIK	S	0	-	52.1
		598.42	1194.82	1195.57	-0.75	2	151	162	K	SADDATAFIGTK	K	0	-	75.0
		684.85	1367.69	1367.60	0.09	2	190	201	R	SDYDFGHTLDAK	N	0	-	47.0
		726.91	1451.81	1452.71	-0.89	2	367	379	K	SEPIPETNNEPVK	V	0	-	39.4
		796.97	1591.93	1591.82	0.11	2	471	483	R	TKEDIQFIENSR	D	1	-	94.0
		1047.57	2093.13	2092.97	0.16	2	90	107	K	VDANEENKDLASQYEV	G	1	-	51.2
		702.94	1403.86	1403.77	0.10	2	380	392	K	VVVGDSLQDVVFK	S	0	-	99.5
		593.41	1184.81	1185.54	-0.73	2	290	298	K	YREAAEEYR	K	1	-	34.0
7	chr1.CM0295.260.nd	566.35	1130.69	1130.59	0.10	2	368	376	K	AWIQVNVCK	G	0	Propionamide (C)	38.7
		630.36	1258.71	1258.62	0.10	2	236	246	K	DEEQDKGAIVR	V	1	-	67.6
		494.97	987.92	988.55	-0.63	2	459	466	R	FNFLVPPR	E	0	-	47.4
		459.77	917.53	917.46	0.07	2	408	414	K	FNYSISFK	T	0	-	30.9
		1018.57	2035.13	2034.94	0.19	2	179	194	R	FYLSGNQENEFQYQR	Q	0	-	59.9
		563.37	1124.73	1124.62	0.12	2	249	259	K	GGLSVITPPER	Q	0	-	68.1
		597.85	1190.54	1191.70	-1.16	3	265	279	R	GSEEEEEDEEDRPSR	H	0	-	28.0
		1126.91	2251.81	2252.05	-0.24	2	46	64	R	IESEAGFIETWNPTNNQFR	C	0	-	30.3
		520.85	1039.69	1039.58	0.12	2	37	45	R	LNALKPDNR	I	0	-	73.0
		541.94	1081.87	1082.55	-0.68	2	336	345	K	LSAEHGSINR	N	0	-	82.0
		809.94	1617.86	1617.72	0.14	2	24	36	R	QQSQQQNECQLR	L	0	-	54.7
		845.96	1689.91	1688.75	1.15	2	24	36	R	QQSQQQNECQLR	L	0	Propionamide (C)	70.1
		975.00	1947.98	1947.80	0.18	2	264	279	R	RGSEEEEEDEEDRPSR	H	1	-	58.4
		712.88	1423.74	1424.63	-0.89	2	307	319	K	SSSPDFYNPQAGR	I	0	-	56.0
		718.92	1435.82	1435.70	0.12	2	403	414	R	STSDKFNYISFK	T	1	-	55.6
		565.80	1129.59	1129.50	0.09	2	415	423	K	THEMPWMAK	L	0	-	40.5
		573.80	1145.59	1145.50	0.09	2	415	423	K	THEMPWMAK	L	0	Oxidation (M)	33.1
		618.93	1235.85	1236.62	-0.77	2	322	332	K	TISSMDFFALR	W	0	-	52.6
		626.92	1251.83	1252.61	-0.79	2	322	332	K	TISSMDFFALR	W	0	Oxidation (M)	52.4
		676.96	1351.90	1351.78	0.12	2	247	259	R	VKGGLSVITPPER	Q	1	-	73.2
8	chr5.CM0357.550.nc	612.96	1223.90	1224.68	-0.78	2	216	226	K	AIITLVNPNDR	E	0	-	41.7
		721.42	1440.82	1441.71	-0.89	2	381	392	R	DFDIFLSSTEIR	E	0	-	51.0
		486.50	970.99	971.54	-0.55	2	328	335	R	DLIQQLSR	H	0	-	37.1
		585.35	1168.68	1168.54	0.14	2	358	367	R	DPIYSNEFGK	H	0	-	39.8
		710.89	1419.77	1418.69	1.08	2	393	404	R	EGSIFLPHYNSR	S	0	-	55.5
		717.41	1432.81	1432.68	0.13	2	510	522	K	EIAFPGSAEDIER	L	0	-	74.6
		588.35	1174.68	1174.54	0.14	2	159	167	R	FQNEYGYVR	V	0	-	47.4
		1295.73	2589.45	2589.26	0.19	2	234	257	R	GDVLVHPAGTIIAYVANHDDNENLR	I	0	-	71.4
		513.81	1025.61	1025.50	0.10	2	368	375	K	HFEINPNR	N	0	-	38.5
		872.01	1742.01	1741.86	0.15	2	491	506	R	HFLAGDDNVISQIEK	V	0	-	51.8
		598.47	1194.93	1195.60	-0.67	2	178	186	K	LFENLQNYR	I	0	-	72.6
		457.51	913.01	913.52	-0.52	2	317	324	R	QEGLIVK	V	0	-	22.8
		515.28	1028.55	1028.49	0.06	2	85	92	R	RLEDPPER	E	1	-	32.2
		909.46	1816.90	1816.73	0.17	2	431	444	R	RNEDEEEEEEQPR	I	1	-	47.9
		706.42	1410.82	1410.73	0.10	2	176	186	R	SKLFENLQNYR	I	1	-	71.4
		706.90	1411.78	1411.67	0.10	2	356	367	R	SRDPIYSNEFGK	H	1	-	67.8
		593.48	1184.94	1185.67	-0.73	2	405	415	R	TSVILVVNEGR	G	0	-	30.0
		638.86	1275.70	1275.61	0.09	2	345	355	R	TSSEPEPFNL	S	0	-	52.9
9	LjSGA_084876.1	456.48	910.95	911.46	-0.51	2	159	166	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	159	166	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		502.47	1002.93	1003.48	-0.56	2	91	99	K	AQEETGEIK	G	0	-	39.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		733.90	1465.79	1466.61	-0.82	2	65	76	K	DDENVNSQPFMR	W	0	Oxidation (M)	62.7
		511.95	1021.89	1022.47	-0.57	2	214	221	R	DDFVEKDR	S	1	-	58.2
		594.38	1186.74	1186.66	0.08	2	149	158	R	DNGLLLHIHR	A	0	-	56.0
		415.49	828.96	829.43	-0.47	2	303	309	R	EGNEIIR	E	0	-	45.4
		638.01	1274.00	1274.72	-0.72	2	203	213	R	EITLGFVDLLR	D	0	-	84.7
		1085.57	2169.13	2168.98	0.15	2	58	76	R	GGLDFTKDDENVNSQPFMR	W	1	-	79.2
		733.41	1464.81	1464.71	0.09	2	183	197	R	MSGGDHIHAGTVVGK	L	0	-	64.3
		740.95	1479.88	1480.71	-0.83	2	183	197	R	MSGGDHIHAGTVVGK	L	0	Oxidation (M)	67.3
		732.94	1463.87	1464.75	-0.88	2	10	22	K	TFQGPPHGIQVER	D	0	-	80.4
9	LjSGA_124257.1	456.48	910.95	911.46	-0.51	2	232	239	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	232	239	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		502.47	1002.93	1003.48	-0.56	2	164	172	K	AQEETGEIK	G	0	-	39.6
		733.90	1465.79	1466.61	-0.82	2	138	149	K	DDENVNSQPFMR	W	0	Oxidation (M)	62.7
		511.95	1021.89	1022.47	-0.57	2	287	294	R	DDFVEKDR	S	1	-	58.2
		594.38	1186.74	1186.66	0.08	2	222	231	R	DNGLLLHIHR	A	0	-	56.0
		638.01	1274.00	1274.72	-0.72	2	276	286	R	EITLGFVDLLR	D	0	-	84.7
		1085.57	2169.13	2168.98	0.15	2	131	149	R	GGLDFTKDDENVNSQPFMR	W	1	-	79.2
		733.41	1464.81	1464.71	0.09	2	256	270	R	MSGGDHIHAGTVVGK	L	0	-	64.3
		740.95	1479.88	1480.71	-0.83	2	256	270	R	MSGGDHIHAGTVVGK	L	0	Oxidation (M)	67.3
		732.94	1463.87	1464.75	-0.88	2	83	95	K	TFQGPPHGIQVER	D	0	-	80.4
9	LjSGA_134471.1	456.48	910.95	911.46	-0.51	2	22	29	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	22	29	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		511.95	1021.89	1022.47	-0.57	2	77	84	R	DDFVEKDR	S	1	-	58.2
		594.38	1186.74	1186.66	0.08	2	12	21	R	DNGLLLHIHR	A	0	-	56.0
		415.49	828.96	829.43	-0.47	2	166	172	R	EGNEIIR	E	0	-	45.4
		638.01	1274.00	1274.72	-0.72	2	66	76	R	EITLGFVDLLR	D	0	-	84.7
		733.41	1464.81	1464.71	0.09	2	46	60	R	MSGGDHIHAGTVVGK	L	0	-	64.3
		740.95	1479.88	1480.71	-0.83	2	46	60	R	MSGGDHIHAGTVVGK	L	0	Oxidation (M)	67.3
9	LjSGA_149364.1	456.48	910.95	911.46	-0.51	2	25	32	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	25	32	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		511.95	1021.89	1022.47	-0.57	2	80	87	R	DDFVEKDR	S	1	-	58.2
		594.38	1186.74	1186.66	0.08	2	15	24	R	DNGLLLHIHR	A	0	-	56.0
		638.01	1274.00	1274.72	-0.72	2	69	79	R	EITLGFVDLLR	D	0	-	84.7
		733.41	1464.81	1464.71	0.09	2	49	63	R	MSGGDHIHAGTVVGK	L	0	-	64.3
		740.95	1479.88	1480.71	-0.83	2	49	63	R	MSGGDHIHAGTVVGK	L	0	Oxidation (M)	67.3
9	LjSGA_113307.1	456.48	910.95	911.46	-0.51	2	18	25	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	18	25	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		594.38	1186.74	1186.66	0.08	2	8	17	R	DNGLLLHIHR	A	0	-	56.0
		638.01	1274.00	1274.72	-0.72	2	62	72	R	EITLGFVDLLR	D	0	-	84.7
9	LjSGA_105267.1	511.95	1021.89	1022.47	-0.57	2	81	88	R	DDFVEKDR	S	1	-	58.2
		415.49	828.96	829.43	-0.47	2	170	176	R	EGNEIIR	E	0	-	45.4
		638.01	1274.00	1274.72	-0.72	2	70	80	R	EITLGFVDLLR	D	0	-	84.7
9	LjSGA_136714.1	502.47	1002.93	1003.48	-0.56	2	220	228	K	AQEETGEIK	G	0	-	39.6
		733.90	1465.79	1466.61	-0.82	2	194	205	K	DDENVNSQPFMR	W	0	Oxidation (M)	62.7
		1085.57	2169.13	2168.98	0.15	2	187	205	R	GGLDFTKDDENVNSQPFMR	W	1	-	79.2
		732.94	1463.87	1464.75	-0.88	2	139	151	K	TFQGPPHGIQVER	D	0	-	80.4
9	LjSGA_040977.3	456.48	910.95	911.46	-0.51	2	47	54	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	47	54	R	AMHAVIDR	Q	0	Oxidation (M)	54.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		594.38	1186.74	1186.66	0.08	2	37	46	R	DNGLLLHIHR	A	0	-	56.0
		733.41	1464.81	1464.71	0.09	2	71	85	R	MSGGDHIHAGTVVGK	L	0	-	64.3
		740.95	1479.88	1480.71	-0.83	2	71	85	R	MSGGDHIHAGTVVGK	L	0	Oxidation (M)	67.3
9	LjSGA_106428.1	511.95	1021.89	1022.47	-0.57	2	10	17	R	DDFVEKDR	S	1	-	58.2
		415.49	828.96	829.43	-0.47	2	99	105	R	EGNEIIR	E	0	-	45.4
9	chr5.CM0019.360.nc	456.48	910.95	911.46	-0.51	2	19	26	R	AMHAVIDR	X	0	-	42.3
		464.47	926.93	927.46	-0.53	2	19	26	R	AMHAVIDR	X	0	Oxidation (M)	54.6
9	LjSGA_117887.1	415.49	828.96	829.43	-0.47	2	50	56	R	EGNEIIR	E	0	-	45.4
10	chr3.CM0115.240.nc	1035.44	2068.87	2070.04	-1.17	2	469	488	K	DDGALTPLAIELSLPDSESK	V	0	-	68.6
		479.98	957.94	958.45	-0.51	2	272	279	R	DENFGHLK	S	0	-	21.5
		865.97	1729.92	1730.89	-0.97	2	596	610	K	DWVFTDQALPADLIK	R	0	-	70.6
		751.44	1500.87	1501.74	-0.87	2	379	391	R	EMIAGVNPVICR	L	0	Oxidation (M); Propionamide (C)	54.8
		603.42	1204.83	1205.52	-0.69	2	791	800	R	ENPEWTSDTK	A	0	-	45.7
		744.50	1486.99	1487.85	-0.86	2	832	844	R	FGPAQLPYTLRL	S	0	-	50.9
		899.96	1797.91	1798.96	-1.04	2	37	56	K	GGIPGIAGNIFGLATDAAGK	V	0	-	70.1
		719.43	1436.84	1437.67	-0.83	2	612	625	R	GMAVEDPSAPHGVR	L	0	Oxidation (M)	56.0
		644.93	1287.85	1288.60	-0.75	2	780	790	R	HASDEIYLGER	E	0	-	66.0
		581.00	1159.98	1160.67	-0.69	2	96	106	K	HIPSLPTLGAR	Q	0	-	34.2
		835.43	1668.85	1669.84	-0.98	2	171	185	R	IFFTNDAYLPGSTPK	A	0	-	75.0
		866.92	1731.82	1732.82	-1.00	2	737	751	R	LIPEPGTPEYDEMVK	S	0	Oxidation (M)	41.0
		551.99	1101.97	1102.61	-0.63	2	692	700	K	MQTLQELIK	S	0	-	27.3
		559.98	1117.95	1118.60	-0.65	2	692	700	K	MQTLQELIK	S	0	Oxidation (M)	33.3
		715.99	1429.97	1430.78	-0.81	2	24	36	K	NVLDFNALTSPK	G	0	-	65.3
		672.40	1342.78	1343.55	-0.77	2	368	378	K	SAWMTDEEFGK	E	0	Oxidation (M)	68.5
		615.41	1228.81	1229.52	-0.71	2	311	320	K	SEFDSFDEVR	D	0	-	46.6
		611.45	1220.89	1221.60	-0.71	2	399	409	R	SNLDVAIYGDR	T	0	-	66.4
		543.46	1084.91	1085.54	-0.63	2	280	289	K	SSDFLGYGK	S	0	-	53.3
		565.51	1129.01	1129.67	-0.66	2	68	78	R	SVAIQLISATK	T	0	-	56.4
		606.98	1211.94	1212.65	-0.71	2	290	300	K	SVSHDLIPAFK	S	0	-	64.0
		504.48	1006.95	1007.53	-0.58	2	87	95	K	VGNLTYVDK	H	0	-	51.7
		603.98	1205.94	1206.66	-0.72	2	57	67	K	VVDFSTAILSR	S	0	-	68.1
10	chr3.CM0115.260.nc	479.98	957.94	958.45	-0.51	2	242	249	R	DENFGHLK	S	0	-	21.5
		719.43	1436.84	1437.67	-0.83	2	594	607	R	GMAVEDPSAPHGVR	L	0	Oxidation (M)	56.0
		644.93	1287.85	1288.60	-0.75	2	762	772	R	HASDEIYLGER	E	0	-	66.0
		581.00	1159.98	1160.67	-0.69	2	67	77	K	HIPSLPTLGAR	Q	0	-	34.2
10	chr3.CM0115.140.nd	479.98	957.94	958.45	-0.51	2	109	116	R	DENFGHLK	S	0	-	21.5
		865.97	1729.92	1730.89	-0.97	2	440	454	K	DWVFTDQALPADLIK	R	0	-	70.6
11	chr4.CM0126.1570.nc	733.90	1465.79	1466.61	-0.82	2	202	213	K	DDENVNSQPFMR	W	0	Oxidation (M)	62.7
		511.95	1021.89	1022.47	-0.57	2	351	358	R	DDFVEKDR	S	1	-	58.2
		510.97	1019.93	1020.52	-0.59	2	33	41	K	DTDILAAFR	V	0	-	49.8
		415.49	828.96	829.43	-0.47	2	440	446	R	EGNEIIR	E	0	-	45.4
		638.01	1274.00	1274.72	-0.72	2	340	350	R	EITLGFVDLLR	D	0	-	84.7
		1085.57	2169.13	2168.98	0.15	2	195	213	R	GGLDFTKDDENVNSQPFMR	W	1	-	79.2
		697.38	1392.74	1392.64	0.09	2	22	32	K	LTYTTPDYETK	D	0	-	52.6
		732.94	1463.87	1464.75	-0.88	2	147	159	K	TFQCPPHGIQVER	D	0	-	80.4
11	chr3.CM0106.360.nd	697.38	1392.74	1392.64	0.09	2	22	32	K	LTYTTPDYETK	D	0	-	52.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
11	LjSGA_096321.1	697.38	1392.74	1392.64	0.09	2	22	32	K	LTYTPDYETK	E	0	-	52.6
11	LjSGA_102132.1	510.97	1019.93	1020.52	-0.59	2	23	31	K	DTDILAAFR	V	0	-	49.8
12	LjSGA_043185.1	630.88	1259.75	1260.51	-0.75	2	179	190	K	CCHNGNTTANAR	A	0	-	39.1
		468.58	1402.72	1402.58	0.14	3	179	190	K	CCHNGNTTANAR	A	0	2 Propionamide (C)	65.3
		523.96	1045.90	1046.52	-0.63	2	73	81	K	DTVTTQVEK	L	0	-	46.7
		543.99	1085.97	1086.61	-0.64	2	87	96	K	GETGWALLIK	G	0	-	69.9
		422.96	843.90	844.41	-0.51	2	127	133	K	GFEFAFK	E	0	-	31.1
		740.97	1479.93	1480.84	-0.91	2	97	111	K	GPFFVAVGHGTTVLK	T	0	-	68.3
		1014.04	2026.07	2027.14	-1.08	2	38	55	K	IPIGLFNLESLQSNITTR	F	0	-	79.7
		486.96	971.91	972.51	-0.59	2	126	133	K	KGFEFAFK	E	1	-	43.7
		603.45	1204.88	1205.67	-0.79	2	24	34	K	LASTFAIELNK	E	0	-	86.9
		660.93	1319.84	1320.65	-0.80	2	14	23	K	NKDVIQEFNK	L	1	-	57.5
		638.46	1274.90	1275.67	-0.77	2	71	81	K	TKDVTVTQVEK	L	1	-	78.2
		566.94	1131.86	1132.55	-0.69	2	170	178	R	TMEVFISYK	C	0	Oxidation (M)	47.2
		411.96	821.91	822.41	-0.51	2	112	118	K	TVAEFEK	W	0	-	30.3
		473.46	944.91	945.50	-0.58	2	6	13	K	YVFIYGGK	N	0	-	54.1
13	LjT41N19.20.nd	406.52	811.02	811.49	-0.47	2	611	617	R	EGLPLRK	S	1	-	32.2
		599.94	1197.86	1198.57	-0.71	2	19	28	K	FALESFWDGK	T	0	-	49.4
		419.96	837.91	838.40	-0.49	2	130	136	K	FAYSSHK	A	0	-	23.4
		734.98	1467.94	1467.80	0.13	2	597	610	K	GGINVIQIDEAALR	E	0	-	59.0
		903.51	1805.00	1805.95	-0.95	2	556	571	K	GMLTGPVTILNWSFVR	N	0	Oxidation (M)	39.7
		640.92	1279.83	1280.57	-0.74	2	100	111	R	GNATVPAMEMTK	W	0	2 Oxidation (M)	30.4
		632.93	1263.85	1264.58	-0.73	2	100	111	R	GNATVPAMEMTK	W	0	Oxidation (M)	38.3
		563.46	1124.91	1125.57	-0.65	2	705	714	R	IPPTDEIADR	I	0	-	57.0
		505.46	1008.91	1009.50	-0.58	2	458	465	K	ISEEEYIK	Q	0	-	48.8
		693.00	1383.99	1384.79	-0.81	2	358	371	K	IVEVNALATALSGK	K	0	-	100.5
		617.31	1848.92	1850.00	-1.08	3	739	755	R	KYTEVKPALTNMVAALK	Q	1	Oxidation (M)	44.5
		1155.46	2308.90	2309.30	-0.40	2	427	447	K	LNLPILPPTTIGSFPPQTVELR	R	0	-	76.0
		437.49	872.96	873.48	-0.52	2	412	419	R	RATNVSAR	L	1	-	35.6
		552.53	1103.04	1103.66	-0.62	2	174	183	K	SFSLLSLLPK	V	0	-	39.0
		510.98	1019.94	1020.54	-0.60	2	349	357	K	SWLAFAAQK	I	0	-	28.2
		882.95	1763.88	1764.96	-1.08	2	254	270	K	TLTSLSGVTAYGLDLVR	G	0	-	50.2
		438.98	875.95	876.46	-0.51	2	29	36	K	TSADDLKK	V	1	-	46.4
		829.98	1657.96	1657.82	0.13	2	689	704	K	YGAGIGPGVYDIHSPR	I	0	-	80.6
		548.47	1094.93	1095.57	-0.64	2	287	296	K	YLFAGVVDGR	N	0	-	54.8
13	chr5.CM0341.20.nc	599.94	1197.86	1198.57	-0.71	2	19	28	K	FALESFWDGK	S	0	-	49.4
13	LjSGA_056527.2	599.94	1197.86	1198.57	-0.71	2	19	28	K	FALESFWDGK	S	0	-	49.4
13	LjSGA_094289.1	406.52	811.02	811.49	-0.47	2	164	170	R	EGLPLRK	S	1	-	32.2
		903.51	1805.00	1805.95	-0.95	2	109	124	K	GMLTGPVTILNWSFVR	D	0	Oxidation (M)	39.7
14	LjT17C10.10.nd	488.45	974.88	975.44	-0.56	2	21	30	K	AGFAGDDAPR	A	0	-	73.3
		591.43	1180.84	1181.52	-0.68	2	53	63	K	DAYVGDEAQSK	R	0	-	52.0
		669.87	1337.73	1337.62	0.11	2	53	64	K	DAYVGDEAQSKR	G	1	-	45.7
		573.98	1145.94	1146.60	-0.66	2	318	328	K	EITALAPSSMK	I	0	-	32.3
		581.97	1161.93	1162.59	-0.66	2	318	328	K	EITALAPSSMK	I	0	Oxidation (M)	48.7
		723.40	1444.79	1444.66	0.13	2	362	374	K	GEYDESGPSIVHR	K	0	-	125.9
		581.44	1160.87	1161.51	-0.64	2	199	208	R	GYMFTTSAER	E	0	-	20.5
		589.43	1176.84	1177.51	-0.67	2	199	208	R	GYMFTTSAER	E	0	Oxidation (M)	56.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		572.83	1143.64	1143.55	0.09	2	42	52	R	HTGVMVGMGQK	D	0	-	59.4
		588.45	1174.88	1175.54	-0.67	2	42	52	R	HTGVMVGMGQK	D	0	2 Oxidation (M)	23.0
		580.45	1158.89	1159.55	-0.66	2	42	52	R	HTGVMVGMGQK	D	0	Oxidation (M)	26.2
		888.03	1774.05	1773.89	0.16	2	241	256	K	NYELPDGQVITIGAER	F	0	-	107.8
		977.41	1952.81	1953.06	-0.24	2	98	115	R	VAPEEHPVLLTEAPLNPK	A	0	-	67.9
14	LjSGA_019708.2	488.45	974.88	975.44	-0.56	2	21	30	K	AGFAGDDAPR	A	0	-	73.3
		591.43	1180.84	1181.52	-0.68	2	53	63	K	DAYVGDEAQSK	R	0	-	52.0
		669.87	1337.73	1337.62	0.11	2	53	64	K	DAYVGDEAQSKR	G	1	-	45.7
		572.83	1143.64	1143.55	0.09	2	42	52	R	HTGVMVGMGQK	D	0	-	59.4
		588.45	1174.88	1175.54	-0.67	2	42	52	R	HTGVMVGMGQK	D	0	2 Oxidation (M)	23.0
		580.45	1158.89	1159.55	-0.66	2	42	52	R	HTGVMVGMGQK	D	0	Oxidation (M)	26.2
		977.41	1952.81	1953.06	-0.24	2	98	115	R	VAPEEHPVLLTEAPLNPK	A	0	-	67.9
15	LjT29P04.130.nd	588.94	1175.87	1175.63	0.24	2	302	312	K	AGISLNNNFVK	L	0	-	30.1
		417.46	832.90	832.46	0.44	2	7	14	K	IGINGFGR	I	0	-	48.8
		471.85	941.69	941.59	0.10	2	121	129	K	KVIISAPSK	D	1	-	59.8
		407.50	812.98	813.50	-0.52	2	122	129	K	VIISAPSK	D	0	-	42.3
		750.01	1498.01	1497.84	0.17	2	238	251	R	VPTVDVSVVDLTVR	I	0	-	107.1
16	LjSGA_086307.1	717.41	1432.81	1433.75	-0.94	2	72	86	R	AASFNIIPSSTGAAK	A	0	-	49.3
		454.94	907.87	908.46	-0.59	2	123	130	K	AASYEQIK	A	0	-	21.9
		1017.16	2032.30	2032.07	0.24	2	39	57	R	FGIVEGLMTTTHAITATQK	T	0	Oxidation (M)	25.5
		750.01	1498.01	1497.84	0.17	2	106	119	R	VPTVDVSVVDLTVR	L	0	-	107.1
17	LjB12N13.20.nc	436.97	871.93	872.47	-0.54	2	164	171	R	ALGQISER	L	0	-	57.2
		522.95	1043.88	1044.52	-0.64	2	143	151	K	EFAPSIPIER	N	0	-	59.0
		976.20	2925.59	2926.53	-0.94	3	28	55	R	GVMLGPDQPVLHMLDIPPAESLNGVK	M	0	Oxidation (M)	22.1
		681.94	1361.87	1362.71	-0.85	2	299	310	K	IVQGLSIDEFSR	K	0	-	73.3
		759.99	1517.96	1517.78	0.18	2	312	324	K	KLDLTAEEELTEEK	A	1	-	63.5
		695.94	1389.87	1389.69	0.18	2	313	324	K	LDLTAEEELTEEK	A	0	-	65.0
		815.50	1628.98	1628.79	0.19	2	241	256	K	LSSALSAASGACDHIR	D	0	Propionamide (C)	27.4
		471.98	941.94	942.54	-0.60	2	172	180	R	LSVPVSDVK	N	0	-	54.1
		673.95	1345.89	1345.73	0.16	2	56	67	K	MELVDAAFPLLK	G	0	-	61.3
		681.95	1361.89	1361.73	0.16	2	56	67	K	MELVDAAFPLLK	G	0	Oxidation (M)	78.4
		416.96	831.91	832.43	-0.52	2	112	119	K	SQASALEK	H	0	-	38.5
		477.47	952.93	953.53	-0.60	2	203	211	K	TPAGEKPVIR	E	0	-	76.4
		824.97	1647.92	1648.99	-1.07	2	127	142	K	VLVVANPANTNALILK	E	0	-	58.0
17	chr5.CM0071.650.nc	436.97	871.93	872.47	-0.54	2	141	148	R	ALGQISER	L	0	-	57.2
		976.20	2925.59	2926.53	-0.94	3	5	32	R	GVMLGPDQPVLHMLDIPPAESLNGVK	M	0	Oxidation (M)	22.1
		681.94	1361.87	1362.71	-0.85	2	276	287	K	IVQGLSIDEFSR	K	0	-	73.3
		673.95	1345.89	1345.73	0.16	2	33	44	K	MELVDAAFPLLK	G	0	-	61.3
		681.95	1361.89	1361.73	0.16	2	33	44	K	MELVDAAFPLLK	G	0	Oxidation (M)	78.4
		416.96	831.91	832.43	-0.52	2	89	96	K	SQASALEK	H	0	-	38.5
		824.97	1647.92	1648.99	-1.07	2	104	119	K	VLVVANPANTNALILK	E	0	-	58.0
17	LjSGA_070021.1	976.20	2925.59	2926.53	-0.94	3	28	55	R	GVMLGPDQPVLHMLDIPPAESLNGVK	M	0	Oxidation (M)	22.1
		673.95	1345.89	1345.73	0.16	2	56	67	K	MELVDAAFPLLK	G	0	-	61.3
		681.95	1361.89	1361.73	0.16	2	56	67	K	MELVDAAFPLLK	G	0	Oxidation (M)	78.4
18	LjSGA_116237.1	456.48	910.95	911.46	-0.51	2	284	291	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	284	291	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		502.47	1002.93	1003.48	-0.56	2	216	224	K	AQEETGEIK	G	0	-	39.6
		733.90	1465.79	1466.61	-0.82	2	190	201	K	DDENVNSQPFR	W	0	Oxidation (M)	62.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		594.38	1186.74	1186.66	0.08	2	274	283	R	DNGLLLHIHR	A	0	-	56.0
		510.97	1019.93	1020.52	-0.59	2	21	29	K	DTDILAAFR	V	0	-	49.8
		1085.57	2169.13	2168.98	0.15	2	183	201	R	GGLDFTKDDENVNSQPFMR	W	1	-	79.2
		697.38	1392.74	1392.64	0.09	2	10	20	K	LTYYTPDYETK	D	0	-	52.6
		733.41	1464.81	1464.71	0.09	2	308	322	R	MSGGDHIHAGTVVGK	L	0	-	64.3
		740.95	1479.88	1480.71	-0.83	2	308	322	R	MSGGDHIHAGTVVGK	L	0	Oxidation (M)	67.3
		732.94	1463.87	1464.75	-0.88	2	135	147	K	TFQGPPIHGIQVER	D	0	-	80.4
		1285.50	3853.46	3853.86	-0.40	3	30	67	R	VTPQGPVPEEAGAAVAESSTGTWTTVWTDGLTSLDR	Y	0	-	74.0
18	LjSGA_141109.1	502.47	1002.93	1003.48	-0.56	2	222	230	K	AQEETGEIK	G	0	-	39.6
		733.90	1465.79	1466.61	-0.82	2	196	207	K	DDENVNSQPFMR	W	0	Oxidation (M)	62.7
		510.97	1019.93	1020.52	-0.59	2	27	35	K	DTDILAAFR	V	0	-	49.8
		1085.57	2169.13	2168.98	0.15	2	189	207	R	GGLDFTKDDENVNSQPFMR	W	1	-	79.2
		697.38	1392.74	1392.64	0.09	2	16	26	K	LTYYTPDYETK	D	0	-	52.6
		732.94	1463.87	1464.75	-0.88	2	141	153	K	TFQGPPIHGIQVER	D	0	-	80.4
		1285.50	3853.46	3853.86	-0.40	3	36	73	R	VTPQGPVPEEAGAAVAESSTGTWTTVWTDGLTSLDR	Y	0	-	74.0
18	LjSGA_138404.1	510.97	1019.93	1020.52	-0.59	2	33	41	K	DTDILAAFR	V	0	-	49.8
		697.38	1392.74	1392.64	0.09	2	22	32	K	LTYYTPDYETK	D	0	-	52.6
		732.94	1463.87	1464.75	-0.88	2	147	159	K	TFQGPPIHGIQVER	D	0	-	80.4
		1285.50	3853.46	3853.86	-0.40	3	42	79	R	VTPQGPVPEEAGAAVAESSTGTWTTVWTDGLTSLDR	Y	0	-	74.0
19	chr3.LjT44N20.60.nd	953.05	1904.09	1903.95	0.14	2	371	388	K	DSTTIIADAASKDELQAR	V	1	-	53.6
		751.87	1501.73	1502.68	-0.95	2	395	407	K	ELFATDSVYDSEK	L	0	-	80.9
		531.21	530.21	530.34	-0.14	1	270	274	K	ISAIK	D	0	-	26.5
		778.51	1555.01	1554.90	0.11	2	145	160	K	LGLLSVTSGANPVSLK	R	0	-	63.2
		602.71	1203.41	1203.61	-0.21	2	81	91	R	NVVLEDFGSPK	V	0	-	64.1
		486.50	970.99	970.56	0.43	2	58	66	R	RALQAGIDK	L	1	-	37.1
		818.76	1635.50	1635.77	-0.27	2	124	140	R	TNDSAGDGTITASVLAR	E	0	-	114.6
		607.97	1213.92	1214.68	-0.75	2	166	176	K	TVAALIEELEK	K	0	-	53.7
		671.97	1341.92	1342.77	-0.85	2	166	177	K	TVAALIEELEKK	A	1	-	63.5
		645.70	1289.39	1289.61	-0.22	2	424	435	K	VGAATETELEDK	K	0	-	79.2
20	chr4.CM0007.1000.nc	491.80	981.58	981.52	0.06	2	95	102	R	ELEVIHSR	W	0	-	58.3
		491.95	981.89	982.49	-0.60	2	124	131	K	FGEAVWFK	A	0	-	52.3
		1176.54	3526.59	3527.73	-1.15	3	175	209	R	IAGGFLGEVTDPLYPGGSFDPLGLADDPEAFELK	V	0	-	52.1
		767.94	1533.86	1533.76	0.10	2	40	53	K	KVSSGSPWYGPDR	V	1	-	84.8
		417.95	1250.83	1251.67	-0.84	3	93	102	K	NRELEVIHSR	W	1	-	55.5
		703.34	1404.66	1405.66	-1.00	2	41	53	K	VVSSGSPWYGPDR	V	0	-	65.9
20	LjSGA_017687.2	491.80	981.58	981.52	0.06	2	95	102	R	ELEVIHSR	W	0	-	58.3
		491.95	981.89	982.49	-0.60	2	124	131	K	FGEAVWFK	A	0	-	52.3
		1176.54	3526.59	3527.73	-1.15	3	175	209	R	IAGGFLGEVTDPLYPGGSFDPLGLADDPEAFELK	V	0	-	52.1
		417.95	1250.83	1251.67	-0.84	3	93	102	K	NRELEVIHSR	W	1	-	55.5
20	LjSGA_061139.1	491.80	981.58	981.52	0.06	2	95	102	R	ELEVIHSR	W	0	-	58.3
		491.95	981.89	982.49	-0.60	2	124	131	K	FGEAVWFK	V	0	-	52.3
		1176.54	3526.59	3527.73	-1.15	3	175	209	R	IAGGFLGEVTDPLYPGGSFDPLGLADDPEAFELK	V	0	-	52.1
		417.95	1250.83	1251.67	-0.84	3	93	102	K	NRELEVIHSR	W	1	-	55.5
21	LjSGA_030216.1	566.35	1130.69	1130.59	0.10	2	191	199	R	AWIQVNCNCK	G	0	Propionamide (C)	38.7
		630.36	1258.71	1258.62	0.10	2	59	69	R	DEEQDKGAIVR	V	1	-	67.6
		494.97	987.92	988.55	-0.63	2	282	289	R	FNFLVPPR	E	0	-	47.4
		1025.59	2049.16	2048.96	0.20	2	2	17	R	FYLSGNQEQLQYQR	Q	0	-	28.2
		563.37	1124.73	1124.62	0.12	2	72	82	K	GGLSVITPPER	Q	0	-	68.1

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		597.85	1790.54	1791.70	-1.16	3	88	102	R	GSEEEEEDEEDRPSR	H	0	-	28.0
		541.94	1081.87	1082.55	-0.68	2	159	168	K	LSAEHGSLNR	N	0	-	82.0
		975.00	1947.98	1947.80	0.18	2	87	102	R	RGSEEEEEDEEDRPSR	H	1	-	58.4
		726.91	1451.80	1451.68	0.12	2	226	237	R	SMSDKFNYVAFK	T	1	Oxidation (M)	36.6
		687.91	1373.80	1374.65	-0.86	2	130	142	K	SSSPDIFNPQAGR	I	0	-	64.8
		598.36	1194.71	1194.60	0.11	2	145	155	K	TATGFDFPALR	F	0	-	64.3
		676.96	1351.90	1351.78	0.12	2	70	82	R	VKGGLSVITPPER	Q	1	-	73.2
22	chr3.CM0152.120.nc	761.40	1520.79	1520.69	0.10	2	225	238	R	AGHPWELPDDAGK	Y	0	-	23.6
		475.27	1422.78	1423.71	-0.93	3	374	386	R	EHIEVAGENALSR	Y	0	-	81.8
		499.91	997.80	998.44	-0.64	2	164	171	R	ENMSDFLK	S	0	Oxidation (M)	34.7
		647.40	1292.78	1293.62	-0.84	2	134	144	K	EYLTVGVDNER	I	0	-	47.9
		456.47	910.93	911.53	-0.60	2	469	476	K	IPDDVLLK	A	0	-	40.8
		789.90	1577.78	1578.80	-1.02	2	271	284	K	LLNHGQDQILDEANK	A	0	-	66.3
		905.48	1808.94	1809.89	-0.95	2	422	436	R	LSDDLQSQSNFDIFR	K	0	-	96.2
		768.82	1535.62	1536.60	-0.98	2	442	454	K	MHADQDYCADPGK	Y	0	Oxidation (M); Propionamide (C)	50.5
		760.82	1519.63	1520.60	-0.97	2	442	454	K	MHADQDYCADPGK	Y	0	Propionamide (C)	56.4
		768.94	1535.86	1535.76	0.10	2	132	144	R	NKEYLTVGVDNER	I	1	-	53.7
		1078.95	2155.89	2157.03	-1.14	2	354	373	R	SDVDSGPEELVQVLSGGWR	E	0	-	105.6
		977.02	1952.04	1951.90	0.13	2	306	323	K	SESHAELTAGYYNLGNNR	D	0	-	42.3
		506.92	1011.82	1011.49	0.33	2	251	259	R	SNGTYLTEK	G	0	-	61.1
		674.89	1347.76	1348.62	-0.87	2	150	160	R	TAIELYSIDYMK	S	0	Oxidation (M)	58.1
		751.90	1501.79	1501.68	0.11	2	239	250	K	YNDVPQSTEFFR	S	0	-	60.3
23	LjSGA_018057.1	482.45	962.89	963.48	-0.60	2	100	107	K	CGVNIPIYK	I	0	Propionamide (C)	25.2
		626.43	1250.84	1251.61	-0.77	2	108	118	K	ISTSTNCNTIK	A	0	Propionamide (C)	57.9
		919.39	1836.77	1837.91	-1.14	2	80	99	K	NAAGSMPLNAGNAAALPGK	C	0	-	75.9
		927.38	1852.75	1853.91	-1.15	2	80	99	K	NAAGSMPLNAGNAAALPGK	C	0	Oxidation (M)	90.1
		615.42	1228.82	1229.60	-0.78	2	60	71	K	NLNAAASTTPDR	K	0	-	73.5
		679.43	1356.85	1357.69	-0.84	2	60	72	K	NLNAAASTTPDRK	T	1	-	72.7
24	chr1.CM0378.190.nd	903.03	1804.05	1803.94	0.12	2	35	52	R	AAVPSGASTGIYEALRL	D	0	-	111.2
		455.97	909.93	910.40	-0.48	2	53	61	R	DGGSIDYLGK	G	0	-	57.8
		401.03	800.04	800.46	-0.43	2	227	233	K	EGLELLK	T	0	-	54.8
		977.02	1952.03	1951.89	0.14	2	17	34	R	GNPTVEVDITCSDGTFR	A	0	Propionamide (C)	20.2
		469.02	936.02	936.51	-0.50	2	138	146	K	HIANIAGNK	N	0	-	40.7
		927.44	1852.86	1853.94	-1.08	2	168	184	K	LAMQEFMVLPGASSFK	E	0	-	47.1
		944.03	1886.05	1885.93	0.12	2	168	184	K	LAMQEFMVLPGASSFK	E	0	2 Oxidation (M)	57.4
		706.62	2116.85	2117.14	-0.29	3	147	167	K	NLVLPVPAPFNVIINGGSHAGNK	L	0	-	76.3
		1126.45	2250.88	2251.12	-0.24	2	382	403	R	SGETEDTFIADLAVGLSTGQIK	T	0	-	33.4
		944.48	1886.95	1886.83	0.12	2	262	277	K	TYDLNFKEDNNDGSQK	I	1	-	60.6
		800.99	1599.97	1600.84	-0.87	2	353	367	K	VNQIGSVTESIEAVR	M	0	-	79.9
		403.52	805.02	805.44	-0.43	2	416	421	K	YNQLLR	I	0	-	44.9
25	chr3.CM0452.230.nd	837.88	1673.74	1674.72	-0.98	2	227	242	K	ATAGDTHLGGEDFDNR	L	0	-	72.6
		664.92	1327.83	1328.61	-0.78	2	308	317	R	FEELNMDLFR	K	0	Oxidation (M)	57.0
		829.96	1657.91	1658.89	-0.97	2	176	191	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	176	192	R	IINEPTAAAIAYGLDKK	A	1	-	77.9
		402.98	803.94	803.44	0.50	2	507	513	K	ITITNDK	G	0	-	41.3
		687.71	1373.40	1373.60	-0.20	2	546	556	K	NALENYAYNMR	N	0	Oxidation (M)	39.4
		841.00	1679.99	1679.83	0.17	2	145	159	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
		838.92	1675.82	1675.80	0.02	2	60	74	K	NQVAMNPQNTVFDAK	R	0	-	48.2
		451.50	900.99	901.52	-0.53	2	423	430	R	NTTIPTKK	E	1	-	46.1
		743.94	1485.86	1486.69	-0.84	2	40	52	R	TTPSYVAFTDTER	L	0	-	54.9

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		614.45	1226.89	1227.62	-0.73	2	29	39	R	VEIIANDQGNR	T	0	-	68.8
		718.95	1435.89	1435.75	0.14	2	352	363	K	VQQLLQDFNKG	E	0	-	49.7
25	chr4.CM0179.510.nd	837.88	1673.74	1674.72	-0.98	2	226	241	K	ATAGDTHLGGEDFDNR	M	0	-	72.6
		664.92	1327.83	1328.61	-0.78	2	307	316	R	FEELNMDLFR	K	0	Oxidation (M)	57.0
		829.96	1657.91	1658.89	-0.97	2	175	190	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	175	191	R	IINEPTAAAIAYGLDKK	A	1	-	77.9
		841.00	1679.99	1679.83	0.17	2	144	158	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
		838.92	1675.82	1675.80	0.02	2	59	73	K	NQVAMNPQNTVFDAK	R	0	-	48.2
		743.94	1485.86	1486.69	-0.84	2	39	51	R	TTPSYVAFTDTER	L	0	-	54.9
25	LjSGA_025770.1	829.96	1657.91	1658.89	-0.97	2	198	213	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	198	214	R	IINEPTAAAIAYGLDKK	G	1	-	77.9
		614.45	1226.89	1227.62	-0.73	2	52	62	R	VEIIANDQGNR	I	0	-	68.8
25	LjSGA_069657.1	829.96	1657.91	1658.89	-0.97	2	176	191	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	176	192	R	IINEPTAAAIAYGLDKK	V	1	-	77.9
25	chr1.LjT14113.160.nd	829.96	1657.91	1658.89	-0.97	2	182	197	R	IINEPTAAAIAYGLDK	T	0	-	94.3
25	chr6.CM0118.670.nc	451.50	900.99	901.52	-0.53	2	427	434	K	NTTIPTKK	E	1	-	46.1
		743.94	1485.86	1486.69	-0.84	2	40	52	R	TTPSYVAFTDTER	L	0	-	54.9
25	chr6.CM0118.650.nc	743.94	1485.86	1486.69	-0.84	2	40	52	R	TTPSYVAFTDTER	L	0	-	54.9
25	LjSGA_050585.1	614.45	1226.89	1227.62	-0.73	2	29	39	R	VEIIANDQGNR	T	0	-	68.8
25	LjSGA_042820.1	841.00	1679.99	1679.83	0.17	2	53	67	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
25	LjSGA_024670.1	841.00	1679.99	1679.83	0.17	2	68	82	K	NAVVTVPAYFNDSQR	K	0	-	60.8
25	chr1.LjT16O03.90.nd	718.95	1435.89	1435.75	0.14	2	309	320	K	VQQLLQDFNKG	E	0	-	49.7
25	LjSGA_089217.1	718.95	1435.89	1435.75	0.14	2	223	234	K	VQQLLQDFNKG	E	0	-	49.7
25	chr1.LjT23O20.220.nd	402.98	803.94	803.44	0.50	2	309	315	R	ITITNDK	E	0	-	41.3
26	LjSGA_031559.1	744.42	1486.82	1487.72	-0.91	2	159	171	K	CSRPVVVADCGQL	-	0	2 Propionamide (C)	45.0
		484.93	967.85	968.46	-0.61	2	90	97	K	FADENFVK	K	0	-	23.9
		548.95	1095.89	1096.56	-0.66	2	90	98	K	FADENFVKK	H	1	-	50.2
		812.46	1622.90	1623.90	-1.00	2	133	147	K	HVVFGQVVEGLDVVK	N	0	-	78.9
		695.46	1388.90	1389.73	-0.84	2	20	31	R	IVMELFADVTPR	T	0	-	56.7
		703.43	1404.84	1405.73	-0.89	2	20	31	R	IVMELFADVTPR	T	0	Oxidation (M)	75.2
		464.97	927.93	928.51	-0.58	2	49	56	R	SGKPLHYK	G	0	-	32.2
		747.91	1493.80	1494.73	-0.93	2	6	19	K	VFFDMTIGGQPAGR	I	0	-	77.3
		755.89	1509.77	1510.72	-0.95	2	6	19	K	VFFDMTIGGQPAGR	I	0	Oxidation (M)	77.4
		926.53	2776.57	2777.24	-0.67	3	63	89	R	VIPNFMCGGQDFTAGNGTGGESIYGAK	F	0	Oxidation (M); Propionamide (C)	36.0
26	LjSGA_090105.1	484.93	967.85	968.46	-0.61	2	90	97	K	FADENFVK	K	0	-	23.9
		548.95	1095.89	1096.56	-0.66	2	90	98	K	FADENFVKK	H	1	-	50.2
		695.46	1388.90	1389.73	-0.84	2	20	31	R	IVMELFADVTPR	T	0	-	56.7
		703.43	1404.84	1405.73	-0.89	2	20	31	R	IVMELFADVTPR	T	0	Oxidation (M)	75.2
		464.97	927.93	928.51	-0.58	2	49	56	R	SGKPLHYK	G	0	-	32.2
27	LjT36L22.20.nd	642.45	1282.89	1283.71	-0.82	2	282	292	R	DLINILEDATR	N	0	-	54.3
		860.87	1719.73	1720.81	-1.09	2	378	394	K	DSTTIVGDGSTQEAVNK	R	0	-	67.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		501.95	1001.88	1002.52	-0.64	2	353	361	R	EEVGLTLDK	A	0	-	35.3
		752.88	1503.75	1504.71	-0.96	2	248	260	R	GYISPYFVTDEK	M	0	-	61.0
		507.97	1013.92	1014.57	-0.65	2	100	109	K	IVNDGVTVAK	E	0	-	44.3
		530.34	1058.66	1058.60	0.07	2	222	231	R	KGVVTLLEEGK	S	1	-	62.7
		591.48	1180.94	1181.70	-0.76	2	74	85	K	LADLVGVTLGPK	G	0	-	70.6
		414.52	827.02	827.55	-0.53	2	270	276	K	LLLVDDK	I	1	-	27.7
		614.96	1227.90	1228.68	-0.78	2	444	454	K	LRVEDALNATK	A	1	-	31.7
		580.93	1159.84	1159.58	0.26	2	509	520	K	NAGVNGSVVSEK	V	0	-	67.4
		847.96	1693.91	1693.78	0.13	2	401	414	K	NQIEAAEQDYEKEK	L	1	-	38.3
		917.41	1832.81	1833.98	-1.17	2	336	352	K	SQYLDLIAILTGGTIVIR	E	0	-	52.9
		480.45	958.88	959.49	-0.61	2	446	454	R	VEDALNATK	A	0	-	66.1
		468.94	935.87	936.47	-0.60	2	521	528	K	VLSSDNFR	Y	0	-	54.6
		640.48	1278.94	1279.76	-0.82	2	157	169	K	VVAAGANPVLITR	G	0	-	88.2
		768.40	1534.79	1535.75	-0.97	2	538	551	K	YEDLMAAGIIDPTK	V	0	-	79.3
		776.39	1550.77	1551.75	-0.98	2	538	551	K	YEDLMAAGIIDPTK	V	0	Oxidation (M)	73.8
		472.43	942.84	943.44	-0.60	2	529	537	R	YGYNAATGK	Y	0	-	59.7
27	LjSGA_075236.1	642.45	1282.89	1283.71	-0.82	2	23	33	R	DLINILEDAIR	N	0	-	54.3
		860.87	1719.73	1720.81	-1.09	2	119	135	K	DSTTIIVGDGSTQEAVNK	R	0	-	67.7
		501.95	1001.88	1002.52	-0.64	2	94	102	R	EEVGLTLDK	A	0	-	35.3
		917.41	1832.81	1833.98	-1.17	2	77	93	K	SQYLDLIAILTGGTIVIR	E	0	-	52.9
28	chr3.CM0282.370.nc	795.46	1588.90	1589.91	-1.02	2	94	109	K	ALEGADIVIIIPAGVPR	K	0	-	89.8
		659.43	1316.85	1317.69	-0.84	2	116	127	R	DDLFINAGIVK	G	0	-	25.9
		495.44	988.87	989.50	-0.63	2	326	334	K	GELQSSIEK	G	0	-	48.1
		609.96	1217.91	1218.70	-0.79	2	171	181	R	LFGVTTLDVVR	A	0	-	66.9
		695.44	1388.86	1388.69	0.17	2	234	246	K	RTQDGGTEVVEAK	A	1	-	65.9
		761.39	1520.76	1521.73	-0.97	2	80	93	R	SEVVGYQGEEQLGK	A	0	-	90.3
		616.91	1231.81	1232.59	-0.78	2	235	246	R	TQDGGTEVVEAK	A	0	-	75.5
		897.46	1792.91	1794.04	-1.14	2	32	50	K	VAVLGAAGGIGQPLSLLMK	L	0	-	86.6
		905.45	1808.89	1810.04	-1.15	2	32	50	K	VAVLGAAGGIGQPLSLLMK	L	0	Oxidation (M)	50.4
28	chr3.CM0282.420.nc	609.96	1217.91	1218.70	-0.79	2	9	19	R	LFGVTTLDVVR	A	0	-	66.9
		695.44	1388.86	1388.69	0.17	2	72	84	K	RTQDGGTEVVEAK	A	1	-	65.9
		616.91	1231.81	1232.59	-0.78	2	73	84	R	TQDGGTEVVEAK	A	0	-	75.5
28	chr3.CM0282.440.nc	495.44	988.87	989.50	-0.63	2	30	38	K	GELQSSIEK	G	0	-	48.1
29	chr1.LjT16O03.100.nd	527.42	1052.83	1053.50	-0.66	2	106	115	K	DYTGDAVSVK	N	0	-	45.2
		798.44	1594.86	1595.79	-0.93	2	49	61	R	HQADVCHAYQILK	K	0	Propionamide (C)	69.8
		508.25	1521.72	1522.61	-0.89	3	272	283	K	MHSHVMQYGDMR	M	0	2 Oxidation (M)	25.2
		513.58	1537.70	1538.61	-0.90	3	272	283	K	MHSHVMQYGDMR	M	0	3 Oxidation (M)	30.1
		754.40	1506.79	1506.62	0.18	2	272	283	K	MHSHVMQYGDMR	M	0	Oxidation (M)	22.4
		587.44	1172.86	1172.58	0.28	2	95	105	R	NGPNVYEGVPK	D	0	-	60.8
		415.97	829.92	830.40	-0.49	2	258	263	K	QYEHVR	K	0	-	32.8
		679.91	1357.81	1358.65	-0.84	2	286	297	R	SDYLATYLGSNR	E	0	-	63.4
		759.42	1516.82	1517.81	-0.99	2	368	381	K	SVNLIGNLLFGEDK	S	0	-	60.6
30	chr6.LjT23A02.60.nc	805.33	1608.64	1609.66	-1.02	2	398	411	R	AMDEYTSEIFMGKK	N	0	2 Oxidation (M)	45.7
		487.96	973.90	974.52	-0.62	2	487	494	R	AMLENILR	A	0	Oxidation (M)	27.5
		749.49	1496.97	1497.76	-0.79	2	99	112	R	ANYFGSLTQASAIR	V	0	-	94.2
		779.95	1557.89	1558.91	-1.01	2	469	484	K	APLVPPTGTPVFNALSK	Q	0	-	53.5
		499.97	997.93	998.58	-0.65	2	204	211	K	EQIQQIIK	D	0	-	31.2
		564.05	1126.08	1126.67	-0.59	2	203	211	K	KEQIQQIIK	D	1	-	63.6
		660.89	1319.77	1318.70	1.07	2	37	47	R	NGSYQQWIVPKK	S	0	-	23.2

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		532.92	1063.82	1064.51	-0.69	2	299	308	K	NSLIGGDDFK	S	0	-	56.4
		489.01	976.00	976.52	-0.52	2	158	165	R	VFDIDLQK	Q	0	-	31.8
		785.98	1569.94	1570.77	-0.82	2	113	126	R	VGSFQGEIYAPFK	S	0	-	73.4
		644.02	1286.02	1286.70	-0.68	2	225	235	R	VVVLWTANTER	Y	0	-	51.8
30	chr4.CM0307.90.nc	779.95	1557.89	1558.91	-1.01	2	469	484	K	APLVPPGTPVNVNALS	Q	0	-	53.5
		532.92	1063.82	1064.51	-0.69	2	299	308	K	NSLIGGDDFK	S	0	-	56.4
		489.01	976.00	976.52	-0.52	2	158	165	R	VFDIDLQK	Q	0	-	31.8
		785.98	1569.94	1570.77	-0.82	2	113	126	R	VGSFQGEIYAPFK	S	0	-	73.4
31	LjSGA_133863.1	1099.60	2197.19	2197.02	0.17	2	137	155	K	DETKHEVTTTTTTTQDPR	N	1	-	34.1
		707.89	1413.76	1413.66	0.10	2	63	75	K	DKTQQAHSSTGDR	T	1	-	77.5
		862.97	1723.93	1723.81	0.12	2	141	155	K	EHVTTTTTTTQDPR	N	0	-	55.6
		1035.52	2069.02	2068.88	0.15	2	96	115	R	ESAQAGNDNTGGFMQQTGEK	V	0	-	82.9
		1043.52	2085.02	2084.87	0.15	2	96	115	R	ESAQAGNDNTGGFMQQTGEK	V	0	Oxidation (M)	39.0
		647.86	1293.70	1293.62	0.07	2	129	140	K	STLGMGQKDETK	E	1	-	54.7
		655.86	1309.71	1309.62	0.09	2	129	140	K	STLGMGQKDETK	E	1	Oxidation (M)	34.3
		674.40	1346.78	1346.69	0.10	2	116	128	K	VKDMAQGATEAVK	S	1	-	46.8
		682.39	1362.76	1362.68	0.08	2	116	128	K	VKDMAQGATEAVK	S	1	Oxidation (M)	51.4
32	chr1.CM0001.670.nc	649.92	1297.82	1297.74	0.08	2	135	146	R	EHALLAFTLGVK	Q	0	-	58.6
		404.97	807.93	808.41	-0.48	2	311	318	R	GFVASNSK	D	0	-	40.9
		668.38	1334.74	1334.65	0.09	2	311	323	R	GFVASNSKDDPAK	E	1	-	63.7
		496.99	991.96	992.53	-0.57	2	165	172	K	GRYEEIVK	E	1	-	26.4
		513.03	1024.05	1024.60	-0.55	2	244	254	K	IGGIGTVPVGR	V	0	-	58.5
		487.99	973.97	974.54	-0.58	2	236	243	R	LPLQDVYK	I	0	-	51.8
		457.55	913.08	913.56	-0.48	2	419	427	R	QTVAVGVK	S	0	-	34.5
		513.46	1024.90	1025.48	-0.58	2	205	212	R	STNLDWYK	G	0	-	51.2
		560.48	1118.95	1119.59	-0.64	2	21	30	K	STTTGHLIYK	L	0	-	54.2
		488.98	1463.92	1464.68	-0.77	3	85	96	K	YYCTVIDAPGHR	D	0	Propionamide (C)	66.2
32	chr2.LjT12G08.20.nc	649.92	1297.82	1297.74	0.08	2	135	146	R	EHALLAFTLGVK	Q	0	-	58.6
		404.97	807.93	808.41	-0.48	2	311	318	R	GFVASNSK	D	0	-	40.9
		668.38	1334.74	1334.65	0.09	2	311	323	R	GFVASNSKDDPAK	E	1	-	63.7
		513.03	1024.05	1024.60	-0.55	2	244	254	K	IGGIGTVPVGR	V	0	-	58.5
		487.99	973.97	974.54	-0.58	2	236	243	R	LPLQDVYK	I	0	-	51.8
		457.55	913.08	913.56	-0.48	2	419	427	R	QTVAVGVK	S	0	-	34.5
		513.46	1024.90	1025.48	-0.58	2	205	212	R	STNLDWYK	G	0	-	51.2
		560.48	1118.95	1119.59	-0.64	2	21	30	K	STTTGHLIYK	L	0	-	54.2
		488.98	1463.92	1464.68	-0.77	3	85	96	K	YYCTVIDAPGHR	D	0	Propionamide (C)	66.2
32	chr5.CM0909.50.nc	404.97	807.93	808.41	-0.48	2	311	318	R	GFVASNSK	D	0	-	40.9
		668.38	1334.74	1334.65	0.09	2	311	323	R	GFVASNSKDDPAK	E	1	-	63.7
		513.03	1024.05	1024.60	-0.55	2	244	254	K	IGGIGTVPVGR	V	0	-	58.5
		487.99	973.97	974.54	-0.58	2	236	243	R	LPLQDVYK	I	0	-	51.8
		457.55	913.08	913.56	-0.48	2	419	427	R	QTVAVGVK	S	0	-	34.5
		560.48	1118.95	1119.59	-0.64	2	21	30	K	STTTGHLIYK	L	0	-	54.2
		488.98	1463.92	1464.68	-0.77	3	85	96	K	YYCTVIDAPGHR	D	0	Propionamide (C)	66.2
32	chr1.CM0192.320.nd	404.97	807.93	808.41	-0.48	2	157	164	R	GFVASNSK	D	0	-	40.9
		668.38	1334.74	1334.65	0.09	2	157	169	R	GFVASNSKDDPAK	E	1	-	63.7
		513.03	1024.05	1024.60	-0.55	2	90	100	K	IGGIGTVPVGR	V	0	-	58.5
		487.99	973.97	974.54	-0.58	2	82	89	R	LPLQDVYK	I	0	-	51.8
		513.46	1024.90	1025.48	-0.58	2	51	58	R	STNLDWYK	G	0	-	51.2

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
32	LjSGA_022872.2	560.48	1118.95	1119.59	-0.64	2	17	26	K	STTTGHLIYK	L	0	-	54.2
32	LjSGA_053227.1	560.48	1118.95	1119.59	-0.64	2	21	30	K	STTTGHLIYK	L	0	-	54.2
32	LjSGA_132154.1	560.48	1118.95	1119.59	-0.64	2	21	30	K	STTTGHLIYK	L	0	-	54.2
33	LjSGA_082137.1	604.49	1206.96	1207.59	-0.63	2	20	31	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		717.01	1432.01	1432.77	-0.76	2	222	235	R	FVQAGSEVSALLGR	M	0	-	98.1
		984.44	1966.86	1968.03	-1.17	2	54	71	R	IFNVLGEPIDNLGPVDTR	T	0	-	84.2
		487.97	973.92	974.55	-0.64	2	112	122	K	IGLFGGAGVGK	T	0	-	55.6
		716.39	1430.77	1430.68	0.09	2	323	334	R	IVGEEHYETAQR	V	0	-	38.0
		504.03	1006.04	1006.57	-0.53	2	90	98	K	LSIFETGIK	V	0	-	57.2
		595.51	1189.01	1189.63	-0.63	2	79	89	R	SAPAFIQLDTK	L	0	-	58.9
		735.96	1469.90	1470.85	-0.95	2	123	135	K	TVLIMELINNIK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	123	135	K	TVLIMELINNIK	A	0	Oxidation (M)	49.9
33	LjSGA_135295.1	604.49	1206.96	1207.59	-0.63	2	4	15	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		717.01	1432.01	1432.77	-0.76	2	206	219	R	FVQAGSEVSALLGR	M	0	-	98.1
		984.44	1966.86	1968.03	-1.17	2	38	55	R	IFNVLGEPIDNLGPVDTR	T	0	-	84.2
		487.97	973.92	974.55	-0.64	2	96	106	K	IGLFGGAGVGK	T	0	-	55.6
		504.03	1006.04	1006.57	-0.53	2	74	82	K	LSIFETGIK	V	0	-	57.2
		595.51	1189.01	1189.63	-0.63	2	63	73	R	SAPAFIQLDTK	L	0	-	58.9
		735.96	1469.90	1470.85	-0.95	2	107	119	K	TVLIMELINNIK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	107	119	K	TVLIMELINNIK	A	0	Oxidation (M)	49.9
33	LjB15P09.140.nc	487.97	973.92	974.55	-0.64	2	175	185	K	IGLFGGAGVGK	T	0	-	55.6
		504.03	1006.04	1006.57	-0.53	2	153	161	K	LSIFETGIK	V	0	-	57.2
		595.51	1189.01	1189.63	-0.63	2	142	152	R	SAPAFIQLDTK	L	0	-	58.9
		735.96	1469.90	1470.85	-0.95	2	186	198	K	TVLIMELINNIK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	186	198	K	TVLIMELINNIK	A	0	Oxidation (M)	49.9
33	LjSGA_067288.1	487.97	973.92	974.55	-0.64	2	93	103	K	IGLFGGAGVGK	T	0	-	55.6
		504.03	1006.04	1006.57	-0.53	2	71	79	K	LSIFETGIK	V	0	-	57.2
		735.96	1469.90	1470.85	-0.95	2	104	116	K	TVLIMELINNIK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	104	116	K	TVLIMELINNIK	A	0	Oxidation (M)	49.9
33	LjSGA_081554.1	717.01	1432.01	1432.77	-0.76	2	18	31	R	FVQAGSEVSALLGR	M	0	-	98.1
		716.39	1430.77	1430.68	0.09	2	119	130	R	IVGEEHYETAQR	V	0	-	38.0
33	LjSGA_114982.1	717.01	1432.01	1432.77	-0.76	2	96	109	R	FVQAGSEVSALLGR	M	0	-	98.1
		716.39	1430.77	1430.68	0.09	2	197	208	R	IVGEEHYETAQR	V	0	-	38.0
33	LjSGA_129516.1	717.01	1432.01	1432.77	-0.76	2	56	69	R	FVQAGSEVSALLGR	M	0	-	98.1
		716.39	1430.77	1430.68	0.09	2	157	168	R	IVGEEHYETAQR	V	0	-	38.0
34	chr2.CM0373.1010.nd	730.40	1458.79	1458.67	0.11	2	362	374	K	AEYDESGPSIVHR	K	0	-	28.9
		488.45	974.88	975.44	-0.56	2	21	30	K	AGFAGDDAPR	A	0	-	73.3
		591.43	1180.84	1181.52	-0.68	2	53	63	K	DAYVGDEAQS	R	0	-	52.0
		669.87	1337.73	1337.62	0.11	2	53	64	K	DAYVGDEAQS	G	1	-	45.7
		566.97	1131.93	1132.58	-0.65	2	318	328	K	EISALAPSSMK	I	0	-	63.6
		574.97	1147.92	1148.57	-0.65	2	318	328	K	EISALAPSSMK	I	0	Oxidation (M)	40.2
		572.83	1143.64	1143.55	0.09	2	42	52	R	HTGVMVGMGQK	D	0	-	59.4
		588.45	1174.88	1175.54	-0.67	2	42	52	R	HTGVMVGMGQK	D	0	2 Oxidation (M)	23.0
		580.45	1158.89	1159.55	-0.66	2	42	52	R	HTGVMVGMGQK	D	0	Oxidation (M)	26.2
		873.95	1745.89	1746.88	-0.99	2	241	256	K	SYELPDQQVITIGAER	F	0	-	85.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		977.41	1952.81	1953.06	-0.24	2	98	115	R	VAPEEHPVLLTEAPLNPK	A	0	-	67.9
34	chr6.CM0314.690.nc	488.45	974.88	975.44	-0.56	2	21	30	K	AGFAGDDAPR	A	0	-	73.3
		591.43	1180.84	1181.52	-0.68	2	53	63	K	DAYVGDEAQS	R	0	-	52.0
		669.87	1337.73	1337.62	0.11	2	53	64	K	DAYVGDEAQS	G	1	-	45.7
		566.97	1131.93	1132.58	-0.65	2	318	328	K	EISALAPSSMK	I	0	-	63.6
		574.97	1147.92	1148.57	-0.65	2	318	328	K	EISALAPSSMK	I	0	Oxidation (M)	40.2
		572.83	1143.64	1143.55	0.09	2	42	52	R	HTGVMVGMGQK	D	0	-	59.4
		588.45	1174.88	1175.54	-0.67	2	42	52	R	HTGVMVGMGQK	D	0	2 Oxidation (M)	23.0
		580.45	1158.89	1159.55	-0.66	2	42	52	R	HTGVMVGMGQK	D	0	Oxidation (M)	26.2
		873.95	1745.89	1746.88	-0.99	2	241	256	K	SYELPDGQVITIGAER	F	0	-	85.0
		977.41	1952.81	1953.06	-0.24	2	98	115	R	VAPEEHPVLLTEAPLNPK	A	0	-	67.9
34	chr1.LjT23O20.150.nd	730.40	1458.79	1458.67	0.11	2	362	374	K	AEYDESGPSIVHR	K	0	-	28.9
		488.45	974.88	975.44	-0.56	2	21	30	K	AGFAGDDAPR	A	0	-	73.3
		591.43	1180.84	1181.52	-0.68	2	53	63	K	DAYVGDEAQS	R	0	-	52.0
		669.87	1337.73	1337.62	0.11	2	53	64	K	DAYVGDEAQS	G	1	-	45.7
		566.97	1131.93	1132.58	-0.65	2	318	328	K	EISALAPSSMK	I	0	-	63.6
		574.97	1147.92	1148.57	-0.65	2	318	328	K	EISALAPSSMK	I	0	Oxidation (M)	40.2
		572.83	1143.64	1143.55	0.09	2	42	52	R	HTGVMVGMGQK	D	0	-	59.4
		588.45	1174.88	1175.54	-0.67	2	42	52	R	HTGVMVGMGQK	D	0	2 Oxidation (M)	23.0
		580.45	1158.89	1159.55	-0.66	2	42	52	R	HTGVMVGMGQK	D	0	Oxidation (M)	26.2
		977.41	1952.81	1953.06	-0.24	2	98	115	R	VAPEEHPVLLTEAPLNPK	A	0	-	67.9
34	LjSGA_131797.1	566.97	1131.93	1132.58	-0.65	2	100	110	K	EISALAPSSMK	I	0	-	63.6
		574.97	1147.92	1148.57	-0.65	2	100	110	K	EISALAPSSMK	I	0	Oxidation (M)	40.2
		873.95	1745.89	1746.88	-0.99	2	23	38	K	SYELPDGQVITIGAER	F	0	-	85.0
34	LjSGA_146200.1	873.95	1745.89	1746.88	-0.99	2	89	104	K	SYELPDGQVITIGAER	F	0	-	85.0
35	LjSGA_043401.1	717.41	1432.81	1433.75	-0.94	2	189	203	R	AASFNIIPSSGA	V	0	-	49.3
		989.60	1977.19	1977.03	0.16	2	51	68	K	DANTLLFGDKPVTVFANR	N	0	-	66.0
		1017.16	2032.30	2032.07	0.24	2	156	174	R	FGIVEGLMTTVHSITATQK	T	0	-	85.3
		1025.16	2048.31	2048.06	0.25	2	156	174	R	FGIVEGLMTTVHSITATQK	T	0	Oxidation (M)	84.0
		424.96	847.90	848.45	-0.55	2	44	50	K	HHEVTVK	D	0	-	26.1
		471.85	941.69	941.59	0.10	2	106	114	K	KVIISAPSK	D	1	-	59.8
		407.50	812.98	813.50	-0.52	2	107	114	K	VIISAPSK	D	0	-	42.3
		544.82	1087.63	1087.51	0.12	2	35	43	K	YDSVHGPK	H	0	-	46.7
36	chr1.CM0231.140.nd	812.46	1622.90	1623.90	-1.00	2	133	147	K	HVVFGQVVEGLDVVK	E	0	-	78.9
		464.97	927.93	928.51	-0.58	2	49	56	R	SGKPLHYK	G	0	-	32.2
		737.97	1473.92	1473.75	0.17	2	159	172	K	TSKPVVVADCGQLS	-	0	Propionamide (C)	31.9
		747.91	1493.80	1494.73	-0.93	2	6	19	K	VFFDMTIGGQPAGR	I	0	-	77.3
		755.89	1509.77	1510.72	-0.95	2	6	19	K	VFFDMTIGGQPAGR	I	0	Oxidation (M)	77.4
		926.53	2776.57	2777.24	-0.67	3	63	89	R	VIPNFMCGGDFTAGNGTGGESIYGAK	F	0	Oxidation (M); Propionamide (C)	36.0
37	LjSGA_042035.1	414.98	827.95	828.47	-0.52	2	1	7	-	ALIEEVR	G	0	-	67.4
		575.42	1148.82	1149.55	-0.73	2	180	189	K	GMVVWTSNEK	E	0	-	39.8
		583.85	1165.68	1165.54	0.14	2	180	189	K	GMVVWTSNEK	E	0	Oxidation (M)	61.7
		438.97	875.93	876.52	-0.59	2	158	165	K	HPNLVGIK	E	0	-	30.7
		819.40	1636.79	1637.89	-1.09	2	143	157	R	TAQDIPPSVVEILEK	H	0	-	41.2
		790.91	1579.80	1580.81	-1.01	2	63	76	K	VMLIGHTVHQFGDK	V	0	-	71.5
		799.51	1597.00	1596.81	0.19	2	63	76	K	VMLIGHTVHQFGDK	V	0	Oxidation (M)	64.7
38	chr3.LjT05P05.90.nd	784.93	1567.84	1568.89	-1.05	2	210	223	K	ALLSDPVFRPLVDK	Y	0	-	48.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		437.45	872.88	873.46	-0.57	2	32	38	K	CAPLMRL	L	0	Propionamide (C)	33.6
		416.93	1247.78	1248.61	-0.83	3	120	130	R	EDKPQPPPEGR	L	0	-	48.3
		556.96	1111.90	1112.61	-0.71	2	200	209	K	EGLLQLPTDK	A	0	-	63.3
		610.24	1827.70	1827.93	-0.23	3	62	79	K	HAAELAHGANGLDIAVR	L	0	-	103.8
		666.39	1330.76	1330.67	0.10	2	39	50	R	LAWHSAGTFDVK	T	0	-	23.9
		629.40	1256.79	1257.59	-0.79	2	4	14	K	SYPTVSADYQK	A	0	-	46.5
		455.92	909.82	910.42	-0.60	2	53	61	K	TGGPFGTMK	H	0	Oxidation (M)	38.9
		1147.17	2292.33	2292.15	0.18	2	148	170	K	TMGLNDVDIVALSGGHTLGAAHK	E	0	Oxidation (M)	85.9
39	chr3.CM0091.630.nd	658.41	1314.81	1315.63	-0.82	2	27	38	K	AFSTYGEIVDSK	V	0	-	75.6
		753.86	1505.71	1505.64	0.07	2	64	77	K	DAIEGMNQDIDGR	N	0	Oxidation (M)	92.9
		775.88	1549.75	1550.71	-0.96	2	50	63	R	GFGFVTFASEQSMK	D	0	Oxidation (M)	41.2
		550.95	1099.88	1100.56	-0.68	2	78	87	R	NVTVNEAQR	G	0	-	53.5
		818.34	1634.67	1635.67	-0.99	2	116	135	R	YSGGGGGYGGSGGGYGGGR	R	0	-	126.2
		507.41	1012.81	1013.42	-0.61	2	155	163	R	YSSGGSWRD	-	1	-	40.7
40	chr2.CM0210.60.nc	628.48	1254.95	1255.69	-0.73	2	88	99	K	ADLVNNLGTIAR	S	0	-	56.1
		526.95	1051.89	1052.52	-0.63	2	318	326	R	APFDLFDTK	K	0	-	34.6
		501.48	1000.95	1001.54	-0.58	2	548	556	K	DVLGDKVEK	V	1	-	20.6
		661.92	1321.84	1322.60	-0.76	2	180	189	K	EDQLEYLEER	R	0	-	58.4
		794.91	1587.81	1588.73	-0.91	2	457	470	K	EGQSDIYYITGESK	K	0	-	52.8
		637.95	1273.89	1274.64	-0.74	2	34	45	R	ELISNASDALDK	I	0	-	88.1
		663.95	1325.89	1326.66	-0.76	2	253	263	K	EVSHWSLVNK	Q	0	-	59.9
		419.96	837.92	838.41	-0.49	2	48	54	R	FESLTDK	S	0	-	50.7
		445.96	889.90	890.42	-0.51	2	408	414	K	FYEAFSK	N	0	-	25.2
		763.96	1525.91	1526.79	-0.88	2	358	371	K	GIVDSEDPLNISR	E	0	-	77.0
		577.46	1152.90	1153.57	-0.67	2	418	427	K	LGIHEDTQNK	T	0	-	44.4
		604.97	1207.92	1208.62	-0.70	2	317	326	K	RAPFDLFDTK	K	1	-	46.4
		474.97	947.93	948.48	-0.55	2	441	449	K	SGDELTSK	D	0	-	44.0
		574.96	1147.91	1148.57	-0.66	2	472	481	K	SVENSPFLEK	L	0	-	36.9
		840.44	1678.87	1679.84	-0.97	2	72	87	K	TNNSLTLIDSGIGMTK	A	0	Oxidation (M)	39.9
40	LjT02J13.90.nc	628.48	1254.95	1255.69	-0.73	2	88	99	K	ADLVNNLGTIAR	S	0	-	56.1
		661.92	1321.84	1322.60	-0.76	2	180	189	K	EDQLEYLEER	R	0	-	58.4
		637.95	1273.89	1274.64	-0.74	2	34	45	R	ELISNASDALDK	I	0	-	88.1
		419.96	837.92	838.41	-0.49	2	48	54	R	FESLTDK	T	0	-	50.7
		474.97	947.93	948.48	-0.55	2	441	449	K	SGDELTSK	D	0	-	44.0
40	LjSGA_033246.1	637.95	1273.89	1274.64	-0.74	2	34	45	R	ELISNASDALDK	I	0	-	88.1
		419.96	837.92	838.41	-0.49	2	48	54	R	FESLTDK	S	0	-	50.7
40	CM1324.20.nd	637.95	1273.89	1274.64	-0.74	2	108	119	R	ELISNASDALDK	I	0	-	88.1
41	CM1729.90.nc	943.40	1884.79	1885.95	-1.15	2	257	274	R	ITVITQGADPVCVAEDGK	V	0	Propionamide (C)	81.5
		550.96	1099.91	1099.59	0.33	2	33	42	K	LNNAILAEDK	H	0	-	68.1
		1060.37	2118.73	2119.11	-0.37	2	288	308	K	LVDITNGAGDAFVGGLAQLVR	E	0	-	89.0
		869.91	1737.81	1738.85	-1.04	2	229	243	K	VHGWEITDNVEEIALK	I	0	-	56.4
		620.04	1238.06	1238.80	-0.74	2	275	285	K	VTLFPVILLPK	E	0	-	55.8
41	chr1.CM0033.1040.nc	943.40	1884.79	1885.95	-1.15	2	256	273	R	ITVITQGADPVCVAEDGK	V	0	Propionamide (C)	81.5
42	LjSGA_038906.1	607.97	1213.93	1214.64	-0.72	2	164	175	K	DAGVIAGLNVMR	I	0	-	54.2
		615.97	1229.92	1230.64	-0.72	2	164	175	K	DAGVIAGLNVMR	I	0	Oxidation (M)	28.1
		591.43	1180.85	1181.56	-0.70	2	81	91	R	FSDASVQSDVK	L	0	-	80.8
		841.00	1679.99	1679.83	0.17	2	145	159	K	NAVVTVPAYFNDQR	Q	0	-	60.8

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		830.93	1659.84	1660.82	-0.98	2	60	74	K	NQVAMNPINTVFDAK	R	0	-	74.6
		838.92	1675.82	1676.82	-1.00	2	60	74	K	NQVAMNPINTVFDAK	R	0	Oxidation (M)	82.5
		743.94	1485.86	1486.69	-0.84	2	40	52	R	TTPSYVAFTDTER	L	0	-	54.9
		614.45	1226.89	1227.62	-0.73	2	29	39	R	VEIIANDQGNR	T	0	-	68.8
42	LjSGA_076792.1	841.00	1679.99	1679.83	0.17	2	145	159	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
		830.93	1659.84	1660.82	-0.98	2	60	74	K	NQVAMNPINTVFDAK	R	0	-	74.6
		838.92	1675.82	1676.82	-1.00	2	60	74	K	NQVAMNPINTVFDAK	R	0	Oxidation (M)	82.5
		614.45	1226.89	1227.62	-0.73	2	29	39	R	VEIIANDQGNR	T	0	-	68.8
43	chr5.CM0052.430.nd	642.34	1282.66	1282.56	0.10	2	150	159	R	DEV DYKEEEK	H	1	-	35.1
		1105.17	2208.33	2208.15	0.17	2	163	183	K	KLEHLGELGTTAAGAYALHEK	H	1	-	64.0
		819.90	1637.79	1638.71	-0.93	2	16	29	K	NEDRPTDTTETGYNK	T	0	-	48.7
		591.83	1181.64	1181.54	0.10	2	186	195	K	SEKDPENahr	H	1	-	43.0
		850.42	1698.83	1698.70	0.13	2	49	64	K	SSYETSGGGYETGYNK	T	0	-	49.0
		1122.04	2242.06	2241.89	0.17	2	65	86	K	TSSYSTDEPNsggggydsgyNK	T	0	-	58.7
		964.96	1927.91	1927.76	0.15	2	30	47	K	TSYSTDEPSGGDYDSGYK	K	0	-	61.2
		1029.01	2056.01	2055.85	0.16	2	30	48	K	TSYSTDEPSGGDYDSGYK	S	1	-	74.7
		692.97	1383.93	1383.77	0.16	2	266	280	R	AAALNIVPTSTGAAK	A	0	-	62.3
		512.54	1023.06	1023.67	-0.61	2	281	290	K	AVALLVPLTK	G	0	-	65.2
44	chr1.CM0222.50.nc	806.95	1611.88	1612.83	-0.95	2	90	105	K	DSPLDVIaINDTGGVK	Q	0	-	73.2
		778.43	1554.85	1554.67	0.18	2	239	252	K	GTMTTTHSYTGDQR	L	0	-	27.1
		524.26	1569.75	1570.67	-0.92	3	239	252	K	GTMTTTHSYTGDQR	L	0	Oxidation (M)	67.0
		405.98	809.95	810.43	-0.49	2	253	259	R	LLDASHR	D	0	-	23.6
		417.46	832.90	832.46	0.44	2	69	76	K	VAINGFR	I	0	-	32.0
		897.00	1791.98	1793.03	-1.05	2	300	316	R	VPTPNVSVVDLVVQVTK	K	0	-	98.9
		728.47	1454.92	1455.77	-0.86	2	389	401	R	VVDLADIVANNWK	-	0	-	62.7
		607.97	1213.93	1214.64	-0.72	2	92	103	K	DAGVIAGLNVMR	I	0	-	54.2
		615.97	1229.92	1230.64	-0.72	2	92	103	K	DAGVIAGLNVMR	I	0	Oxidation (M)	28.1
		647.45	1292.89	1293.68	-0.79	2	61	72	R	EIAEAYLGSTIK	N	0	-	43.7
45	LjSGA_147202.1	829.96	1657.91	1658.89	-0.97	2	104	119	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	104	120	R	IINEPTAAAIAYGLDKK	A	1	-	77.9
		841.00	1679.99	1679.83	0.17	2	73	87	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
		591.42	1180.82	1181.52	-0.71	2	9	19	R	VSDASVQSDMK	L	0	Oxidation (M)	62.8
46	LjSGA_131247.1	604.49	1206.96	1207.59	-0.63	2	38	49	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		984.44	1966.86	1968.03	-1.17	2	72	89	R	IFNVLGEPIDNLGPVDTR	T	0	-	84.2
		487.97	973.92	974.55	-0.64	2	130	140	K	IGLFGGAGVGK	T	0	-	55.6
		504.03	1006.04	1006.57	-0.53	2	108	116	K	LSIFETGIK	V	0	-	57.2
		638.03	1274.04	1274.71	-0.67	2	2	12	K	MPNIYNALIVK	G	0	-	54.0
		595.51	1189.01	1189.63	-0.63	2	97	107	R	SAPAFIQLDTK	L	0	-	58.9
		735.96	1469.90	1470.85	-0.95	2	141	153	K	TVLIMELINNIaK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	141	153	K	TVLIMELINNIaK	A	0	Oxidation (M)	49.9
		984.44	1966.86	1968.03	-1.17	2	71	88	R	IFNVLGEPIDNLGPVDTR	T	0	-	84.2
46	LjSGA_143694.1	487.97	973.92	974.55	-0.64	2	129	139	K	IGLFGGAGVGK	T	0	-	55.6
		504.03	1006.04	1006.57	-0.53	2	107	115	K	LSIFETGIK	V	0	-	57.2
		638.03	1274.04	1274.71	-0.67	2	1	11	-	MPNIYNALIVK	G	0	-	54.0
		595.51	1189.01	1189.63	-0.63	2	96	106	R	SAPAFIQLDTK	L	0	-	58.9
		735.96	1469.90	1470.85	-0.95	2	140	152	K	TVLIMELINNIaK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	140	152	K	TVLIMELINNIaK	A	0	Oxidation (M)	49.9
		487.97	973.92	974.55	-0.64	2	108	118	K	IGLFGGAGVGK	T	0	-	55.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		504.03	1006.04	1006.57	-0.53	2	86	94	K	LSIFETGIK	V	0	-	57.2
		638.03	1274.04	1274.71	-0.67	2	2	12	K	MPNIYNALIVK	G	0	-	54.0
		595.51	1189.01	1189.63	-0.63	2	75	85	R	SAPAFIQLDTK	L	0	-	58.9
		735.96	1469.90	1470.85	-0.95	2	119	131	K	TVLMELINNIK	A	0	-	70.2
		743.98	1485.95	1486.84	-0.89	2	119	131	K	TVLMELINNIK	A	0	Oxidation (M)	49.9
46	LjSGA_096734.1	604.49	1206.96	1207.59	-0.63	2	53	64	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		984.44	1966.86	1968.03	-1.17	2	87	104	R	IFNVLGEPIDNLGPVDTR	T	0	-	84.2
		504.03	1006.04	1006.57	-0.53	2	123	131	K	LSIFETGIK	V	0	-	57.2
		638.03	1274.04	1274.71	-0.67	2	17	27	K	MPNIYNALIVK	G	0	-	54.0
		595.51	1189.01	1189.63	-0.63	2	112	122	R	SAPAFIQLDTK	L	0	-	58.9
46	LjSGA_077431.1	604.49	1206.96	1207.59	-0.63	2	37	48	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		638.03	1274.04	1274.71	-0.67	2	1	11	-	MPNIYNALIVK	G	0	-	54.0
47	LjSGA_011421.2	488.45	974.88	975.44	-0.56	2	21	30	K	AGFAGDDAPR	A	0	-	73.3
		599.43	1196.84	1197.51	-0.67	2	53	63	K	DSYVGDEAQS	R	0	-	47.4
		581.44	1160.87	1161.51	-0.64	2	199	208	R	GYMFTTSAER	E	0	-	20.5
		589.43	1176.84	1177.51	-0.67	2	199	208	R	GYMFTTSAER	E	0	Oxidation (M)	56.7
		572.83	1143.64	1143.55	0.09	2	42	52	R	HTGVMVGMGQK	D	0	-	59.4
		588.45	1174.88	1175.54	-0.67	2	42	52	R	HTGVMVGMGQK	D	0	2 Oxidation (M)	23.0
		580.45	1158.89	1159.55	-0.66	2	42	52	R	HTGVMVGMGQK	D	0	Oxidation (M)	26.2
		977.41	1952.81	1953.06	-0.24	2	98	115	R	VAPEEHPVLLTEAPLNPK	A	0	-	67.9
48	LjT35D18.30.nc	637.93	1273.84	1273.74	0.10	2	212	222	K	EHVIKPVVPEK	Y	0	-	42.3
		727.43	1452.85	1452.75	0.11	2	238	252	R	FVIGGPHGDAGLTGR	K	0	-	87.5
		648.03	1294.04	1294.79	-0.74	2	328	338	K	IPDKEILQIVK	E	1	-	65.5
		926.99	1851.97	1851.83	0.14	2	75	91	R	NIGFVSDVDGLDADNCK	V	0	Propionamide (C)	74.5
		489.96	977.91	978.47	-0.56	2	364	372	K	TAAYGHFGR	D	0	-	65.8
		571.35	1140.69	1140.60	0.08	2	228	237	K	TIFHLNPSGR	F	0	-	37.5
		498.44	994.87	995.44	-0.57	2	40	47	K	VACETCTK	T	0	2 Propionamide (C)	53.7
48	LjSGA_030253.1	727.43	1452.85	1452.75	0.11	2	170	184	R	FVIGGPHGDAGLTGR	K	0	-	87.5
		489.96	977.91	978.47	-0.56	2	297	305	K	TAAYGHFGR	D	0	-	65.8
48	LjSGA_140570.1	498.44	994.87	995.44	-0.57	2	40	47	K	VACETCTK	T	0	2 Propionamide (C)	53.7
49	chr5.CM0260.320.nc	786.37	1570.73	1571.77	-1.04	2	169	183	K	DGSIPEVESAVIDNK	L	0	-	70.3
		502.93	1003.85	1004.52	-0.67	2	85	93	R	DIVTGPFEK	F	0	-	37.3
		923.45	1844.89	1845.99	-1.10	2	143	159	K	DQTFPPGSSILFTVLPK	G	0	-	49.0
		875.87	1749.72	1750.89	-1.17	2	70	84	K	GKPVDELTESTVQFFR	D	0	-	84.4
		454.95	907.89	908.50	-0.61	2	160	168	K	GSLAISFSK	D	0	-	65.1
		631.35	1260.68	1260.60	0.08	2	122	132	K	HLGIYTDEEGK	A	0	-	78.1
50	LjSGA_077045.1	519.98	1037.94	1038.56	-0.62	2	21	29	R	ALSSQHQIR	V	0	-	60.3
		474.45	946.89	947.44	-0.55	2	68	76	K	AMDDAGLQK	N	0	-	44.2
		482.44	962.86	963.43	-0.57	2	68	76	K	AMDDAGLQK	N	0	Oxidation (M)	22.9
		613.69	1225.37	1225.56	-0.19	2	100	109	K	DYFEGKEPNK	G	1	-	24.2
		662.41	1322.80	1323.58	-0.78	2	269	279	R	EAEFEAEEDKK	V	1	-	74.8
		584.98	1167.94	1168.62	-0.69	2	207	217	K	FDLSGIPPAPR	G	0	-	58.9
		648.43	1294.85	1295.61	-0.76	2	50	59	R	FEELNNDLFR	K	0	-	76.0
		409.49	816.97	817.45	-0.49	2	249	255	K	ITITNEK	G	0	-	33.7
		495.29	988.57	988.48	0.08	2	258	265	R	LSQEEIDR	M	0	-	80.1
		750.46	1498.91	1499.79	-0.88	2	77	90	K	NQIDEIVLVGGSTR	I	0	-	68.4
		1009.48	2016.95	2018.02	-1.07	2	30	47	R	VEIESLFDGVDLSEPLTR	A	0	-	104.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
51	chr2.CM1731.130.nc	749.82	1497.63	1498.62	-0.98	2	226	238	R	ETTENESANEGYR	F	0	-	67.3
		657.43	1312.84	1313.71	-0.87	2	313	323	R	VINTWADIINR	A	0	-	43.5
51	chr4.CM0126.1600.nc	657.43	1312.84	1313.71	-0.87	2	313	323	R	VINTWADIINR	A	0	-	43.5
51	LjSGA_137513.1	657.43	1312.84	1313.71	-0.87	2	37	47	R	VINTWADIINR	A	0	-	43.5
52	LjSGA_007175.1	850.97	1699.93	1700.90	-0.97	2	65	79	R	AVFVDLEPTVIDEVR	T	0	-	90.9
		503.95	1005.88	1006.45	-0.57	2	97	105	K	EDAANNFAR	G	0	-	66.6
		698.93	1395.85	1395.75	0.10	2	85	96	R	QLFHPEQLISGK	E	0	-	26.5
		988.89	1975.77	1976.88	-1.10	2	41	60	K	TVGGGDDAFNTFFSETGAGK	H	0	-	124.5
52	chr4.CM0399.240.nd	850.97	1699.93	1700.90	-0.97	2	66	80	R	AVFVDLEPTVIDEVR	A	0	-	90.9
		503.95	1005.88	1006.45	-0.57	2	98	106	K	EDAANNFAR	G	0	-	66.6
		698.93	1395.85	1395.75	0.10	2	86	97	R	QLFHPEQLISGK	E	0	-	26.5
52	chr1.CM0033.1170.nc	503.95	1005.88	1006.45	-0.57	2	63	71	K	EDAANNFAR	G	0	-	66.6
53	chr1.CM0033.1130.nc	649.47	1296.93	1297.65	-0.72	2	370	381	R	EIDIGVPDEVGR	L	0	-	44.4
		608.96	1823.87	1824.89	-1.02	3	492	506	R	ELQETVQYPVEHPEK	F	0	-	33.5
		484.52	967.02	967.57	-0.55	2	222	229	R	ELVELPLR	H	0	-	41.0
		579.50	1156.99	1157.64	-0.65	2	244	255	K	GILLYGPPGSGK	T	0	-	47.4
		559.95	1117.89	1118.50	-0.60	2	591	603	R	GSSVGDAGGAADR	V	0	-	77.7
		632.97	1263.92	1264.63	-0.71	2	517	528	K	GVLFYGPPEGCK	T	0	Propionamide (C)	39.6
		723.51	1445.01	1445.82	-0.81	2	328	340	R	IVSQLLTLMGGLK	S	0	Oxidation (M)	30.5
		537.97	1073.92	1074.53	-0.61	2	282	291	K	LAGESESNLR	K	0	-	82.3
		696.95	1391.88	1392.65	-0.77	2	202	214	R	LDEVGYDDVGGVR	K	0	-	23.4
		893.46	1784.91	1785.91	-1.00	2	643	657	R	LDQLIYIPLPDEDSR	H	0	-	73.0
		921.47	1840.93	1841.98	-1.05	2	300	316	K	NAPSIIFIDEIDSIAPK	R	0	-	89.7
		431.48	860.94	861.42	-0.48	2	750	757	R	SVSDADIR	K	0	-	32.2
		728.45	1454.90	1455.71	-0.82	2	759	770	K	YQSFATLQQSR	G	0	-	45.2
53	LjSGA_044103.1	649.47	1296.93	1297.65	-0.72	2	115	126	R	EIDIGVPDEVGR	L	0	-	44.4
		608.96	1823.87	1824.89	-1.02	3	237	251	R	ELQETVQYPVEHPEK	F	0	-	33.5
		559.95	1117.89	1118.50	-0.60	2	309	321	R	GSSVGDAGGAADR	V	0	-	77.7
		632.97	1263.92	1264.63	-0.71	2	262	273	K	GVLFYGPPEGCK	T	0	Propionamide (C)	39.6
		723.51	1445.01	1445.82	-0.81	2	73	85	R	IVSQLLTLMGGLK	S	0	Oxidation (M)	30.5
		537.97	1073.92	1074.53	-0.61	2	27	36	K	LAGESESNLR	K	0	-	82.3
		921.47	1840.93	1841.98	-1.05	2	45	61	K	NAPSIIFIDEIDSIAPK	R	0	-	89.7
53	LjSGA_042412.1	484.52	967.02	967.57	-0.55	2	114	121	R	ELVELPLR	H	0	-	41.0
		579.50	1156.99	1157.64	-0.65	2	136	147	K	GILLYGPPGSGK	T	0	-	47.4
		723.51	1445.01	1445.82	-0.81	2	220	232	R	IVSQLLTLMGGLK	S	0	Oxidation (M)	30.5
		537.97	1073.92	1074.53	-0.61	2	174	183	K	LAGESESNLR	K	0	-	82.3
		696.95	1391.88	1392.65	-0.77	2	94	106	R	LDEVGYDDVGGVR	K	0	-	23.4
		921.47	1840.93	1841.98	-1.05	2	192	208	K	NAPSIIFIDEIDSIAPK	R	0	-	89.7
53	chr1.CM0171.740.nd	608.96	1823.87	1824.89	-1.02	3	284	298	R	ELQETVQYPVEHPEK	F	0	-	33.5
		559.95	1117.89	1118.50	-0.60	2	383	395	R	GSSVGDAGGAADR	V	0	-	77.7
		632.97	1263.92	1264.63	-0.71	2	309	320	K	GVLFYGPPEGCK	T	0	Propionamide (C)	39.6
		723.51	1445.01	1445.82	-0.81	2	120	132	R	IVSQLLTLMGGLK	S	0	Oxidation (M)	30.5
		537.97	1073.92	1074.53	-0.61	2	74	83	K	LAGESESNLR	K	0	-	82.3
		431.48	860.94	861.42	-0.48	2	543	550	R	SVSDADIR	K	0	-	32.2
53	chr3.LjT44N20.100.nd	608.96	1823.87	1824.89	-1.02	3	32	46	R	ELQETVQYPVEHPEK	F	0	-	33.5

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		893.46	1784.91	1785.91	-1.00	2	183	197	R	LDQLIYIPLPDEDSR	H	0	-	73.0
54	LjT37C05.70.nd	656.48	1310.94	1311.67	-0.73	2	228	239	R	EIDIGVPDEIGR	L	0	-	37.5
		608.96	1823.87	1824.89	-1.02	3	350	364	R	ELQETVQYPVVEHPEK	F	0	-	33.5
		484.52	967.02	967.57	-0.55	2	80	87	R	ELVELPLR	H	0	-	41.0
		579.50	1156.99	1157.64	-0.65	2	102	113	K	GILLYGPPGSGK	T	0	-	47.4
		559.95	1117.89	1118.50	-0.60	2	449	461	R	GSSVGDAGGAADR	V	0	-	77.7
		632.97	1263.92	1264.63	-0.71	2	375	386	K	GVLFGPPGCGK	T	0	-	39.6
		723.51	1445.01	1445.82	-0.81	2	186	198	R	IVSQLLTLMGK	S	0	Propionamide (C)	30.5
		537.97	1073.92	1074.53	-0.61	2	140	149	K	LAGESESNLR	K	0	Oxidation (M)	82.3
		696.95	1391.88	1392.65	-0.77	2	60	72	R	LDEVGYDDVGVR	K	0	-	23.4
		878.49	1754.96	1755.94	-0.98	2	501	515	R	LDQLIYIPLPDVDSR	H	0	-	60.4
		921.47	1840.93	1841.98	-1.05	2	158	174	K	NAPSIIFIDEISIAPK	R	0	-	89.7
55	chr6.CM1829.160.nc	915.39	1828.76	1829.92	-1.16	2	36	53	R	ETPSVAGIINPGSEGFQK	L	0	-	71.2
		496.43	990.85	991.47	-0.62	2	448	457	R	FGAIDDAAR	Y	0	-	54.3
		486.97	971.92	972.54	-0.62	2	217	224	R	FNNIPQIK	M	0	-	21.0
		643.92	1285.82	1286.63	-0.81	2	599	608	R	HPWEDVLYTK	-	0	-	25.0
		764.37	1526.74	1527.70	-0.96	2	176	189	K	SGGMSNELYNTIAR	V	0	Oxidation (M)	57.8
		657.94	1313.86	1314.69	-0.83	2	579	590	R	SIGLIGHTFDQK	R	0	-	46.1
		750.27	1498.53	1498.79	-0.26	2	106	120	R	VAAIIAEGVPESDTK	E	0	-	25.4
		793.01	1584.00	1583.90	0.10	2	132	148	K	VVIGPATVGGIQAGAFK	I	0	-	101.8
56	chr6.CM0013.290.nc	641.96	1281.91	1282.64	-0.74	2	718	728	R	AAETLVEFFEK	S	0	-	66.5
		539.45	1076.89	1077.51	-0.62	2	312	320	R	ALENEMLSR	I	0	Oxidation (M)	47.9
		642.00	1281.98	1282.72	-0.74	2	600	611	R	ELVNLVVVAGDR	R	0	-	59.8
		672.49	1342.96	1343.74	-0.78	2	173	183	K	ESLQPLLEFLR	L	0	-	44.9
		495.97	989.92	990.51	-0.59	2	231	238	K	FQEIGLER	G	0	-	39.2
		445.95	889.89	890.39	-0.50	2	239	246	R	GWGDTAER	V	0	-	24.0
		427.48	852.95	853.44	-0.49	2	772	778	K	HVTNLDLR	R	0	-	27.6
		429.50	856.98	857.47	-0.49	2	739	746	K	ISQGGQLQR	I	0	-	61.9
		487.49	972.96	973.51	-0.55	2	16	24	R	LDETLAGQK	N	0	-	42.2
		618.98	1235.94	1235.67	0.27	2	62	72	K	LFNGAFGEILR	S	0	-	74.4
		777.46	1552.91	1553.82	-0.91	2	427	440	K	LGVTQCTIAHALEK	T	0	Propionamide (C)	61.8
		700.95	1399.89	1400.71	-0.82	2	338	350	R	LLPDAVGTTTCGQR	L	0	Propionamide (C)	51.6
		529.50	1057.00	1057.61	-0.62	2	25	33	K	NEILTLLSR	I	0	-	45.8
		603.46	1204.90	1204.62	0.28	2	152	162	K	SIGNGVFEFLMR	H	0	-	72.5
		612.98	1223.94	1224.65	-0.71	2	508	518	R	VVHGIDVDFPK	F	0	-	34.0
56	LjSGA_128664.1	777.46	1552.91	1553.82	-0.91	2	35	48	K	LGVTQCTIAHALEK	T	0	Propionamide (C)	61.8
		612.98	1223.94	1224.65	-0.71	2	116	126	R	VVHGIDVDFPK	F	0	-	34.0
57	chr4.CM0194.140.nc	880.38	1758.74	1759.87	-1.13	2	189	205	K	DGIDYAAVTVQLPGGER	V	0	-	61.2
		671.41	1340.80	1341.66	-0.86	2	133	143	K	FCLEPTSFTVK	A	0	Propionamide (C)	26.4
		788.38	1574.74	1575.76	-1.02	2	245	261	R	GASTGYDNAVALPAGGR	G	0	-	105.1
		687.88	1373.75	1374.63	-0.88	2	262	273	R	GDEEELAKENNK	S	1	-	66.5
		1101.12	2200.22	2200.01	0.21	2	104	124	K	GTGTANQCPTIEGGVESFSFK	A	0	Propionamide (C)	44.3
		540.43	1078.85	1079.55	-0.70	2	89	97	R	LTFDEIQSK	T	0	-	52.5
		580.92	1159.83	1160.58	-0.75	2	150	159	K	NAPLEFQNTK	L	0	-	36.6
		618.90	1235.79	1235.65	0.13	2	88	97	K	RLTFDEIQSK	T	1	-	46.1
		482.83	963.65	963.58	0.07	2	206	213	R	VPFLFTIK	Q	0	-	42.6
57	LjSGA_048614.2	671.41	1340.80	1341.66	-0.86	2	105	115	K	FCLEPTSFTVK	A	0	Propionamide (C)	26.4
		1101.12	2200.22	2200.01	0.21	2	76	96	K	GTGTANQCPTIEGGVESFSFK	A	0	Propionamide (C)	44.3
		540.43	1078.85	1079.55	-0.70	2	61	69	R	LTFDEIQSK	T	0	-	52.5

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		580.92	1159.83	1160.58	-0.75	2	122	131	K	NAPLEFQNTK	L	0	-	36.6
		618.90	1235.79	1235.65	0.13	2	60	69	K	RLTFDEIQSK	T	1	-	46.1
57	LjSGA_118676.1	880.38	1758.74	1759.87	-1.13	2	49	65	K	DGIDYAAVTQVLPGGER	V	0	-	61.2
		482.83	963.65	963.58	0.07	2	66	73	R	VPFLFTIK	Q	0	-	42.6
57	LjSGA_066867.1	687.88	1373.75	1374.63	-0.88	2	60	71	R	GDEELAKENNK	S	1	-	66.5
58	LjSGA_031182.1	634.89	1267.77	1268.59	-0.82	2	38	49	R	DITFENTAGSSK	H	0	-	48.5
		654.88	1307.74	1308.59	-0.86	2	203	215	R	EYQNTGPGAGTSK	R	0	-	81.9
		713.45	1424.88	1424.76	0.12	2	129	141	R	VDPNQNTGIVIQK	C	0	-	58.2
59	LjSGA_091355.1	604.49	1206.96	1207.59	-0.63	2	76	87	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		882.49	1762.96	1764.02	-1.06	2	23	39	R	IAQIIGPVLDTVFPFGK	M	0	-	36.9
		984.44	1966.86	1968.03	-1.17	2	110	127	R	IFNVLCEPIDNLGPVDTR	T	0	-	84.2
		487.97	973.92	974.55	-0.64	2	168	178	K	IGLFGGAGVGK	T	0	-	55.6
		857.00	1711.99	1712.88	-0.89	2	2	17	M	IINPTTSDPEVSALEK	K	0	-	49.2
		504.03	1006.04	1006.57	-0.53	2	146	154	K	LSIFETGIK	V	0	-	57.2
		638.03	1274.04	1274.71	-0.67	2	40	50	K	MPNIYNALIVK	G	0	-	54.0
		595.51	1189.01	1189.63	-0.63	2	135	145	R	SAPAFIQLDTK	L	0	-	58.9
59	LjSGA_135941.1	604.49	1206.96	1207.59	-0.63	2	76	87	R	AVAMSATDGLTR	G	0	Oxidation (M)	61.5
		882.49	1762.96	1764.02	-1.06	2	23	39	R	IAQIIGPVLDTVFPFGK	M	0	-	36.9
		857.00	1711.99	1712.88	-0.89	2	2	17	M	IINPTTSDPEVSALEK	K	0	-	49.2
		638.03	1274.04	1274.71	-0.67	2	40	50	K	MPNIYNALIVK	G	0	-	54.0
59	LjSGA_098067.1	882.49	1762.96	1764.02	-1.06	2	23	39	R	IAQIIGPVLDTVFPFGK	M	0	-	36.9
		857.00	1711.99	1712.88	-0.89	2	2	17	M	IINPTTSDPEVSALEK	K	0	-	49.2
		638.03	1274.04	1274.71	-0.67	2	40	50	K	MPNIYNALIVK	G	0	-	54.0
60	LjSGA_052805.1	829.96	1657.91	1658.89	-0.97	2	130	145	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	130	146	R	IINEPTAAAIAYGLDKK	A	1	-	77.9
		639.44	1276.87	1277.62	-0.75	2	197	206	R	MVNHVFQEFK	R	0	-	74.7
		647.88	1293.74	1293.62	0.12	2	197	206	R	MVNHVFQEFK	R	0	Oxidation (M)	31.8
		477.42	952.82	952.39	0.43	2	443	450	R	MVSNMCPK	R	0	Oxidation (M)	26.0
		841.00	1679.99	1679.83	0.17	2	99	113	K	NAVVTVPAYFNDSSQR	Q	0	-	60.8
61	chr2.CM0002.140.nc	552.49	1102.96	1103.60	-0.64	2	928	937	R	DPTLAVVAYR	R	0	-	55.9
		777.47	1552.93	1553.80	-0.87	2	393	407	K	EAAELAAESPQGILR	T	0	-	77.3
		717.99	1433.97	1434.74	-0.77	2	1133	1145	R	EGLVSDAIESFIR	A	0	-	40.1
		560.48	1118.94	1119.57	-0.63	2	382	390	R	FHELFAQTK	Y	0	-	25.5
		719.44	1436.86	1437.67	-0.81	2	190	201	K	GNMQLFSVDQQR	S	0	Oxidation (M)	43.2
		607.66	1819.97	1821.01	-1.04	3	243	259	K	LHVIELGAQPGKPSFTK	K	0	-	31.9
		642.96	1283.90	1284.62	-0.72	2	1220	1230	R	LYDEALYEAAK	I	0	-	51.8
		531.47	1060.93	1061.53	-0.60	2	1251	1260	K	QFQGAVDAAR	K	0	-	47.0
		630.49	1258.97	1259.70	-0.73	2	927	937	K	RDPITLAVVAYR	R	1	-	44.2
		752.47	1502.93	1503.78	-0.85	2	152	164	R	TANLANNQIINRYR	S	0	-	70.5
		494.49	986.96	987.52	-0.56	2	483	491	K	TVDNDLALK	I	0	-	26.2
		635.97	1269.93	1270.64	-0.72	2	1184	1194	K	VDESLIYAYAK	I	0	-	45.5
		680.46	1358.90	1359.67	-0.76	2	1117	1128	R	VEEDAVWSQVAK	A	0	-	57.7
		542.48	1082.95	1083.56	-0.61	2	1413	1421	K	VGNVELYYK	A	0	-	52.2
		553.47	1104.92	1105.54	-0.62	2	974	982	K	VLTPDNEYR	R	0	-	47.8
		845.46	1688.90	1689.86	-0.96	2	217	232	K	VPGNENPSTLISFSTK	T	0	-	61.9
		499.98	997.94	998.51	-0.57	2	814	821	R	YIEGYVQK	V	0	-	21.5

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
61	LjSGA_147823.1	552.49	1102.96	1103.60	-0.64	2	85	94	R	DPTLAVVAYR	R	0	-	55.9
		630.49	1258.97	1259.70	-0.73	2	84	94	K	RDPTLAVVAYR	R	1	-	44.2
61	LjSGA_067209.1	635.97	1269.93	1270.64	-0.72	2	223	233	K	VDSELIYAYAK	I	0	-	45.5
62	LjSGA_000862.1	601.99	1201.97	1202.65	-0.68	2	7	17	R	AAELTTLESR	I	0	-	72.9
		513.53	1025.04	1025.59	-0.54	2	154	163	K	AVDSLVPIGR	G	0	-	56.0
		442.49	882.96	883.41	-0.46	2	121	128	R	GALSDHER	R	0	-	55.8
		650.53	1299.05	1299.74	-0.69	2	178	189	K	TAIAIDTILNQK	Q	0	-	94.6
		522.02	1042.02	1042.57	-0.55	2	93	103	R	TGSIVDVPAGK	A	0	-	83.0
		605.52	1209.03	1209.67	-0.64	2	109	120	R	VVDALGVPIDGR	G	0	-	71.1
		486.52	971.03	971.54	-0.51	2	33	42	R	VVSGDGIAR	V	0	-	52.3
63	chr3.CM0112.180.nd	799.40	1596.79	1596.82	-0.03	2	66	81	K	AIEVTGPNQAVQGTR	R	0	-	89.8
		788.34	1574.67	1575.64	-0.98	2	92	111	R	GGGGYGGGGYGGGGYGGGR	G	0	-	44.3
		400.78	799.54	800.40	-0.86	2	82	91	R	RGGAGGGGR	G	1	-	23.6
64	chr2.CM0323.140.nc	880.38	1758.74	1759.87	-1.13	2	191	207	K	DGIDYAAVTVQLPGER	V	0	-	61.2
		788.38	1574.74	1575.76	-1.02	2	247	263	R	GASTGYDNAVALPAGGR	G	0	-	105.1
		687.88	1373.75	1374.63	-0.88	2	264	275	R	GDEELAKENNK	S	1	-	66.5
		540.43	1078.85	1079.55	-0.70	2	91	99	R	LTFDEIQSK	T	0	-	52.5
		618.90	1235.79	1235.65	0.13	2	90	99	K	RLTFDEIQSK	T	1	-	46.1
		475.48	948.95	949.56	-0.62	2	208	215	R	VPFLFTVK	Q	0	-	43.5
65	chr1.CM0122.480.nc	544.99	1087.97	1088.62	-0.66	2	118	127	R	DAVLLVFANK	Q	0	-	64.7
		543.98	1085.95	1086.61	-0.66	2	20	30	R	ILMVGLDAAGK	T	0	-	72.8
		551.98	1101.94	1102.61	-0.66	2	20	30	R	ILMVGLDAAGK	T	0	Oxidation (M)	38.3
		509.93	1017.85	1018.48	-0.62	2	110	117	R	MLNEDELRL	D	0	-	62.0
		517.93	1033.84	1034.47	-0.63	2	110	117	R	MLNEDELRL	D	0	Oxidation (M)	32.3
		782.91	1563.81	1564.75	-0.94	2	60	73	K	NISFTVWDVGGQDK	I	0	-	43.0
		815.40	1628.78	1629.77	-0.98	2	128	142	K	QDLPNAMNAAEITDK	L	0	-	100.1
		823.39	1644.76	1645.76	-1.00	2	128	142	K	QDLPNAMNAAEITDK	L	0	Oxidation (M)	65.5
65	chr2.CM0008.210.nc	544.99	1087.97	1088.62	-0.66	2	118	127	R	DAVLLVFANK	Q	0	-	64.7
		543.98	1085.95	1086.61	-0.66	2	20	30	R	ILMVGLDAAGK	T	0	-	72.8
		551.98	1101.94	1102.61	-0.66	2	20	30	R	ILMVGLDAAGK	T	0	Oxidation (M)	38.3
		509.93	1017.85	1018.48	-0.62	2	110	117	R	MLNEDELRL	D	0	-	62.0
		517.93	1033.84	1034.47	-0.63	2	110	117	R	MLNEDELRL	D	0	Oxidation (M)	32.3
		782.91	1563.81	1564.75	-0.94	2	60	73	K	NISFTVWDVGGQDK	I	0	-	43.0
		815.40	1628.78	1629.77	-0.98	2	128	142	K	QDLPNAMNAAEITDK	L	0	-	100.1
		823.39	1644.76	1645.76	-1.00	2	128	142	K	QDLPNAMNAAEITDK	L	0	Oxidation (M)	65.5
65	LjSGA_037475.1	544.99	1087.97	1088.62	-0.66	2	45	54	R	DAVLLVFANK	Q	0	-	64.7
		509.93	1017.85	1018.48	-0.62	2	37	44	R	MLNEDELRL	D	0	-	62.0
		517.93	1033.84	1034.47	-0.63	2	37	44	R	MLNEDELRL	D	0	Oxidation (M)	32.3
		815.40	1628.78	1629.77	-0.98	2	55	69	K	QDLPNAMNAAEITDK	L	0	-	100.1
		823.39	1644.76	1645.76	-1.00	2	55	69	K	QDLPNAMNAAEITDK	L	0	Oxidation (M)	65.5
65	chr2.CM0250.220.nd	543.98	1085.95	1086.61	-0.66	2	20	30	R	ILMVGLDAAGK	T	0	-	72.8
		551.98	1101.94	1102.61	-0.66	2	20	30	R	ILMVGLDAAGK	T	0	Oxidation (M)	38.3
65	LjSGA_070137.1	782.91	1563.81	1564.75	-0.94	2	10	23	K	NISFTVWDVGGQDK	I	0	-	43.0
66	LjT05F15.160.nd	595.93	1189.84	1190.63	-0.79	2	348	360	R	AVAGAGVLAGYDK	L	0	-	78.7
		422.96	843.90	843.46	0.44	2	140	147	R	GNTANVIR	Y	0	-	45.3

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		672.92	1343.82	1343.71	0.11	2	100	110	K	LLIQNQDEMIK	A	0	-	22.2
		680.41	1358.80	1359.71	-0.90	2	100	110	K	LLIQNQDEMIK	A	0	Oxidation (M)	57.9
		558.37	1114.73	1115.47	-0.74	2	308	317	R	MMMTSGEAVK	Y	0	2 Oxidation (M)	39.8
		566.36	1130.71	1131.46	-0.75	2	308	317	R	MMMTSGEAVK	Y	0	3 Oxidation (M)	38.8
		414.46	826.90	827.45	-0.55	2	90	97	K	TAAAPIER	V	0	-	52.5
		611.42	1220.83	1221.64	-0.81	2	233	244	K	TLASDGVAGLYR	G	0	-	67.7
		723.40	1444.78	1445.73	-0.95	2	148	159	R	YFPTQALNFAFK	D	0	-	50.6
66	LjSGA_104961.1	595.93	1189.84	1190.63	-0.79	2	71	83	R	AVAGAGVLAGYDK	L	0	-	78.7
		558.37	1114.73	1115.47	-0.74	2	31	40	R	MMMTSGEAVK	Y	0	2 Oxidation (M)	39.8
		566.36	1130.71	1131.46	-0.75	2	31	40	R	MMMTSGEAVK	Y	0	3 Oxidation (M)	38.8
67	chr5.CM0328.790.nd	679.93	1357.84	1358.70	-0.86	2	9	22	R	GILAI DESNATAGK	R	0	-	55.6
		702.44	1402.87	1402.71	0.17	2	24	36	R	LASIGLDNTETNR	Q	0	-	86.7
		1024.86	3071.55	3072.58	-1.03	3	152	179	R	YAAISQDNLVPIVEPILLDGDHPPIER	T	0	-	28.8
		664.36	1326.71	1326.56	0.16	2	319	330	R	YSAEGESEEAQK	G	0	-	87.9
68	chr3.CM0160.510.nc	595.93	1189.84	1190.63	-0.79	2	339	351	R	AVAGAGVLAGYDK	L	0	-	78.7
		422.96	843.90	843.46	0.44	2	132	139	R	GNTANVIR	Y	0	-	45.3
		672.92	1343.82	1343.71	0.11	2	92	102	K	LLIQNQDEMIK	S	0	-	22.2
		680.41	1358.80	1359.71	-0.90	2	92	102	K	LLIQNQDEMIK	S	0	Oxidation (M)	57.9
		558.37	1114.73	1115.47	-0.74	2	299	308	R	MMMTSGEAVK	Y	0	2 Oxidation (M)	39.8
		566.36	1130.71	1131.46	-0.75	2	299	308	R	MMMTSGEAVK	Y	0	3 Oxidation (M)	38.8
		414.46	826.90	827.45	-0.55	2	82	89	K	TAAAPIER	I	0	-	52.5
		646.92	1291.82	1292.67	-0.85	2	224	235	K	TIQSDGIAGLYR	G	0	-	57.7
		723.40	1444.78	1445.73	-0.95	2	140	151	R	YFPTQALNFAFK	D	0	-	50.6
69	chr4.CM0006.600.nc	640.98	1279.94	1280.67	-0.73	2	717	727	R	AADLLVEFFEK	V	0	-	52.8
		642.00	1281.98	1282.72	-0.74	2	599	610	R	ELVNLVVVAGDR	R	0	-	59.8
		676.99	1351.96	1352.75	-0.78	2	172	182	K	ESLHPLLEFLR	L	0	-	41.2
		495.97	989.92	990.51	-0.59	2	230	237	K	FQEIGLER	G	0	-	39.2
		445.95	889.89	890.39	-0.50	2	238	245	R	GWGDTAER	V	0	-	24.0
		516.47	1030.93	1031.52	-0.60	2	15	23	R	LDET LATNR	N	0	-	51.4
		777.46	1552.91	1553.82	-0.91	2	426	439	K	LGVTQCTIAHALEK	T	0	Propionamide (C)	61.8
		700.95	1399.89	1400.71	-0.82	2	337	349	R	LLPDAVGTTTCGQR	L	0	Propionamide (C)	51.6
		588.97	1175.93	1176.61	-0.69	2	61	71	K	LTDGAFGEVLR	S	0	-	76.8
		603.46	1204.90	1204.62	0.28	2	151	161	K	SIGNGVFEFLNR	H	0	-	72.5
		439.47	876.93	877.43	-0.50	2	190	196	K	TLMLNDR	I	0	Oxidation (M)	42.5
		612.98	1223.94	1224.65	-0.71	2	507	517	R	VVHGIDVDFPK	F	0	-	34.0
69	LjT48H14.80.nd	603.46	1204.90	1204.62	0.28	2	35	45	K	SIGNGVFEFLNR	H	0	-	72.5
		439.47	876.93	877.43	-0.50	2	74	80	K	TLMLNDR	I	0	Oxidation (M)	42.5
69	LjSGA_038745.1	495.97	989.92	990.51	-0.59	2	41	48	R	FQEIGLER	G	0	-	39.2
		445.95	889.89	890.39	-0.50	2	49	56	R	GWGDTAER	V	0	-	24.0
		439.47	876.93	877.43	-0.50	2	1	7	-	TLMLNDR	I	0	Oxidation (M)	42.5
70	chr2.CM0191.170.nc	491.80	981.58	981.52	0.06	2	96	103	R	ELEVIHSR	W	0	-	58.3
		491.95	981.89	982.49	-0.60	2	125	132	K	FGEAVWFK	A	0	-	52.3
		417.95	1250.83	1251.67	-0.84	3	94	103	K	NRELEVIHSR	W	1	-	55.5
		415.49	828.96	828.45	0.51	2	19	25	K	QQNELLR	K	0	-	45.4
		534.25	1599.74	1600.80	-1.06	3	43	56	K	SAPQSIWYGPDPRPK	Y	0	-	61.2
71	chr2.CM0056.380.nc	614.44	1226.87	1227.63	-0.77	2	124	135	K	ASTDIPDPSPVK	D	0	-	43.5
		722.96	1443.90	1444.78	-0.87	2	102	116	K	GTISVIAVGEGSEVK	W	0	-	59.8

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		657.46	1312.90	1313.70	-0.80	2	57	68	R	HITYAEGSPLVK	S	0	-	65.6
		502.44	1002.87	1003.48	-0.61	2	74	82	K	IDAADDEKK	T	1	-	43.7
		783.91	1565.81	1566.76	-0.94	2	141	153	K	NFLEVDEVVLQQA	-	0	-	31.8
		530.45	1058.89	1059.54	-0.65	2	41	50	K	SIEILEGDGK	A	0	-	68.8
		930.92	1859.83	1860.95	-1.12	2	83	98	K	TVSYAVIDGELLQYYK	K	0	-	87.0
72	chr2.CM0304.350.nc	810.91	1619.81	1620.75	-0.94	2	29	42	K	EELANIGDVFEEEK	K	0	-	52.8
		640.00	1916.98	1918.11	-1.13	3	313	329	K	IILKPLPELVTETEPAR	F	0	-	67.6
		755.43	1508.85	1509.74	-0.88	2	98	111	K	SAGAEFFSLPVEEK	E	0	-	72.2
		700.97	1399.93	1400.75	-0.82	2	9	22	R	VESLSGSGIQSIPK	E	0	-	65.1
		583.50	1164.99	1165.67	-0.68	2	44	54	K	VGPQVPTIDLK	D	0	-	45.9
		821.40	1640.79	1641.74	-0.95	2	114	129	K	YANDQAAGNVQYGSK	L	0	-	95.5
73	LjSGA_000588.1	513.53	1025.04	1025.59	-0.54	2	79	88	K	AVDSLVPIGR	G	0	-	56.0
		849.00	1695.98	1697.00	-1.02	2	395	409	R	DILSTIKPELLQSLK	G	0	-	65.9
		442.49	882.96	883.41	-0.46	2	46	53	R	GALSDHER	R	0	-	55.8
		642.02	1282.02	1282.69	-0.68	2	358	368	K	QPQYAPLPIEK	Q	0	-	37.9
		650.53	1299.05	1299.74	-0.69	2	103	114	K	TAIAIDTILNQK	Q	0	-	94.6
		605.52	1209.03	1209.67	-0.64	2	34	45	R	VVDALGVPIDGR	G	0	-	71.1
73	LjSGA_000590.1	849.00	1695.98	1697.00	-1.02	2	137	151	R	DILSTIKPELLQSLK	G	0	-	65.9
		642.02	1282.02	1282.69	-0.68	2	100	110	K	QPQYAPLPIEK	Q	0	-	37.9
74	LjSGA_057408.1	577.99	1153.96	1154.64	-0.68	2	142	153	K	DAGVIAGLNVAR	I	0	-	66.0
		829.96	1657.91	1658.89	-0.97	2	154	169	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	154	170	R	IINEPTAAAIAYGLDKK	G	1	-	77.9
		465.46	928.91	929.55	-0.65	2	86	93	R	ISLLDTLR	G	0	-	25.0
75	chr4.LjT30K03.110.nc	600.45	1198.89	1199.65	-0.77	2	134	144	K	APVSLPLDNFK	S	0	-	61.0
		550.94	1099.87	1100.57	-0.70	2	45	55	K	EDVDLAVAAAK	A	0	-	86.5
		645.43	1288.85	1289.67	-0.82	2	392	402	K	EEVFGPVLCKV	T	0	Propionamide (C)	64.0
		563.43	1124.85	1125.57	-0.72	2	234	245	K	IAFTGSSATGSK	V	0	-	61.5
		594.90	1187.79	1188.54	-0.75	2	323	332	K	ISDPLEEGCR	L	0	Propionamide (C)	41.3
		652.92	1303.83	1304.66	-0.83	2	333	344	R	LGPVVSEGQYEK	I	0	-	48.0
		504.98	1007.95	1008.60	-0.64	2	300	308	R	LIVHESIAK	E	0	-	33.5
		877.03	1752.04	1751.92	0.12	2	354	370	K	SEGATILTGSRPEHLK	K	0	-	24.9
		744.92	1487.82	1488.77	-0.95	2	265	277	K	SPLIVFEDVDLDK	A	0	-	63.8
		956.61	1911.21	1911.09	0.12	2	246	264	K	VMTAAQLVKPVSLELGK	S	0	-	46.3
76	LjSGA_014613.2	518.48	1034.95	1035.56	-0.61	2	5	14	K	FAVGTTETIAK	K	0	-	48.7
		786.96	1571.91	1572.84	-0.93	2	23	39	K	GVTTIIGGSDSVAAVEK	V	0	-	79.4
76	LjSGA_047542.1	786.96	1571.91	1572.84	-0.93	2	50	66	K	GVTTIIGGSDSVAAVEK	V	0	-	79.4
77	chr1.CM0032.460.nc	740.95	1479.88	1480.90	-1.02	2	88	102	R	ASITPGTVLILLAGR	F	0	-	71.8
		477.42	952.82	953.45	-0.63	2	65	72	K	FYPADDVK	K	0	-	26.1
		490.96	979.92	980.57	-0.65	2	53	61	K	LKPEAPAQK	A	0	-	35.1
		734.96	1467.90	1468.87	-0.97	2	113	126	R	QLPSGLLLVTGPFK	I	0	-	53.9
		885.91	1769.80	1770.96	-1.17	2	198	214	K	TVDSALLTAIESVPDLK	S	0	-	88.9
78	chr5.CM0077.110.nd	761.40	1520.79	1521.69	-0.90	2	63	76	K	ADLAEEGSFDEAIR	G	0	-	64.4
		723.96	1445.90	1444.78	1.11	2	280	291	K	FKDIPDELDIK	F	1	-	25.1
		517.98	1033.95	1034.58	-0.62	2	47	55	K	HLLELPDAK	T	0	-	39.9
		660.42	1318.82	1318.64	0.19	2	328	340	K	TAETPATNGTTQK	-	0	-	73.1
		547.45	1092.89	1093.54	-0.65	2	271	279	K	YPEFNVPTK	F	0	-	25.4

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
79	LjT22I05.20.nd	785.46	1568.91	1569.84	-0.93	2	24	38	R	APEDPILGVTVAFNK	D	0	-	23.6
		739.46	1476.91	1477.78	-0.87	2	81	93	K	EYLPVGLADFNK	L	0	-	64.8
		753.47	1504.92	1505.79	-0.87	2	112	125	R	ITTVQCLSGTGSRLR	V	0	Propionamide (C)	37.8
		765.45	1528.89	1529.78	-0.89	2	98	111	K	LIFGADSPAIQENR	I	0	-	97.2
		727.49	1452.97	1452.83	0.14	2	54	66	R	TEEGKPLVLNVVR	K	0	-	38.0
		524.32	1569.94	1570.86	-0.92	3	402	416	K	TVPHLADAIHAAVTR	A	0	-	54.2
79	LjSGA_110862.1	739.46	1476.91	1477.78	-0.87	2	48	60	K	EYLPVGLADFNK	L	0	-	64.8
		727.49	1452.97	1452.83	0.14	2	21	33	R	TEEGKPLVLNVVR	K	0	-	38.0
80	chr3.CM0282.260.nc	645.50	1288.98	1289.70	-0.72	2	426	437	R	AIADGSLLDFLR	Q	0	-	64.8
		628.96	1883.85	1884.91	-1.06	3	199	214	K	DITPDDKQELDEALQR	E	1	-	41.6
		581.48	1160.95	1161.59	-0.64	2	875	884	K	DLLEGDPYLK	Q	0	-	21.7
		741.96	2222.87	2223.18	-0.31	3	644	665	R	GGGPTHLAISQPPDTIHGSLR	V	0	-	25.1
		656.00	1309.98	1310.72	-0.74	2	564	576	K	LADLETAPAALAR	L	0	-	64.7
		574.48	1146.95	1147.59	-0.64	2	740	749	R	LATPELEYGR	M	0	-	56.0
		407.99	813.97	814.43	-0.46	2	264	270	K	NIGINER	V	0	-	20.4
		664.94	1327.86	1328.59	-0.73	2	591	602	K	QEVMIIGYSDSGK	D	0	Oxidation (M)	44.7
		603.99	1205.97	1205.68	0.29	2	438	448	R	QVSTFGLSLVR	L	0	-	49.4
		580.94	1159.86	1160.51	-0.65	2	228	237	R	TAPTPQDEMR	A	0	Oxidation (M)	42.1
80	LjSGA_016084.1	741.96	2222.87	2223.18	-0.31	3	427	448	R	GGGPTHLAISQPPDTIHGSLR	V	0	-	25.1
		407.99	813.97	814.43	-0.46	2	49	55	K	NIGINER	V	0	-	20.4
		664.94	1327.86	1328.59	-0.73	2	374	385	K	QEVMIIGYSDSGK	D	0	Oxidation (M)	44.7
		603.99	1205.97	1205.68	0.29	2	221	231	R	QVSTFGLSLVR	L	0	-	49.4
81	LjSGA_045033.1	919.88	1837.74	1838.93	-1.19	2	99	113	K	LIFELDNLNLTYDEK	D	0	-	77.1
		452.00	1352.96	1353.80	-0.83	3	66	77	K	RVPELTKPSSLK	T	1	-	38.1
		599.49	1196.97	1197.70	-0.73	2	67	77	R	VPELTKPSSLK	T	0	-	49.9
82	chr1.CM0122.340.nc	644.93	1287.85	1287.76	0.10	2	213	223	K	EHVIKPIVEK	Y	0	-	33.8
		727.43	1452.85	1452.75	0.11	2	239	253	R	FVIGGPHGDAGLTGR	K	0	-	87.5
		489.96	977.91	978.47	-0.56	2	365	373	K	TAAYGHFGR	D	0	-	65.8
		571.35	1140.69	1140.60	0.08	2	229	238	K	TIFHLNPSGR	F	0	-	37.5
		498.44	994.87	995.44	-0.57	2	41	48	K	VACETCTK	T	0	2 Propionamide (C)	53.7
83	LjT41B11.100.nd	607.97	1213.93	1214.64	-0.72	2	138	149	K	DAGVIAGLNVMR	I	0	-	54.2
		615.97	1229.92	1230.64	-0.72	2	138	149	K	DAGVIAGLNVMR	I	0	Oxidation (M)	28.1
		829.96	1657.91	1658.89	-0.97	2	150	165	R	IINEPTAAAIAYGLDK	I	0	-	94.3
		639.44	1276.87	1277.62	-0.75	2	217	226	R	MVNHVQVEFK	R	0	-	74.7
		647.88	1293.74	1293.62	0.12	2	217	226	R	MVNHVQVEFK	R	0	Oxidation (M)	31.8
		687.71	1373.40	1373.60	-0.20	2	520	530	K	NALENYAYNMR	N	0	Oxidation (M)	39.4
		451.50	900.99	901.52	-0.53	2	397	404	R	NTTIPTKK	E	1	-	46.1
		515.48	1028.95	1029.56	-0.61	2	430	438	R	TRDNNLLGK	F	1	-	45.2
84	LjSGA_009509.2	421.47	840.93	841.47	-0.53	2	85	91	K	ALKEPER	D	1	-	31.2
		892.89	1783.76	1784.83	-1.07	2	151	166	K	DLQQEVTGDGVEVPLE	-	0	-	62.4
		441.00	879.98	880.54	-0.56	2	32	40	K	IGPLGLSPK	K	0	-	59.2
		627.00	1251.99	1252.78	-0.78	2	72	84	K	VSVVPSAALVIK	A	0	-	51.3
		671.96	1341.90	1342.71	-0.81	2	17	31	R	VTGGEVGAASSLAPK	I	0	-	87.7
85	LjSGA_027059.1	657.92	1313.83	1314.70	-0.87	2	133	143	R	DLFHLLPDAFK	G	0	-	52.4
		477.42	952.82	953.42	-0.60	2	184	192	K	GSSSFNEAR	G	0	-	65.0
		541.42	1080.83	1081.52	-0.68	2	183	192	R	KGSSSFNEAR	G	1	-	87.4
		534.95	1067.89	1068.55	-0.66	2	106	114	K	LDFDTAIFK	K	0	-	51.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		678.93	1355.84	1356.70	-0.86	2	118	129	R	VNLAGHDEYIVK	G	0	-	66.0
86	LjSGA_066441.1	829.96	1657.91	1658.89	-0.97	2	131	146	R	IINEPTAAAIAYGLDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	131	147	R	IINEPTAAAIAYGLDKK	I	1	-	77.9
		639.87	1277.73	1278.61	-0.88	2	198	207	R	MVNHFVEEFK	R	0	-	20.6
		647.88	1293.74	1294.60	-0.86	2	198	207	R	MVNHFVEEFK	R	0	Oxidation (M)	24.9
86	LjSGA_077967.1	829.96	1657.91	1658.89	-0.97	2	110	125	R	IINEPTAAAIAYGLDK	R	0	-	94.3
		639.87	1277.73	1278.61	-0.88	2	177	186	R	MVNHFVEEFK	R	0	-	20.6
		647.88	1293.74	1294.60	-0.86	2	177	186	R	MVNHFVEEFK	R	0	Oxidation (M)	24.9
87	chr1.LjT36P09.130.nd	829.96	1657.91	1658.89	-0.97	2	178	193	R	IINEPTAAAIAYGIDK	K	0	-	94.3
		596.31	1785.91	1786.98	-1.07	3	178	194	R	IINEPTAAAIAYGIDKK	A	1	-	77.9
88	chr3.CM0115.330.nc	526.94	1051.86	1052.47	-0.60	2	751	759	K	DAEFDELSK	N	0	-	40.2
		933.40	1864.80	1865.88	-1.08	2	799	815	R	DGGDLWTTDTQALQAFK	K	0	-	71.9
		567.46	1132.90	1133.55	-0.65	2	566	575	R	DTMNINALAR	N	0	Oxidation (M)	51.9
		644.93	1287.85	1288.60	-0.75	2	788	798	R	HASDELYLGER	D	0	-	66.0
		596.49	1190.97	1191.68	-0.70	2	549	558	R	HLSVVHPIYK	L	0	-	27.8
		566.49	1130.96	1131.61	-0.66	2	72	83	K	LISATVADASGK	G	0	-	80.2
		457.52	913.03	913.56	-0.53	2	337	344	K	LSPILPK	E	0	-	29.6
		742.48	1482.95	1483.80	-0.86	2	89	101	K	QTWVEGVITNLPK	L	0	-	51.0
		585.00	1167.98	1168.66	-0.68	2	291	301	K	SATQNVIPALR	S	0	-	41.0
		593.48	1184.94	1185.63	-0.69	2	281	290	K	SSDFLTILK	S	0	-	48.3
88	chr3.LjT02L14.10.nd	644.93	1287.85	1288.60	-0.75	2	779	789	R	HASDELYLGER	D	0	-	66.0
88	LjT30L14.30.nd	567.46	1132.90	1133.55	-0.65	2	34	43	R	DTMNINALAR	N	0	Oxidation (M)	51.9
89	LjSGA_020408.2	837.88	1673.74	1673.74	0.00	2	223	238	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
		829.96	1657.91	1658.89	-0.97	2	172	187	R	IINEPTAAAIAYGLDK	R	0	-	94.3
		639.44	1276.87	1277.66	-0.79	2	239	248	R	MVNHFVKEFK	R	1	-	68.0
		647.88	1293.74	1293.65	0.09	2	239	248	R	MVNHFVKEFK	R	1	Oxidation (M)	31.8
89	chr1.LjT14I13.240.nd	837.88	1673.74	1673.74	0.00	2	229	244	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
		829.96	1657.91	1658.89	-0.97	2	178	193	R	IINEPTAAAIAYGLDK	R	0	-	94.3
89	LjSGA_097163.1	837.88	1673.74	1673.74	0.00	2	63	78	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
89	chr2.CM0120.590.nd	837.88	1673.74	1673.74	0.00	2	230	245	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
90	chr3.CM0106.290.nc	824.95	1647.88	1648.87	-0.99	2	63	76	K	DLVSLTYIIVDVR	A	0	-	89.1
91	chr1.CM0023.30.nc	533.51	1065.00	1065.62	-0.62	2	377	386	K	DLALILHGSK	L	0	-	42.2
		496.95	991.88	992.45	-0.57	2	135	142	R	HAFGDQYR	A	0	-	34.2
		711.38	1420.75	1420.62	0.13	2	193	205	R	SFAEASMATAYEK	K	0	Oxidation (M)	63.1
		678.40	1354.79	1354.68	0.10	2	304	316	K	TIEAEAAHGTVTR	H	0	-	65.5
		838.78	1675.54	1675.75	-0.21	2	8	22	K	VANPIVEMDGDEMTR	V	0	-	44.5
92	chr4.CM0337.850.nd	688.91	1375.81	1376.64	-0.83	2	391	402	K	DVCTSANQELAR	E	0	Propionamide (C)	58.6
		713.92	1425.84	1426.69	-0.86	2	180	193	R	GQETPGEDPVLASK	Y	0	-	72.4
		628.50	1254.98	1255.72	-0.75	2	78	90	K	IGNLVSGAAIVSR	L	0	-	71.9
		511.94	1021.87	1022.48	-0.62	2	372	380	R	LGFFDGDPR	K	0	-	50.3
		583.90	1165.79	1165.66	0.13	2	414	424	K	NRPGSLPLNAK	A	0	-	24.7
93	chr3.CM0091.670.nd	789.38	1576.74	1577.72	-0.98	2	48	61	R	GFQFVFTTSEEAMR	S	0	-	52.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		797.37	1592.73	1593.71	-0.98	2	48	61	R	GFGFVFTTSEEAMR	S	0	Oxidation (M)	43.4
		557.94	1113.86	1114.57	-0.72	2	76	85	R	NITVNEAQR	G	0	-	43.8
		739.86	1477.71	1477.65	0.07	2	62	75	R	SAIEGMNGNELDGR	N	0	Oxidation (M)	79.2
94	chr3.LjT02L14.80.nd	468.00	933.98	934.51	-0.53	2	130	138	R	ALGDYLGVK	V	0	-	37.2
		774.97	1547.93	1548.82	-0.89	2	201	213	K	DQIYDIFQLPGK	I	0	-	68.2
		479.49	956.97	957.51	-0.55	2	119	126	R	ELAAQIEK	V	0	-	30.1
		700.97	1399.93	1400.73	-0.79	2	77	90	K	GLDVIQQAQSGTGK	T	0	-	68.8
		785.92	1569.83	1570.70	-0.87	2	185	197	K	MFVLDEADEMSLR	G	0	Oxidation (M)	58.2
		522.00	1041.98	1042.58	-0.59	2	176	184	R	QSLRPDSIK	M	0	-	23.8
		587.37	1172.72	1172.64	0.08	2	245	254	K	RDELTLEGIK	Q	1	-	50.5
		993.49	1984.97	1984.83	0.14	2	301	318	R	SNDHTVSATHGMDQNTR	D	0	-	37.3
		578.83	1155.65	1155.58	0.07	2	139	149	K	VHACVGCTSVR	E	0	Propionamide (C)	33.0
		557.53	1113.04	1113.68	-0.64	2	332	341	R	VLITTDLLAR	G	0	-	62.5
94	LjSGA_011343.1	468.00	933.98	934.51	-0.53	2	21	29	R	ALGDYLGVK	V	0	-	37.2
		774.97	1547.93	1548.82	-0.89	2	92	104	K	DQIYDIFQLPGK	I	0	-	68.2
		479.49	956.97	957.51	-0.55	2	10	17	R	ELAAQIEK	V	0	-	30.1
		785.92	1569.83	1570.70	-0.87	2	76	88	K	MFVLDEADEMSLR	G	0	Oxidation (M)	58.2
		522.00	1041.98	1042.58	-0.59	2	67	75	R	QSLRPDSIK	M	0	-	23.8
		587.37	1172.72	1172.64	0.08	2	136	145	K	RDELTLEGIK	Q	1	-	50.5
		993.49	1984.97	1984.83	0.14	2	192	209	R	SNDHTVSATHGMDQNTR	D	0	-	37.3
		578.83	1155.65	1155.58	0.07	2	30	40	K	VHACVGCTSVR	E	0	Propionamide (C)	33.0
		557.53	1113.04	1113.68	-0.64	2	223	232	R	VLITTDLLAR	G	0	-	62.5
94	chr6.LjT10I04.10.nd	468.00	933.98	934.51	-0.53	2	111	119	R	ALGDYLGVK	V	0	-	37.2
		479.49	956.97	957.51	-0.55	2	100	107	R	ELAAQIEK	V	0	-	30.1
		700.97	1399.93	1400.73	-0.79	2	58	71	K	GLDVIQQAQSGTGK	T	0	-	68.8
		785.92	1569.83	1570.70	-0.87	2	166	178	K	MFVLDEADEMSLR	G	0	Oxidation (M)	58.2
		587.37	1172.72	1172.64	0.08	2	226	235	K	RDELTLEGIK	Q	1	-	50.5
		578.83	1155.65	1155.58	0.07	2	120	130	K	VHACVGCTSVR	E	0	Propionamide (C)	33.0
		557.53	1113.04	1113.68	-0.64	2	313	322	R	VLITTDLLAR	G	0	-	62.5
95	chr1.CM0113.740.nd	692.97	1383.93	1383.77	0.16	2	288	302	R	AAALNIVPTSTGAAK	A	0	-	62.3
		778.43	1554.85	1554.67	0.18	2	261	274	K	GTMTTTHSYTGDQR	L	0	-	27.1
		524.26	1569.75	1570.67	-0.92	3	261	274	K	GTMTTTHSYTGDQR	L	0	Oxidation (M)	67.0
		581.48	1160.95	1161.63	-0.68	2	251	260	K	ILDEEFGIVK	G	0	-	49.2
		405.98	809.95	810.43	-0.49	2	275	281	R	LLDASHR	D	0	-	23.6
		417.46	832.90	832.46	0.44	2	89	96	K	VAINGFGR	I	0	-	32.0
		576.01	1150.00	1150.67	-0.67	2	412	422	R	VVDLAHLVASK	W	0	-	76.0
96	LjSGA_042776.1.2	713.46	1424.91	1425.76	-0.85	2	8	23	R	LGANVGSAAQPTGLGK	Y	0	-	84.2
97	chr6.CM0302.70.nc	724.96	1447.90	1448.70	-0.80	2	1158	1170	R	AAQNTNAYNDLVR	Y	0	-	27.0
		681.96	1361.91	1362.68	-0.77	2	1146	1157	R	ADDATQFLDVIR	A	0	-	60.3
		552.49	1102.96	1103.60	-0.64	2	928	937	R	DPTLAVVAYR	R	0	-	55.9
		777.47	1552.93	1553.80	-0.87	2	393	407	K	EAAELAAESPQGIILR	T	0	-	77.3
		724.97	1447.93	1448.75	-0.82	2	1133	1145	R	EGLVSEAIIESFIR	A	0	-	38.9
		560.48	1118.94	1119.57	-0.63	2	382	390	R	FHELFAQTK	Y	0	-	25.5
		719.44	1436.86	1437.67	-0.81	2	190	201	K	GNMQLFSVDQQR	S	0	Oxidation (M)	43.2
		607.66	1819.97	1821.01	-1.04	3	243	259	K	LHVIELGAQPGKPSFTK	K	0	-	31.9
		531.47	1060.93	1061.53	-0.60	2	1251	1260	K	QFQGAVDAAR	K	0	-	47.0
		630.49	1258.97	1259.70	-0.73	2	927	937	K	RDPTLAVVAYR	R	1	-	44.2
		752.47	1502.93	1503.78	-0.85	2	152	164	R	TANLANNQIINIR	C	0	-	70.5
		522.51	1043.00	1043.60	-0.59	2	233	242	K	TLNAGQIISK	L	0	-	23.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		494.49	986.96	987.52	-0.56	2	483	491	K	TVNDNLALK	I	0	-	26.2
		635.97	1269.93	1270.64	-0.72	2	1184	1194	K	VDSELYAYAK	I	0	-	45.5
		680.46	1358.90	1359.67	-0.76	2	1117	1128	R	VEEDAVWSQVAK	A	0	-	57.7
		499.98	997.94	998.51	-0.57	2	814	821	R	YIEGVYQK	V	0	-	21.5
98	chr1.CM0078.20.nc	561.94	1121.87	1122.57	-0.70	2	239	248	K	FGVTDVFNPK	D	0	-	67.9
		759.46	1516.90	1517.79	-0.89	2	349	361	K	FITHSVVPFSEINK	A	0	-	60.4
		519.50	1036.98	1037.62	-0.64	2	223	232	R	IIGVDLVPGR	F	0	-	40.5
		455.99	909.97	910.51	-0.54	2	164	172	K	ISPAAPLDK	V	0	-	45.9
		626.39	1250.77	1250.67	0.11	2	238	248	K	KFGVTDVFNPK	D	1	-	74.4
		486.96	971.91	972.51	-0.60	2	330	338	R	SDIPSVVEK	Y	0	-	40.2
		642.34	1282.67	1282.56	0.11	2	108	118	K	SSGSNMCELLR	I	0	Oxidation (M); Propionamide (C)	55.0
		591.93	1181.84	1182.53	-0.70	2	50	58	R	TDVYWDAAK	G	0	-	31.3
99	chr1.CM0206.650.nd	727.43	1452.85	1452.75	0.11	2	238	252	R	FVIGGPHGDAGLTGR	K	0	-	87.5
		571.35	1140.69	1140.60	0.08	2	228	237	K	TIFHLNPSGR	F	0	-	37.5
		734.47	1466.92	1467.76	-0.84	2	48	60	K	TNLVMVFGIEITTK	A	0	Oxidation (M)	44.0
		498.44	994.87	995.44	-0.57	2	40	47	K	VACETCTK	T	0	2 Propionamide (C)	53.7
100	LjSGA_008893.1	856.88	1711.74	1712.84	-1.10	2	149	164	K	DGAADPTFLYFAQGLK	E	0	-	81.3
		781.84	1561.66	1561.71	-0.05	2	22	34	R	EIENGCLWEVDGK	W	0	Propionamide (C)	63.4
		617.41	1232.80	1233.62	-0.83	2	102	111	K	LDEENQVLFK	K	0	-	62.5
		550.92	1099.82	1100.55	-0.73	2	76	84	R	LQEQPPFDK	K	0	-	25.6
		614.92	1227.83	1228.65	-0.81	2	76	85	R	LQEQPPFDKK	M	1	-	31.0
		442.95	883.89	884.48	-0.59	2	86	92	K	MFVTFIK	R	0	-	34.7
		531.94	1061.86	1062.57	-0.71	2	67	75	K	VVDIVDTFR	L	0	-	55.0
100	chr5.CM0299.300.nc	550.92	1099.82	1100.55	-0.73	2	76	84	R	LQEQPPFDK	K	0	-	25.6
		614.92	1227.83	1228.65	-0.81	2	76	85	R	LQEQPPFDKK	Q	1	-	31.0
		531.94	1061.86	1062.57	-0.71	2	67	75	K	VVDIVDTFR	L	0	-	55.0
101	LjT09K03.140.nd	720.42	1438.82	1439.74	-0.92	2	321	332	K	EELFGPVLVYMK	F	0	Oxidation (M)	34.2
		691.47	1380.92	1381.82	-0.89	2	115	128	K	GAPTTPLITIAVTK	L	0	-	48.3
		600.62	1798.84	1799.01	-0.17	3	255	271	K	IGNPLENGILVGPLHTR	S	0	-	97.5
		567.95	1133.89	1134.63	-0.73	2	163	173	R	IPLVSFTGSSK	V	0	-	50.5
		464.47	926.94	927.54	-0.60	2	129	136	K	LVAEVLER	N	0	-	45.5
		455.43	908.84	909.42	-0.58	2	272	279	R	SSAENFQK	G	0	-	31.3
		665.40	1328.80	1328.70	0.09	2	174	185	K	VGLSVQQTVNER	F	0	-	78.1
102	LjSGA_039603.1	472.96	943.92	944.51	-0.59	2	35	42	R	EFPGQVLR	Y	0	-	57.3
		786.37	1570.72	1571.74	-1.02	2	64	77	K	SITDYGSPPEFLSK	V	0	-	69.0
		787.35	1572.69	1573.70	-1.01	2	8	21	K	SMTDFLPYNGDGFK	L	0	-	67.0
		403.98	805.95	806.45	-0.51	2	78	84	K	VDYLLGK	Q	0	-	24.8
102	chr2.LjT36E17.90.nd	786.37	1570.72	1571.74	-1.02	2	144	157	K	SITDYGSPPEFLSK	V	0	-	69.0
		403.98	805.95	806.45	-0.51	2	158	164	K	VDYLLGK	Q	0	-	24.8
103	LjSGA_037126.2	1014.84	2027.67	2027.94	-0.27	2	98	115	R	ADLNVPLDDNQNIITDDTR	I	0	-	84.9
		544.98	1087.95	1088.57	-0.62	2	80	90	K	SVGDLAAELK	G	0	-	59.5
104	chr1.CM1409.60.nd	963.83	1925.65	1926.85	-1.19	2	128	144	R	EADVGDGGQINYEYFVK	V	0	-	71.7
		603.93	1808.77	1808.91	-0.13	3	92	107	R	VFDKQNGFISAAELR	H	1	-	92.4
104	LjSGA_007638.2	963.83	1925.65	1926.85	-1.19	2	19	35	R	EADVGDGGQINYEYFVK	V	0	-	71.7
104	LjSGA_007639.1	963.83	1925.65	1926.85	-1.19	2	31	47	R	EADVGDGGQINYEYFVK	V	0	-	71.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
104	LjSGA_007640.1	963.83	1925.65	1926.85	-1.19	2	15	31	R	EADVGDGQYINEEFVK	V	0	-	71.7
105	chr3.CM0111.290.nc	645.50	1288.98	1289.70	-0.72	2	426	437	R	AIADGSLDLFLR	Q	0	-	64.8
		628.96	1883.85	1884.91	-1.06	3	199	214	K	DITPDDKQELDEALQR	E	1	-	41.6
		581.48	1160.95	1161.59	-0.64	2	875	884	K	EVLEGDPYVK	Q	0	-	21.5
		741.96	2222.87	2223.18	-0.31	3	644	665	R	GGGPTHLAILSQPPDTIHGSLR	V	0	-	25.1
		574.48	1146.95	1147.59	-0.64	2	740	749	R	LATPELEYGR	M	0	-	56.0
		407.99	813.97	814.43	-0.46	2	264	270	K	NIGINER	V	0	-	20.4
		664.94	1327.86	1328.59	-0.73	2	591	602	K	QEVMIQYSDSGK	D	0	Oxidation (M)	44.7
		603.99	1205.97	1205.68	0.29	2	438	448	R	QVSTFGLSLVR	L	0	-	49.4
106	LjSGA_009490.3	837.88	1673.74	1673.74	0.00	2	129	144	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
		664.92	1327.83	1328.61	-0.78	2	210	219	R	FEELNIDMFR	E	0	Oxidation (M)	36.7
		829.96	1657.91	1658.89	-0.97	2	78	93	R	IINEPTAAAIAYGLDK	R	0	-	94.3
106	LjSGA_030928.1	837.88	1673.74	1673.74	0.00	2	186	201	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
		664.92	1327.83	1328.61	-0.78	2	267	276	R	FEELNIDMFR	E	0	Oxidation (M)	36.7
107	chr4.CM0119.240.nc	527.93	1053.85	1054.48	-0.63	2	158	166	K	AVTEEYSEK	L	0	-	48.2
		627.96	1253.91	1254.66	-0.75	2	208	218	K	CPQPDLTLGLK	R	0	Propionamide (C)	45.8
		603.45	1204.89	1205.60	-0.71	2	94	103	K	EFFALPPEEK	L	0	-	25.7
		693.95	1385.88	1386.72	-0.83	2	132	142	R	EIVTYFSYPIR	N	0	-	46.0
		436.99	871.97	872.50	-0.53	2	347	353	K	KLQDLEK	A	1	-	25.5
		715.96	1429.91	1430.77	-0.86	2	174	186	K	LLEVLSEAMGLEK	E	0	-	59.5
		723.96	1445.90	1446.76	-0.87	2	174	186	K	LLEVLSEAMGLEK	E	0	Oxidation (M)	24.0
		749.41	1496.80	1497.69	-0.89	2	275	288	K	NADHQAVVNSNSSR	L	0	-	51.2
		954.43	1906.85	1908.00	-1.14	2	8	24	K	TLTTLAQQNTLESSFVR	D	0	-	66.1
		490.98	979.94	980.53	-0.59	2	200	207	K	VVVNYYPK	C	0	-	40.8
107	LjSGA_025931.2	527.93	1053.85	1054.48	-0.63	2	158	166	K	AVTEEYSEK	L	0	-	48.2
		627.96	1253.91	1254.66	-0.75	2	208	218	K	CPQPDLTLGLK	R	0	Propionamide (C)	45.8
		603.45	1204.89	1205.60	-0.71	2	94	103	K	EFFALPPEEK	L	0	-	25.7
		693.95	1385.88	1386.72	-0.83	2	132	142	R	EIVTYFSYPIR	N	0	-	46.0
		715.96	1429.91	1430.77	-0.86	2	174	186	K	LLEVLSEAMGLEK	E	0	-	59.5
		723.96	1445.90	1446.76	-0.87	2	174	186	K	LLEVLSEAMGLEK	E	0	Oxidation (M)	24.0
		954.43	1906.85	1908.00	-1.14	2	8	24	K	TLTTLAQQNTLESSFVR	D	0	-	66.1
		490.98	979.94	980.53	-0.59	2	200	207	K	VVVNYYPK	C	0	-	40.8
108	LjSGA_117475.1	645.44	1288.86	1289.66	-0.80	2	150	160	R	AQLGEIFELDR	A	0	-	66.3
		742.92	1483.83	1484.73	-0.90	2	35	47	K	LAFYDYIGNNPAK	G	0	-	73.6
		890.40	1778.78	1779.84	-1.06	2	14	30	R	VGAGLAENQSFSEAWSK	I	0	-	88.4
108	LjSGA_122035.1	645.44	1288.86	1289.66	-0.80	2	195	205	R	AQLGEIFELDR	A	0	-	66.3
		742.92	1483.83	1484.73	-0.90	2	80	92	K	LAFYDYIGNNPAK	G	0	-	73.6
		890.40	1778.78	1779.84	-1.06	2	59	75	R	VGAGLAENQSFSEAWSK	I	0	-	88.4
108	LjSGA_123451.1	645.44	1288.86	1289.66	-0.80	2	255	265	R	AQLGEIFELDR	A	0	-	66.3
		742.92	1483.83	1484.73	-0.90	2	140	152	K	LAFYDYIGNNPAK	G	0	-	73.6
		890.40	1778.78	1779.84	-1.06	2	119	135	R	VGAGLAENQSFSEAWSK	I	0	-	88.4
108	LjSGA_114943.1	645.44	1288.86	1289.66	-0.80	2	128	138	R	AQLGEIFELDR	A	0	-	66.3
109	chr3.LjT36L08.60.nc	720.44	1438.87	1438.73	0.14	2	706	720	K	AIGIDHFGASAPAGR	I	0	-	55.7
		801.93	1601.84	1602.79	-0.94	2	419	433	K	ALPTYTPETPADATR	N	0	-	53.1
		681.40	1360.79	1360.67	0.11	2	333	346	K	ANSYSVHGSALGAK	E	0	-	53.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		495.98	989.95	990.54	-0.58	2	89	97	R	FLAVDAVEK	A	0	-	47.2
		617.47	1232.92	1233.65	-0.72	2	72	82	K	KVTTDESIVDK	S	1	-	57.0
		727.47	1452.92	1452.78	0.14	2	600	613	K	LPNLPGTSIEGVEK	G	0	-	30.2
		643.47	1284.93	1285.70	-0.76	2	434	445	R	NLSQTNLNALAK	V	0	-	44.7
		610.97	1219.92	1220.64	-0.72	2	321	332	K	VTITIGFGSPNK	A	0	-	74.2
110	chr3.LjT44N20.110.nd	649.47	1296.93	1296.67	0.27	2	208	219	R	EINIGVPDEVGR	L	0	-	31.6
		484.52	967.02	967.57	-0.55	2	60	67	R	ELVELPLR	H	0	-	41.0
		579.50	1156.99	1157.64	-0.65	2	82	93	K	GILLYGPPGSGK	T	0	-	47.4
		723.51	1445.01	1445.82	-0.81	2	166	178	R	IVSQLLTMDGLK	A	0	Oxidation (M)	30.5
		537.97	1073.92	1074.53	-0.61	2	120	129	K	LAGESESNLR	K	0	-	82.3
		921.47	1840.93	1841.98	-1.05	2	138	154	K	NAPSIIFIDEIDSIAPK	R	0	-	89.7
111	chr2.LjT43N03.40.nd	481.48	960.95	961.53	-0.59	2	155	162	R	IIGFDNKR	Q	1	-	47.3
		753.93	1505.84	1506.78	-0.94	2	126	139	K	LPMFGTTDASQVLK	E	0	-	72.1
		761.92	1521.83	1522.77	-0.94	2	126	139	K	LPMFGTTDASQVLK	E	0	Oxidation (M)	89.4
		457.42	912.83	913.39	-0.56	2	112	119	K	SPGYDGR	Y	0	-	51.0
111	chr1.LjT23D08.110.nc	457.42	912.83	913.39	-0.56	2	116	123	K	SPGYDGR	Y	0	-	51.0
111	chr1.LjT23D08.120.nc	457.42	912.83	913.39	-0.56	2	117	124	K	SPGYDGR	Y	0	-	51.0
111	LjSGA_030971.1	457.42	912.83	913.39	-0.56	2	56	63	K	SPGYDGR	Y	0	-	51.0
111	LjSGA_080821.1	457.42	912.83	913.39	-0.56	2	56	63	K	SPGYDGR	Y	0	-	51.0
112	chr4.CM0558.210.nc	731.47	1460.92	1460.69	0.23	2	325	336	K	EVDQMINVQNK	N	0	Oxidation (M)	47.2
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		538.99	1075.97	1076.53	-0.56	2	155	162	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	R	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
112	LjSGA_119221.2	986.44	1970.87	1971.99	-1.12	2	107	124	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
112	LjSGA_050733.1	538.99	1075.97	1076.53	-0.56	2	24	31	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	122	131	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	167	175	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
113	chr4.CM0007.1330.nd	919.03	1836.05	1835.93	0.12	2	3	19	R	EILHIQGGQCGNQIGAK	F	0	Propionamide (C)	37.1
		731.47	1460.92	1461.68	-0.76	2	325	336	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		538.99	1075.97	1076.53	-0.56	2	155	162	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
113	chr5.CM0148.400.nd	919.03	1836.05	1835.93	0.12	2	3	19	R	EILHIQGGQCGNQIGAK	F	0	Propionamide (C)	37.1
		731.47	1460.92	1461.68	-0.76	2	325	336	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		538.99	1075.97	1076.53	-0.56	2	155	162	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
113	chr6.CM0437.270.nc	919.03	1836.05	1835.93	0.12	2	3	19	R	EILHIQGGQCGNQIGAK	F	0	Propionamide (C)	37.1
		731.47	1460.92	1461.68	-0.76	2	325	336	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		538.99	1075.97	1076.53	-0.56	2	155	162	K	IREEYPDR	M	1	-	23.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
113	LjSGA_012413.2	570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
		919.03	1836.05	1835.93	0.12	2	3	19	R	EILHIQGGCGCNIGAK	F	0	Propionamide (C)	37.1
		731.47	1460.92	1461.68	-0.76	2	325	336	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		538.99	1075.97	1076.53	-0.56	2	155	162	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
		731.47	1460.92	1461.68	-0.76	2	325	336	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
113	chr1.CM0269.190.nc	538.99	1075.97	1076.53	-0.56	2	155	162	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
		919.03	1836.05	1835.93	0.12	2	63	79	R	EILHIQGGCGCNIGAK	F	0	Propionamide (C)	37.1
		986.44	1970.87	1971.99	-1.12	2	164	181	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		538.99	1075.97	1076.53	-0.56	2	212	219	K	IREEYPDR	M	1	-	23.6
		731.47	1460.92	1461.68	-0.76	2	193	204	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		538.99	1075.97	1076.53	-0.56	2	23	30	K	IREEYPDR	M	1	-	23.6
		570.03	1138.04	1138.69	-0.64	2	121	130	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	166	174	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
113	LjSGA_112910.1	731.47	1460.92	1461.68	-0.76	2	99	110	K	EVDEQMINVQNK	N	0	Oxidation (M)	43.1
		555.94	1109.86	1110.43	-0.57	2	72	80	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
		837.88	1673.74	1674.72	-0.98	2	177	192	K	ATAGDTHLGGEDFDNR	M	0	-	72.6
		829.96	1657.91	1657.90	0.01	2	125	140	R	IINEPTAAALAYGLNK	K	0	-	53.6
		893.97	1785.93	1786.00	-0.07	2	125	141	R	IINEPTAAALAYGLNKK	T	1	-	66.3
		841.00	1679.99	1679.83	0.17	2	94	108	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
		515.48	1028.95	1029.56	-0.61	2	406	414	R	TRDNNLLGK	F	1	-	45.2
		829.96	1657.91	1658.89	-0.97	2	42	57	R	IINEPTAAAIAYGIDK	R	0	-	94.3
		639.87	1277.73	1278.61	-0.88	2	109	118	R	MVNHFVEEFK	R	0	-	20.6
		647.88	1293.74	1294.60	-0.86	2	109	118	R	MVNHFVEEFK	R	0	Oxidation (M)	24.9
115	LjSGA_012865.1	841.00	1679.99	1679.83	0.17	2	11	25	K	NAVVTVPAYFNDSQR	K	0	-	60.8
		674.90	1347.78	1348.66	-0.88	2	216	229	K	ADVVAADGSGNFK	T	0	-	60.8
		655.91	1309.80	1310.65	-0.85	2	52	62	R	AVEQNFFTVK	L	0	-	53.5
		602.34	1202.67	1202.59	0.08	2	107	116	K	TLYQHADDLK	T	0	-	32.6
		569.91	1137.80	1138.54	-0.74	2	266	275	K	TNIMFLGDGR	T	0	Oxidation (M)	37.2
		474.96	947.91	948.52	-0.61	2	276	284	R	TTTIITGSR	N	0	-	59.5
		557.44	1112.87	1113.60	-0.73	2	230	241	K	TVSAVAAPAAPEK	S	0	-	63.1
		624.40	1246.79	1247.59	-0.80	2	473	484	K	EVLEASEASGEK	L	0	-	74.8
		846.88	1691.74	1692.82	-1.08	2	112	128	K	LGGLLAEASAEEDFSGK	T	0	-	50.9
		659.48	1316.94	1317.62	-0.68	2	413	424	K	TIEVNNTDAEGR	L	0	-	73.2
117	LjT06N06.10.nd	624.40	1246.79	1247.59	-0.80	2	479	490	K	EVLEASEASGEK	L	0	-	74.8
		846.88	1691.74	1692.82	-1.08	2	118	134	K	LGGLLAEASAEEDFSGK	T	0	-	50.9
		659.48	1316.94	1317.62	-0.68	2	419	430	K	TIEVNNTDAEGR	L	0	-	73.2
		721.44	1440.87	1441.76	-0.89	2	488	500	K	NTPIGDVVDMLIR	E	0	-	63.1
		729.42	1456.83	1457.75	-0.93	2	488	500	K	NTPIGDVVDMLIR	E	0	Oxidation (M)	51.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		401.46	800.91	801.47	-0.56	2	540	546	K	TLNLSVR	K	0	-	23.6
119	chr4.CM0042.2380.nc	731.47	1460.92	1461.68	-0.76	2	325	336	K	EVDEQIMNVQNK	N	0	Oxidation (M)	33.3
		986.44	1970.87	1971.99	-1.12	2	104	121	K	GHYTEGAELIDSVLDVVR	K	0	-	87.2
		570.03	1138.04	1138.69	-0.64	2	253	262	K	LAVNLIPFPR	L	0	-	63.7
		555.94	1109.86	1110.43	-0.57	2	298	306	K	NMCAADPR	H	0	2 Oxidation (M); Propionamide (C)	26.1
120	LjT24E19.100.nc	870.44	1738.87	1739.83	-0.96	2	391	406	R	EALSDPGDFLLSDFSK	F	0	-	68.2
		631.95	1261.89	1262.58	-0.69	2	430	441	R	FPVAGSEDDAQK	L	0	-	47.5
		654.99	1307.96	1308.69	-0.73	2	150	161	R	LFASNVLVSGMR	G	0	Oxidation (M)	26.9
		794.46	1586.91	1586.80	0.11	2	442	457	K	LISIASNINGNSGDGR	L	0	-	69.0
		535.51	1069.00	1069.59	-0.59	2	624	632	R	LNIEALQNR	V	0	-	33.2
		630.98	1259.95	1260.64	-0.70	2	581	591	K	LTITDDDVIEK	S	0	-	74.8
		525.98	1049.94	1050.52	-0.58	2	731	739	R	SEFEGGLEK	T	0	-	24.7
		493.53	985.04	985.61	-0.56	2	383	390	K	VLNFKPLR	E	0	-	37.8
		627.97	1253.93	1254.62	-0.69	2	532	542	R	YDAQISVFGQK	L	0	-	40.8
121	chr4.CM0006.280.nc	1106.15	2210.28	2210.12	0.16	2	191	212	K	EKPSIGTVIAAGPGLTDEEGNR	K	0	-	64.3
		554.35	1106.68	1106.62	0.06	2	60	69	K	HTAIKPLGDR	V	0	-	48.0
		789.00	1575.98	1575.89	0.09	2	213	227	R	KPLSVTPGSTVLYSK	Y	0	-	61.3
		587.45	1172.88	1173.66	-0.78	2	179	190	K	TAGGLLLTEATK	E	0	-	67.3
		651.37	1300.72	1300.59	0.13	2	129	140	K	YAGTEVEFNQSK	H	0	-	56.8
122	chr6.CM0420.60.nd	787.38	1572.74	1573.77	-1.04	2	173	186	K	DDDIVGILETEDIK	D	0	-	55.4
		519.91	1037.81	1038.50	-0.68	2	264	272	K	DGSDYITLR	S	0	-	35.9
		1018.12	2034.23	2034.10	0.13	2	218	238	K	EKPSIGTVIAVGPGLGEEGK	R	0	-	65.4
		786.51	1571.01	1570.91	0.10	2	240	254	R	KPLAIAPGNTVLYSK	Y	0	-	40.6
		587.45	1172.88	1173.66	-0.78	2	206	217	K	TAGGLLLTEATK	E	0	-	67.3
		657.88	1313.74	1314.61	-0.87	2	156	167	K	YAGTEVEFNQTK	H	0	-	70.7
123	chr4.CM0042.1650.nc	916.92	1831.83	1832.84	-1.01	2	865	884	K	ANAEISSSPDSTSGAPSACK	G	0	-	90.6
		726.42	1450.82	1451.61	-0.79	2	892	904	K	EGDTMQVDSPTK	K	0	Oxidation (M)	51.6
		544.02	1086.02	1086.63	-0.61	2	842	852	K	LPTAVLSTSAK	A	0	-	82.6
124	LjSGA_048339.1	566.97	1131.92	1132.58	-0.66	2	288	297	K	AVENSPFLEK	L	0	-	53.5
		501.48	1000.95	1001.54	-0.58	2	364	372	K	DVLGDKVEK	V	1	-	20.6
		808.41	1614.81	1615.74	-0.92	2	273	286	K	EGQNDIYYITGESK	K	0	-	33.9
		663.95	1325.89	1326.66	-0.76	2	69	79	K	EVSHWLSLVNK	Q	0	-	59.9
		445.96	889.90	890.42	-0.51	2	224	230	K	FYEAFSK	N	0	-	25.2
		763.96	1525.91	1526.79	-0.88	2	174	187	K	GIVDSEDLPLNISR	E	0	-	77.0
		630.98	1259.94	1260.67	-0.73	2	287	297	K	KAVENSPFLEK	L	1	-	59.4
		570.45	1138.89	1139.56	-0.66	2	234	243	K	LGIHEDSQNK	N	0	-	52.3
125	chr1.CM0544.400.nd	747.43	1492.85	1492.74	0.11	2	50	62	R	DATTGLHWTNLHK	R	0	-	34.6
		689.50	1376.98	1376.85	0.13	2	38	49	K	SKPNLLVPLQR	D	0	-	68.2
		892.98	1783.94	1783.78	0.16	2	92	105	K	TYQAPFCHSTQCTR	A	0	2 Propionamide (C)	58.2
126	LjSGA_039892.1	780.97	1559.92	1559.78	0.14	2	120	134	K	VIGAFLEGGTPEENK	A	0	-	79.9
127	chr1.CM0378.40.nc	486.45	970.89	971.53	-0.64	2	253	260	K	ALILEEER	V	0	-	65.2
		770.43	1538.85	1539.87	-1.01	2	59	71	R	SLEQIYLHSLPIK	E	0	-	55.6
		603.26	1806.75	1807.94	-1.19	3	237	252	K	SPFQYETDLLAKPTAK	A	0	-	50.7
		827.38	1652.75	1653.84	-1.09	2	186	200	K	VLQFAGIDDVFTSSR	G	0	-	67.5
127	chr2.LjT09A11.20.nc	486.45	970.89	971.53	-0.64	2	268	275	K	ALILEEER	V	0	-	65.2

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		770.43	1538.85	1539.87	-1.01	2	65	77	R	SLEQIYLHSLPIK	E	0	-	55.6
		603.26	1806.75	1807.94	-1.19	3	252	267	K	SPFQEYTDLLAKPTAK	A	0	-	50.7
		827.38	1652.75	1653.84	-1.09	2	201	215	K	VLQFAGIDDVFTSSR	G	0	-	67.5
127	chr4.CM0042.1380.nc	486.45	970.89	971.53	-0.64	2	265	272	K	ALILEEER	V	0	-	65.2
		770.43	1538.85	1539.87	-1.01	2	62	74	R	SLEQIYLHSLPIK	E	0	-	55.6
		603.26	1806.75	1807.94	-1.19	3	249	264	K	SPFQEYTDLLAKPTAK	A	0	-	50.7
		827.38	1652.75	1653.84	-1.09	2	198	212	K	VLQFAGIDDVFTSSR	G	0	-	67.5
127	LjSGA_025794.2	486.45	970.89	971.53	-0.64	2	262	269	K	ALILEEER	V	0	-	65.2
		770.43	1538.85	1539.87	-1.01	2	59	71	R	SLEQIYLHSLPIK	E	0	-	55.6
		603.26	1806.75	1807.94	-1.19	3	246	261	K	SPFQEYTDLLAKPTAK	A	0	-	50.7
		827.38	1652.75	1653.84	-1.09	2	195	209	K	VLQFAGIDDVFTSSR	G	0	-	67.5
127	chr2.CM0803.780.nd	770.43	1538.85	1539.87	-1.01	2	59	71	R	SLEQIYLHSLPIK	E	0	-	55.6
128	chr1.CM0206.500.nd	567.95	1133.89	1134.59	-0.70	2	125	135	K	ALDFVVEAGK	Y	0	-	63.9
		814.39	1626.76	1627.77	-1.01	2	110	124	K	ALQTSPGSYDESVFK	A	0	-	58.3
		572.98	1143.94	1144.69	-0.75	2	328	337	K	KPILITEFGK	S	0	-	54.3
		599.99	1197.97	1198.71	-0.74	2	140	149	K	LILSLVNNWK	D	0	-	67.7
		657.88	1313.74	1314.55	-0.81	2	338	349	K	SSNTPGYTADMR	N	0	Oxidation (M)	35.5
		615.26	1842.77	1843.92	-1.15	3	82	98	K	VTTTFQDASQHLNVAR	T	0	-	45.2
129	chr2.CM0191.240.nc	637.95	1273.89	1274.64	-0.74	2	124	135	R	ELISNASDALDK	L	0	-	88.1
		742.46	1482.91	1483.76	-0.86	2	451	464	K	GVVDSNDLPLNVS	E	0	-	55.6
130	chr6.CM0037.640.nd	1069.63	2137.25	2137.13	0.13	2	267	287	R	ELVNSPANVLTPGVLAEEASK	I	0	-	31.8
		624.40	1246.79	1247.59	-0.80	2	486	497	K	EVIEASEASGEK	L	0	-	74.8
		659.48	1316.94	1317.62	-0.68	2	426	437	K	TIEVNNTDAEGR	L	0	-	73.2
131	chr1.CM0544.80.nc	579.96	1157.90	1158.62	-0.73	2	4	15	K	AVAVLGSSDNVK	G	0	-	58.6
		667.94	1333.86	1334.68	-0.82	2	115	127	R	AVVVHADPDDLK	G	0	-	70.2
		547.43	1092.84	1093.52	-0.68	2	69	78	K	EHGAPEDAIR	H	0	-	59.1
132	chr5.CM0260.80.nd	681.40	1360.79	1360.67	0.11	2	339	352	K	ANSYSVHGSALGAK	E	0	-	53.0
		510.98	1019.94	1020.55	-0.61	2	95	103	R	FLSIDAVEK	A	0	-	50.3
		569.92	1137.82	1137.51	0.31	2	300	309	K	NGNTGYDEIR	A	0	-	64.5
		487.98	973.95	974.53	-0.58	2	80	88	K	TAEVSLVEK	S	0	-	42.0
		610.97	1219.92	1220.64	-0.72	2	327	338	K	VTTTIGFGSPNK	A	0	-	74.2
133	chr1.CM0029.350.nd	500.44	998.86	999.52	-0.66	2	19	26	K	AQCPIIER	L	0	Propionamide (C)	31.0
		463.44	924.86	925.45	-0.59	2	138	146	K	GSSNSYAIK	K	0	-	34.5
		499.46	996.90	997.56	-0.65	2	92	100	R	QAVDISPLR	R	0	-	60.0
		822.89	1643.77	1644.84	-1.06	2	123	137	K	TIAECLADELINAAK	G	0	Propionamide (C)	67.4
		709.95	1417.88	1418.79	-0.90	2	102	114	R	VNQAIYLLTTGAR	E	0	-	65.4
133	LjSGA_013603.1	463.44	924.86	925.45	-0.59	2	64	72	K	GSSNSYAIK	K	0	-	34.5
		499.46	996.90	997.56	-0.65	2	18	26	R	QAVDISPLR	R	0	-	60.0
		822.89	1643.77	1644.84	-1.06	2	49	63	K	TIAECLADELINAAK	G	0	Propionamide (C)	67.4
		709.95	1417.88	1418.79	-0.90	2	28	40	R	VNQAIYLLTTGAR	E	0	-	65.4
134	LjSGA_088368.2	722.89	1443.77	1443.65	0.12	2	102	115	R	AGHQTSAESWGTGR	A	0	-	53.8
		465.49	928.96	929.49	-0.54	2	229	237	K	DSTGIRPGK	G	0	-	48.2
		793.46	1584.90	1584.77	0.14	2	305	318	K	LDSIYGSGFDKPSEK	K	0	-	56.2
		648.48	1294.94	1295.68	-0.74	2	268	279	R	NIPGVEVANVER	L	0	-	63.5
		673.93	1345.85	1345.74	0.12	2	249	261	R	RGPLVVYGTGAK	A	1	-	66.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
134	LjSGA_044287.1	465.49	928.96	929.49	-0.54	2	73	81	K	DSTGIRPGK	G	0	-	48.2
		793.46	1584.90	1584.77	0.14	2	149	162	K	LDSIYGSFDKPSEK	K	0	-	56.2
		648.48	1294.94	1295.68	-0.74	2	112	123	R	NIPGVEVANVER	L	0	-	63.5
		673.93	1345.85	1345.74	0.12	2	93	105	R	RGPLVVYGTGAK	A	1	-	66.6
134	LjSGA_029445.1	722.89	1443.77	1443.65	0.12	2	63	76	R	AGHQTSAESWGTGR	A	0	-	53.8
		465.49	928.96	929.49	-0.54	2	190	198	K	DSTGIRPGK	G	0	-	48.2
		793.46	1584.90	1584.77	0.14	2	266	279	K	LDSIYGSFDKPSEK	K	0	-	56.2
		648.48	1294.94	1295.68	-0.74	2	229	240	R	NIPGVEVANVER	L	0	-	63.5
134	LjSGA_055825.1	722.89	1443.77	1443.65	0.12	2	63	76	R	AGHQTSAESWGTGR	A	0	-	53.8
135	chr4.CM0042.2090.nc	1272.27	2542.52	2542.23	0.28	2	13	36	R	AHTDQVTAIATPIDNSDMIVTASR	D	0	Oxidation (M)	31.6
		714.43	1426.84	1427.77	-0.92	2	214	226	K	DGVILLWDLAEGK	R	0	-	56.2
		667.92	1333.83	1334.68	-0.85	2	107	118	K	DVLSVAFSIDNR	Q	0	-	65.9
		567.42	1132.82	1133.55	-0.73	2	131	139	K	LWNTLGECK	Y	0	Propionamide (C)	38.9
		629.46	1256.90	1257.72	-0.82	2	266	276	K	SIVEDLKVDLK	T	1	-	51.3
		639.88	1277.74	1278.57	-0.83	2	277	289	K	TEADATTGNTNK	K	0	-	54.6
		524.95	1047.88	1047.52	0.36	2	177	184	K	VWNLNCK	L	0	Propionamide (C)	22.2
		1040.58	2079.15	2078.91	0.24	2	140	156	K	YTIQDNDAHSDWVSCVR	F	0	Propionamide (C)	48.8
		958.58	1915.15	1914.99	0.15	2	29	47	K	FTITTFSPPTGVAITSSGK	K	0	-	67.0
		510.44	1018.86	1019.53	-0.67	2	4	13	K	GPGLYTDIGK	K	0	-	43.3
136	chr1.CM0051.30.nc	781.49	1560.97	1560.85	0.12	2	48	61	K	KGELFVADVNTQLK	N	1	-	35.8
		402.46	802.91	803.44	-0.53	2	64	70	K	NITTDIK	V	0	-	31.7
		665.91	1329.80	1329.65	0.15	2	249	260	K	SFFTISGEVDTK	A	0	-	62.3
		462.44	922.87	923.47	-0.60	2	158	166	K	SNAGLSFTK	D	0	-	43.9
		665.91	1329.80	1329.65	0.15	2	9	20	K	SFFTISGEVDTK	A	0	-	62.3
		854.92	1707.83	1708.79	-0.96	2	54	68	K	GLAYDISDDQQDITR	G	0	-	102.7
137	LjSGA_017053.1	576.53	1151.04	1151.71	-0.66	2	138	148	K	VPLILGIWGGK	G	0	-	65.5
		863.52	1725.02	1724.83	0.20	2	131	146	K	GVAADISHCNTPTSQVR	D	0	Propionamide (C)	68.2
138	chr4.CM0087.970.nc	609.96	1217.91	1218.70	-0.79	2	234	244	K	LFGVTTLDVVR	A	0	-	66.9
		880.49	1758.96	1760.09	-1.13	2	95	113	K	VAVLGAAGGIGQLALLIK	M	0	-	64.4
		845.46	1688.91	1689.86	-0.95	2	443	458	K	DFGASPIVPFLVDGEK	A	0	-	68.6
139	chr3.CM0070.20.nc	861.46	1720.90	1720.88	0.02	2	262	277	K	GFAIGNGLTNPEIQYK	A	0	-	73.1
		805.50	1608.98	1609.89	-0.91	2	398	412	R	NLEVGIPTLLEDGIK	V	0	-	51.5
140	LjSGA_046206.1	649.92	1297.82	1297.74	0.08	2	138	149	R	EHALLAFTLGVK	Q	0	-	58.6
		487.99	973.97	974.54	-0.58	2	239	246	R	LPLQDVYK	I	0	-	51.8
		509.45	1016.88	1016.60	0.28	2	386	393	R	MVMLVLR	X	1	-	28.3
		513.46	1024.90	1025.48	-0.58	2	208	215	R	STNLDWYK	G	0	-	51.2
		488.98	1463.92	1464.68	-0.77	3	88	99	K	YYCTVIDAPGHR	D	0	Propionamide (C)	66.2
		712.39	1422.76	1422.66	0.10	2	28	40	R	ELAEDGYSGVEVR	V	0	-	86.7
141	chr1.CM0017.210.nc	481.43	960.86	961.49	-0.63	2	133	141	K	GCEIVSGK	L	0	Propionamide (C)	59.1
		472.96	1415.86	1416.80	-0.94	3	202	214	K	TPLPDIVTIHSPK	E	0	-	57.9
		712.39	1422.76	1422.66	0.10	2	28	40	R	ELAEDGYSGVEVR	V	0	-	86.7
141	LjSGA_042121.1	481.43	960.86	961.49	-0.63	2	17	25	K	GCEIVSGK	L	0	Propionamide (C)	59.1

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
142	chr6.LjT21O06.20.nd	704.29	1406.56	1406.74	-0.18	2	78	90	K	DTHADLLAPVLK	A	0	-	66.9
		645.79	1289.56	1289.72	-0.16	2	240	250	K	FKDEIIPVTTK	I	1	-	50.7
		486.02	970.03	970.60	-0.57	2	319	327	K	GLPILGVFR	T	0	-	43.0
		699.40	1396.78	1396.67	0.11	2	218	229	R	KEQDQAAVESHR	R	1	-	72.7
		852.00	1701.99	1701.87	0.11	2	143	159	R	QCSSGLQAVADVAAAIK	A	0	Propionamide (C)	23.5
143	LjSGA_100436.1	620.39	1238.76	1239.57	-0.81	2	76	86	K	AFMDATGGLWR	T	0	Oxidation (M)	47.5
		531.40	1060.78	1061.47	-0.69	2	67	75	R	FGMMAAQFK	A	0	2 Oxidation (M)	29.4
		736.86	1471.71	1471.63	0.08	2	145	160	K	GGSPYGAGTYAGDGSR	Q	0	-	85.0
143	chr3.LjT01D08.20.nd	531.40	1060.78	1061.47	-0.69	2	82	90	R	FGMMAAQFK	A	0	2 Oxidation (M)	29.4
		736.86	1471.71	1471.63	0.08	2	159	174	K	GGSPYGAGTYAGDGSR	Q	0	-	85.0
144	chr2.LjT30P12.40.nc	630.38	1258.74	1259.52	-0.77	2	159	169	R	MADMADYVGQK	T	0	2 Oxidation (M)	43.3
		585.36	1168.71	1168.62	0.09	2	186	195	K	RTPIITHTDK	-	1	-	33.8
		804.45	1606.88	1606.75	0.13	2	29	42	R	YEAGGINFNQPPQR	Y	0	-	73.4
		595.33	1188.65	1188.55	0.10	2	18	28	R	YETGGANPPQR	Y	0	-	63.5
145	LjT04N09.110.nd	661.91	1321.80	1321.60	0.20	2	53	64	K	FVDDDESPTGLDK	A	0	-	68.3
		775.42	1548.83	1549.81	-0.98	2	75	90	R	GALGLSEGGPLFGFTK	S	0	-	97.1
		460.95	919.89	920.47	-0.58	2	91	98	K	SNELFVGR	L	0	-	34.9
146	CM0319.40.nc	544.96	1087.91	1088.59	-0.68	2	78	87	K	AMQLLESGLK	V	0	-	61.2
		552.96	1103.90	1104.58	-0.69	2	78	87	K	AMQLLESGLK	V	0	Oxidation (M)	56.8
		766.44	1530.87	1531.82	-0.95	2	38	51	K	VLEQLSGQTPVFSK	A	0	-	86.5
		467.97	933.93	934.51	-0.58	2	169	176	K	YEGVILNK	A	0	-	33.2
146	LjT43K05.240.nd	544.96	1087.91	1088.59	-0.68	2	68	77	K	AMQLLESGLK	V	0	-	61.2
		552.96	1103.90	1104.58	-0.69	2	68	77	K	AMQLLESGLK	V	0	Oxidation (M)	56.8
		766.44	1530.87	1531.82	-0.95	2	28	41	K	VLEQLSGQTPVFSK	A	0	-	86.5
		467.97	933.93	934.51	-0.58	2	159	166	K	YEGVILNK	A	0	-	33.2
146	chr1.CM0133.1120.nc	766.44	1530.87	1531.82	-0.95	2	14	27	K	VLEQLSGQTPVFSK	A	0	-	86.5
147	chr3.CM0116.230.nc	763.41	1524.81	1525.82	-1.01	2	161	176	K	AGAIGANNQAAQSILK	Q	0	-	77.1
		457.96	913.90	914.51	-0.61	2	41	49	K	DGVVLVGEK	K	0	-	46.3
		553.93	1105.85	1106.58	-0.73	2	55	64	K	LLQTSTSTEK	M	0	-	68.9
		523.90	1045.79	1046.49	-0.70	2	240	250	K	SGVTQPATESA	-	0	-	31.2
148	LjSGA_129817.1	595.95	1189.88	1190.58	-0.70	2	99	110	K	DAISGGSTQDIK	D	0	-	69.1
		691.23	1380.45	1380.65	-0.20	2	62	73	K	NQADSVVYQTEK	Q	0	-	64.9
149	chr2.CM0210.260.nc	444.49	886.96	887.51	-0.54	2	299	306	R	ALQQSTLK	T	0	-	48.5
		666.45	1330.89	1331.69	-0.81	2	25	38	K	GILAADESTGTIGK	R	0	-	74.2
150	LjSGA_014826.1	705.48	1408.95	1409.81	-0.85	2	92	104	K	KQPMVVVLSPPQK	V	1	-	67.5
		713.48	1424.94	1425.80	-0.86	2	92	104	K	KQPMVVVLSPPQK	V	1	Oxidation (M)	66.7
		649.75	1297.48	1297.71	-0.22	2	93	104	K	QPMVVVLSPPQK	V	0	Oxidation (M)	55.9
151	chr5.LjT43D06.110.nd	846.47	1690.94	1690.81	0.13	2	236	250	K	EVSVGFSATTWNTHR	E	0	-	70.4
		740.43	1478.85	1478.73	0.12	2	48	61	K	FTDDGSLILQGDAK	I	0	-	78.3
152	chr5.CM0359.200.nc	444.49	886.96	887.51	-0.54	2	299	306	R	ALQQSTLK	A	0	-	48.5
		666.45	1330.89	1331.69	-0.81	2	25	38	K	GILAADESTGTIGK	R	0	-	74.2
		414.95	827.88	828.38	-0.50	2	133	139	K	YYEAGAR	F	0	-	28.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
153	chr3.CM0142.570.nd	916.42	1830.82	1831.88	-1.07	2	128	143	R	AYVPVEEVLGDEIDR	W	0	-	77.8
		620.97	1239.92	1240.64	-0.72	2	116	127	K	DDNPIGATLIGR	A	0	-	59.6
		773.95	1545.89	1546.79	-0.89	2	354	368	K	IVVVDSDFPSSGLDK	R	0	-	76.6
154	chr5.CM0357.340.nc	794.47	1586.93	1586.79	0.14	2	215	230	K	AATLQDAEGVASAEVR	N	0	-	56.6
		926.55	1851.09	1850.92	0.17	2	231	251	R	NNPEAGATPGGVAASVAAAAAR	L	0	-	36.5
		570.36	1138.70	1138.61	0.09	2	8	17	R	RTQPGQDPIK	Y	1	-	42.3
		1079.14	2156.27	2156.07	0.20	2	144	164	K	TVGDKPVDQSDASAIQAAEVR	A	0	-	87.3
		962.08	1922.15	1921.98	0.17	2	48	67	R	VLGHTQPGGAAAVMQSAATR	N	0	-	25.1
155	chr1.CM0109.50.nd	532.91	1063.81	1064.51	-0.71	2	197	206	K	EGFEGQISAK	N	0	-	56.6
		575.96	1149.91	1150.67	-0.76	2	103	112	K	EPVPVQLVR	E	0	-	36.0
		763.99	1525.96	1525.87	0.09	2	51	64	K	KLPSILVDEASVQK	I	1	-	50.6
		778.51	1555.01	1554.91	0.10	2	100	112	R	LYKEPIPVQLVR	E	1	-	51.1
		635.45	1268.89	1269.73	-0.84	2	207	218	K	NIEIGIIGADKK	F	1	-	63.3
		831.36	1660.70	1661.80	-1.10	2	221	235	R	VLTPAEIDDLGVEVE	-	0	-	29.8
155	LjSGA_070271.1	575.96	1149.91	1150.67	-0.76	2	26	35	K	EPVPVQLVR	E	0	-	36.0
		778.51	1555.01	1554.91	0.10	2	23	35	R	LYKEPIPVQLVR	E	1	-	51.1
156	chr2.LjT07F03.120.nd	713.92	1425.83	1426.71	-0.88	2	525	536	K	NATSFLLDDIYR	N	0	-	54.3
		493.96	985.91	986.51	-0.61	2	304	312	K	QISDAVQAR	A	0	-	38.4
		734.94	1467.86	1468.77	-0.91	2	136	148	K	TLEITDSVLSTYK	N	0	-	46.1
		1011.06	2020.11	2019.94	0.17	2	36	55	R	VEFGDATTADPSDAPAISR	A	0	-	74.0
		655.97	1309.93	1309.76	0.17	2	212	224	K	VGVVPVTLNGDLK	N	0	-	49.7
156	chr1.CM0315.320.nc	713.92	1425.83	1426.71	-0.88	2	37	48	K	NATSFLLDDIYR	N	0	-	54.3
156	chr2.LjT07F03.160.nd	713.92	1425.83	1426.71	-0.88	2	5	16	K	NATSFLLDDIYR	N	0	-	54.3
157	chr2.CM0608.590.nc	538.41	1074.80	1075.51	-0.71	2	160	169	K	AMNEINAAAR	L	0	Oxidation (M)	42.6
		711.42	1420.82	1421.77	-0.95	2	95	106	K	AQIQAYVFDVIR	A	0	-	49.6
		414.93	827.85	828.40	-0.55	2	83	89	K	AVDAYYK	L	0	-	28.8
		473.43	944.84	945.47	-0.63	2	127	134	K	AVEEELEK	A	0	-	43.8
		818.87	1635.74	1636.79	-1.06	2	216	231	R	DSVLAFSENVPGTSSK	D	0	-	54.1
		598.89	1195.76	1196.54	-0.78	2	112	121	K	MELDSAFEQK	N	0	-	51.1
		606.88	1211.74	1212.53	-0.79	2	112	121	K	MELDSAFEQK	N	0	Oxidation (M)	32.9
		466.97	931.92	932.54	-0.63	2	197	205	K	YLAGLGIAR	Q	0	-	41.9
157	chr2.CM0608.600.nc	538.41	1074.80	1075.51	-0.71	2	160	169	K	AMNEINAAAR	M	0	Oxidation (M)	42.6
		473.43	944.84	945.47	-0.63	2	127	134	K	AVEEELEK	A	0	-	43.8
		466.97	931.92	932.54	-0.63	2	197	205	K	YLAGLGIAR	Q	0	-	41.9
157	chr1.CM0123.430.nd	538.41	1074.80	1075.51	-0.71	2	160	169	R	AMNEINAAAR	L	0	Oxidation (M)	42.6
		473.43	944.84	945.47	-0.63	2	127	134	K	AVEEELEK	A	0	-	43.8
157	chr4.CM0170.300.nc	538.41	1074.80	1075.51	-0.71	2	160	169	R	AMNEINAAAR	L	0	Oxidation (M)	42.6
		473.43	944.84	945.47	-0.63	2	127	134	K	AVEEELEK	A	0	-	43.8
157	chr2.CM0225.110.nc	538.41	1074.80	1075.51	-0.71	2	160	169	R	AMNEINAAAR	M	0	Oxidation (M)	42.6
158	chr2.CM0373.850.nc	837.88	1673.74	1674.72	-0.98	2	225	240	K	ATAGDTHLGGEDFDNR	M	0	-	72.6
		829.96	1657.91	1657.90	0.01	2	174	189	R	IINEPTAAGLAYGLQK	K	0	-	26.0
		893.97	1785.93	1786.00	-0.07	2	174	190	R	IINEPTAAGLAYGLQKK	S	1	-	39.2
		553.93	1105.85	1106.56	-0.71	2	521	529	R	LIQEAENYK	A	0	-	21.3

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		841.00	1679.99	1679.83	0.17	2	143	157	K	NAVVTVPAYFNDSQR	K	0	-	60.8
159	chr6.CM0139.590.nd	822.45	1642.89	1643.91	-1.02	2	14	29	K	SLELVDTLSSGALLGTR	S	0	-	109.0
		650.93	1299.84	1300.65	-0.81	2	44	55	K	TLNVEEAPSDEVK	V	0	-	56.3
160	chr4.CM0042.300.nc	613.89	1225.76	1225.67	0.09	2	339	349	R	AVLVKDKQNP	W	1	-	65.2
		743.99	1485.97	1486.84	-0.87	2	237	250	K	LLLPETISSFGGNK	S	0	-	66.7
		697.89	1393.77	1393.64	0.14	2	225	236	R	YESNPESQAQLK	L	0	-	41.5
161	chr5.CM0909.680.nc	588.41	1174.81	1175.57	-0.75	2	402	413	K	IGGASEAEVSEK	K	0	-	68.5
		532.43	1062.84	1063.53	-0.69	2	450	458	K	LQTANFDQK	I	0	-	41.3
		793.92	1585.82	1585.71	0.11	2	372	385	R	SAIENSTSDYDKEK	L	1	-	30.1
		745.39	1488.77	1489.73	-0.96	2	203	215	K	TLENELEVVEGMK	L	0	-	74.6
161	LjSGA_060796.1	745.39	1488.77	1489.73	-0.96	2	97	109	K	TLENELEVVEGMK	L	0	-	74.6
162	chr3.CM0634.370.nd	759.76	758.75	758.42	0.34	1	400	406	K	AVEIAEK	A	0	-	29.7
		1061.46	2120.91	2122.03	-1.12	2	168	187	R	DVLGGSVAFVETLEDDLAK	L	0	-	102.2
		482.97	963.92	964.52	-0.60	2	234	242	K	FTSALEAVK	T	0	-	38.0
		699.86	1397.71	1396.67	1.04	2	221	233	R	GWDQVPLGEASHK	F	0	-	27.7
		661.96	1321.91	1322.73	-0.83	2	327	337	R	HYLVSPPLIER	T	0	-	46.7
		534.44	1066.87	1067.53	-0.66	2	350	358	R	IFACSETVK	F	0	Propionamide (C)	47.4
		542.00	1081.99	1082.67	-0.68	2	140	148	R	LDQLQLLLK	G	0	-	48.0
163	chr2.CM0168.100.nd	435.97	869.92	870.50	-0.58	2	29	37	R	KGNAAVGVR	G	1	-	50.7
		817.40	1632.79	1633.86	-1.07	2	97	110	R	LTVEDPVTVEYITR	Y	0	-	82.2
163	LjSGA_019093.1	435.97	869.92	870.50	-0.58	2	29	37	R	KGNAAVGVR	G	1	-	50.7
164	CM0385.200.nd	891.02	1780.02	1779.86	0.16	2	244	259	R	DVCTPAHNELALEAAR	Q	0	Propionamide (C)	55.8
		512.97	1023.93	1024.57	-0.64	2	269	278	K	GNALPLSPTR	H	0	-	50.3
		707.23	1412.44	1412.68	-0.24	2	35	48	R	GQETPGEDPTLAAR	Y	0	-	46.0
		564.94	1127.88	1128.57	-0.69	2	172	182	R	TPEEAAAIAIK	A	0	-	47.9
		823.54	1645.08	1644.93	0.14	2	367	381	R	VGLLLPGHQELVSR	V	0	-	45.0
165	LjT19C19.50.nd	852.96	1703.90	1703.80	0.10	2	380	394	K	GVEQGPQIDTEQFEK	I	0	-	41.0
		548.92	1095.83	1096.54	-0.71	2	283	293	K	LAFTGSTDTGK	V	0	-	75.0
		934.51	1867.00	1866.87	0.13	2	87	104	R	TGVDIAHVAEGDAEDVNR	A	0	-	58.7
166	LjSGA_011457.1	542.41	1082.80	1083.47	-0.67	2	33	42	K	ATDEGYDVSK	L	0	-	53.8
		927.86	1853.71	1854.81	-1.10	2	46	62	K	TPQSDTPPEEGPQDTK	G	0	-	67.6
167	chr1.CM0318.150.nd	634.30	1266.58	1266.73	-0.15	2	170	180	R	LPNLLSLMLDR	-	0	-	67.9
168	LjSGA_015149.2	705.93	1409.84	1409.70	0.13	2	178	190	R	AVGYLGDKTEETK	Q	1	-	41.1
		711.88	1421.75	1421.63	0.12	2	66	78	K	DNHAPADIDANR	G	0	-	56.4
		1001.10	2000.18	2000.01	0.18	2	79	97	R	GEVVEVIGGTEEDVKGEVR	D	1	-	89.0
		605.34	1208.67	1208.57	0.10	2	119	130	K	VGGESTDFAAQK	A	0	-	36.1
169	LjSGA_028864.1	837.88	1673.74	1674.72	-0.98	2	117	132	K	ATAGDTHLGGEDFDNR	M	0	-	72.6
		829.96	1657.91	1657.90	0.01	2	66	81	K	IINEPTAAGLAYGLQK	K	0	-	26.0
		893.97	1785.93	1786.00	-0.07	2	66	82	R	IINEPTAAGLAYGLQKK	S	1	-	39.2
		639.44	1276.87	1277.66	-0.79	2	133	142	R	MVNHVKEFK	R	1	-	68.0
		647.88	1293.74	1293.65	0.09	2	133	142	R	MVNHVKEFK	R	1	Oxidation (M)	31.8
170	chr1.CM0222.290.nd	491.93	981.85	982.45	-0.60	2	74	81	R	LTEGCSFR	K	0	Propionamide (C)	31.1

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
171	LjSGA_085408.1	763.90	1525.79	1526.74	-0.95	2	25	37	R	LVQSPNSFFMDVK	C	0	Oxidation (M)	46.1
		960.42	1918.82	1920.02	-1.20	2	1	17	-	VLQNDIDLLNPFAELEK	R	0	-	73.0
		615.66	1229.31	1229.52	-0.21	2	81	91	R	FSDASVQSDMK	L	0	Oxidation (M)	63.0
171	LjSGA_046788.2	729.91	1457.81	1458.66	-0.85	2	40	52	R	TTPSYVGFTDSEK	L	0	-	45.3
		614.45	1226.89	1227.62	-0.73	2	29	39	R	VEIIANDQGNR	T	0	-	68.8
		615.66	1229.31	1229.52	-0.21	2	68	78	R	FSDASVQSDMK	L	0	Oxidation (M)	63.0
172	chr3.CM0106.300.nc	675.96	1349.90	1349.74	0.16	2	43	57	K	APGGAPANVAIAVSR	L	0	-	74.8
		754.46	1506.90	1506.71	0.19	2	167	179	K	DAGCLLSYDPNLR	L	0	Propionamide (C)	38.2
		764.97	1527.93	1527.74	0.19	2	280	292	K	IVDDQSIIEDEPR	L	0	-	79.7
173	chr4.CM0042.1220.nc	640.41	1278.80	1278.66	0.14	2	74	85	R	EAPAGEKPEPVR	T	0	-	46.5
		924.90	1847.79	1848.90	-1.12	2	27	43	R	GVLDLALLDMSTDELVK	L	0	Oxidation (M)	99.6
		668.92	1335.82	1335.68	0.14	2	72	83	R	EAPQGEKPEPVR	T	0	-	42.5
174	chr5.CM1574.170.nc	924.90	1847.79	1848.90	-1.12	2	25	41	R	GVLDLALLDMSTDELVK	L	0	Oxidation (M)	99.6
		585.98	1169.94	1170.66	-0.72	2	48	59	K	GKDLAEVIAAGK	E	1	-	79.6
		503.98	1005.95	1006.57	-0.62	2	39	47	R	IASFLSELK	G	0	-	30.7
175	LjSGA_021840.1	644.91	1287.80	1288.59	-0.79	2	26	38	K	IIGSVGGDADDDR	I	0	-	79.4
		585.98	1169.94	1170.66	-0.72	2	48	59	K	GKDLAEVIAAGK	E	1	-	79.6
		503.98	1005.95	1006.57	-0.62	2	39	47	R	IASFLSELK	G	0	-	30.7
175	LjSGA_090516.1	644.91	1287.80	1288.59	-0.79	2	26	38	K	IIGSVGGDADDDR	I	0	-	79.4
		565.93	1694.78	1695.82	-1.05	3	46	61	K	IKTDTPTYGTGGGMNLR	N	1	Oxidation (M)	25.9
		719.89	1437.76	1438.65	-0.89	2	48	61	K	TDTPYGTGGGMNLR	N	0	-	35.1
176	chr3.CM0279.310.nc	727.88	1453.76	1454.65	-0.89	2	48	61	K	TDTPYGTGGGMNLR	N	0	Oxidation (M)	52.8
		831.37	1660.72	1661.76	-1.04	2	83	97	K	YGANVDGYSPIYDTK	D	0	-	85.4
		485.48	968.95	969.52	-0.57	2	351	358	K	HIETTLTR	V	0	-	37.6
177	LjB14K02.60.nc	691.23	1380.45	1380.65	-0.20	2	593	604	K	NQADSVVYQTEK	Q	0	-	64.9
		430.98	859.95	860.46	-0.51	2	471	478	R	NTTLPTSK	S	0	-	28.2
		789.95	1577.88	1578.80	-0.93	2	118	131	R	QAVVNPENTFFSVK	R	0	-	55.4
178	LjSGA_021837.1	678.40	1354.79	1354.68	0.10	2	31	43	K	TLEAEAAHGTVTR	H	0	-	65.5
179	chr6.LjT34E09.150.nc	906.36	1810.71	1811.88	-1.16	2	218	232	R	DEFIQSCDIVAFNKI	-	1	Propionamide (C)	52.3
		422.47	842.93	843.48	-0.55	2	161	167	K	KLEEAVR	S	1	-	42.5
		855.00	1707.99	1707.80	0.19	2	86	100	K	LDASAEDDLKDFQK	V	1	-	55.3
179	LjT39M07.170.nd	459.99	917.97	918.55	-0.59	2	181	189	K	LVAVGYGIK	K	0	-	48.9
		712.39	1422.77	1423.68	-0.91	2	168	180	R	SVEMPGGLFWGASK	L	0	Oxidation (M)	64.3
		572.91	1143.81	1144.54	-0.73	2	25	34	K	TYVSGDQFTK	D	0	-	22.8
179	LjT39M07.170.nd	422.47	842.93	843.48	-0.55	2	107	113	K	KLEEAVR	S	1	-	42.5
180	chr3.LjT58I15.10.nd	548.93	1095.84	1096.49	-0.65	2	9	17	R	LTTFEDDEK	E	0	-	41.3
		668.44	1334.86	1334.73	0.13	2	48	59	R	VGHDLNLIGEIR	L	0	-	77.6
		690.76	1379.50	1379.74	-0.25	2	178	190	K	VTYVAPAGQYALK	D	0	-	30.1
181	chr2.CM0608.90.nd	535.48	1068.95	1069.60	-0.65	2	30	38	R	ALHNLFSIR	I	0	-	35.8
		527.99	1053.97	1054.61	-0.64	2	21	29	K	KVPISQIDR	A	1	-	44.9
		523.95	1045.89	1046.54	-0.65	2	41	50	R	LGLFDGNPSK	L	0	-	53.6
		769.45	1536.89	1536.76	0.13	2	51	64	K	LTYGSIGNPNQVCSK	Q	0	Propionamide (C)	68.1

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		506.31	1515.91	1516.84	-0.93	3	122	134	K	LVTLLQGFQHYAK	D	0	-	29.6
		687.76	1373.50	1373.72	-0.22	2	192	204	K	QQELINSVASASK	K	0	-	43.9
182	LjSGA_021523.1	859.44	1716.86	1717.84	-0.98	2	135	150	K	VPIDVFEGITDEDAK	V	0	-	108.7
183	chr5.LjT43D06.20.nd	740.43	1478.85	1478.73	0.12	2	39	52	K	FTDDGSLILQGDAK	I	0	-	78.3
		562.39	1122.76	1122.66	0.09	2	59	69	R	LALPSDPLIGK	T	0	-	51.6
184	LjSGA_043096.1	422.94	843.87	844.41	-0.54	2	89	95	R	EHFVGEK	D	0	-	26.3
		455.48	908.94	909.57	-0.63	2	66	73	R	LPFVPLPK	A	0	-	49.6
		406.96	811.91	812.41	-0.51	2	27	33	K	NPELNAR	L	0	-	57.7
		551.96	1101.91	1102.65	-0.74	2	76	84	R	RVEFVNLVK	D	1	-	50.3
185	chr4.CM0307.10.nc	784.44	1566.87	1567.78	-0.91	2	146	160	K	IQSQFTSGASSISQK	A	0	-	71.2
		677.53	1353.04	1353.82	-0.79	2	67	78	K	KLLEEIAQIVAK	Y	1	-	79.2
185	chr6.LjT23A02.90.nc	784.44	1566.87	1567.78	-0.91	2	212	226	K	IQSQFTSGASSISQK	A	0	-	71.2
186	LjSGA_119931.1	768.94	1535.86	1536.71	-0.85	2	162	175	K	DLQDDFMGGAEIVK	S	0	-	35.4
		776.93	1551.84	1552.71	-0.87	2	162	175	K	DLQDDFMGGAEIVK	S	0	Oxidation (M)	64.6
		445.51	889.00	889.50	-0.50	2	101	108	K	FSVSPVVR	V	0	-	36.8
		602.47	1202.93	1203.60	-0.67	2	29	39	R	IMGPNYVPGEK	K	0	-	42.3
		610.46	1218.90	1219.59	-0.69	2	29	39	R	IMGPNYVPGEK	K	0	Oxidation (M)	47.6
		453.48	904.95	905.46	-0.51	2	176	183	K	SDPVVSFR	E	0	-	37.9
187	LjSGA_039295.1	743.30	1484.58	1485.68	-1.10	2	62	74	K	AISTSNAYNDQFR	E	0	-	43.5
		667.24	1332.46	1332.64	-0.18	2	124	136	R	LADDTGTIEAAK	W	0	-	107.5
188	chr2.CM0008.290.nc	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjT12A09.240.nd	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_014576.1	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_047101.1	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_049093.1	519.92	1037.82	1038.51	-0.69	2	3	11	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	33	41	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	24	32	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_056269.1	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_010124.3	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
188	LjSGA_044371.1	519.92	1037.82	1038.51	-0.69	2	116	124	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	146	154	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	137	145	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_103437.1	519.92	1037.82	1038.51	-0.69	2	23	31	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	53	61	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	44	52	R	TLADYNIQK	E	0	-	49.4
188	chr3.CM0292.520.nc	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjT12A09.340.nd	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	chr5.CM0956.190.nd	519.92	1037.82	1038.51	-0.69	2	34	42	K	EGIPPDQQR	L	0	-	25.0
		533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_029363.2	533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
188	LjSGA_063041.1	533.99	1065.96	1066.61	-0.66	2	64	72	K	ESTLHLVLR	L	0	-	51.9
		532.95	1063.90	1064.55	-0.66	2	55	63	R	TLADYNIQK	E	0	-	49.4
189	LjT04M14.100.nd	667.95	1333.88	1333.66	0.23	2	498	510	K	ATQQVNSGTVSSR	R	0	-	69.3
		559.45	1116.89	1117.53	-0.63	2	24	34	K	ESLEGNDVGAK	I	0	-	82.4
		619.45	1236.88	1237.58	-0.71	2	178	188	K	FLSTEQDPSSK	R	0	-	39.2
190	chr2.CM0225.70.nc	505.93	1009.86	1010.52	-0.66	2	158	166	K	FNAGLNFTK	A	0	-	51.4
		510.44	1018.86	1019.53	-0.67	2	4	13	K	GPGLYTDIGK	R	0	-	43.3
		781.49	1560.97	1560.85	0.12	2	48	61	K	KGELFVADVNTQLK	N	1	-	35.8
		402.46	802.91	803.44	-0.53	2	64	70	K	NITTDLK	V	0	-	31.7
		665.91	1329.80	1329.65	0.15	2	249	260	K	SFFTISGEVDTK	A	0	-	62.3
191	chr5.CM0048.40.nd	645.49	1288.97	1289.74	-0.77	2	112	123	R	IVFGLFGDVVPK	T	0	-	70.7
		525.45	1048.88	1049.50	-0.62	2	233	241	R	TLESQETSR	S	0	-	58.9
192	LjSGA_029072.1	765.95	1529.89	1530.90	-1.01	2	54	67	R	LISQIISSLTTSR	F	0	-	67.1
193	chr4.CM0087.380.nc	1109.18	2216.35	2216.10	0.25	2	70	88	K	KLEDIVPSSHNCVPHVTR	T	1	Propionamide (C)	24.1
		663.98	1325.94	1326.74	-0.80	2	117	128	K	LPTDDALLTQIK	E	0	-	87.6
		567.46	1132.91	1133.58	-0.67	2	19	28	K	TPPQAGTIR	K	0	-	40.4
		424.47	846.93	847.47	-0.53	2	42	49	K	VVEVSTSK	T	0	-	50.6
193	chr4.CM0179.120.nc	424.47	846.93	847.47	-0.53	2	42	49	K	VVEVSTSK	T	0	-	50.6
193	LjT33K05.120.nd	424.47	846.93	847.47	-0.53	2	1	8	-	VVEVSTSK	T	0	-	50.6
193	LjSGA_031436.1	424.47	846.93	847.47	-0.53	2	1	8	-	VVEVSTSK	T	0	-	50.6
194	chr4.CM0165.150.nd	781.90	1561.79	1562.79	-1.00	2	68	82	K	AVVQVFEGTSGIDNK	F	0	-	63.6
		614.85	1227.69	1228.47	-0.77	2	225	234	R	DFEENGSMER	V	0	Oxidation (M)	29.0
		615.37	1228.72	1228.64	0.07	2	57	67	R	RGQVLEVDGEK	A	1	-	45.4
		684.47	1366.92	1367.80	-0.89	2	23	36	R	TVSGVAGPLVLDK	V	0	-	49.4

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
195	LjSGA_078699.1	573.98	1145.94	1146.60	-0.66	2	166	176	K	EITALAPSSMK	I	0	-	32.3
		581.97	1161.93	1162.59	-0.66	2	166	176	K	EITALAPSSMK	I	0	Oxidation (M)	48.7
		873.95	1745.89	1746.88	-0.99	2	89	104	K	SYELPDGQVITIGAER	F	0	-	85.0
196	chr6.CM0014.300.nc	568.95	1135.89	1136.57	-0.68	2	259	268	R	EDGGYEVIKK	A	1	-	56.6
		672.91	1343.81	1344.61	-0.80	2	279	290	K	EHIAAYGEGNER	R	0	-	32.7
		526.92	1577.73	1577.69	0.04	3	241	255	K	GDWNGAGAHTNYSTK	T	0	-	45.5
		614.94	1841.79	1842.90	-1.11	3	296	311	R	HETADINTFLWGVANR	G	0	-	59.7
		537.27	1608.80	1609.76	-0.96	3	277	290	R	HKEHIAAYGEGNER	R	1	-	24.5
		718.48	1434.94	1434.77	0.17	2	39	52	R	TLPGPVSDPSQLPK	W	0	-	35.3
196	LjSGA_019428.1	672.91	1343.81	1344.61	-0.80	2	39	50	K	EHIAAYGEGNER	R	0	-	32.7
		614.94	1841.79	1842.90	-1.11	3	56	71	K	HETADINTFLWGVANR	G	0	-	59.7
		537.27	1608.80	1609.76	-0.96	3	37	50	K	HKEHIAAYGEGNER	R	1	-	24.5
197	LjSGA_091217.1	602.47	1202.93	1203.60	-0.67	2	216	226	R	IMGPNYVPGEK	K	0	-	42.3
		610.46	1218.90	1219.59	-0.69	2	216	226	R	IMGPNYVPGEK	K	0	Oxidation (M)	47.6
		712.45	1422.88	1423.68	-0.79	2	49	60	R	LWGENFFDPATK	K	0	-	43.5
		1033.43	2064.84	2066.00	-1.16	2	156	173	R	VENLYEGPLDDQYATAIR	N	0	-	68.3
197	LjSGA_018952.1	712.45	1422.88	1423.68	-0.79	2	232	243	R	LWGENFFDPATK	K	0	-	43.5
197	LjSGA_036784.1	712.45	1422.88	1423.68	-0.79	2	232	243	R	LWGENFFDPATK	K	0	-	43.5
198	chr3.LjT39G24.130.nd	535.98	1069.94	1070.63	-0.70	2	18	28	K	LLLIGDSGVGK	S	0	-	70.8
		658.42	1314.82	1315.65	-0.83	2	66	76	K	LQIWDTAGQER	F	0	-	47.8
		819.40	1636.78	1637.84	-1.06	2	162	175	K	TNLMVEEVFFSIAR	D	0	-	56.0
198	chr5.CM0180.240.nd	535.98	1069.94	1070.63	-0.70	2	19	29	K	LLLIGDSGVGK	S	0	-	70.8
		658.42	1314.82	1315.65	-0.83	2	67	77	K	LQIWDTAGQER	F	0	-	47.8
		819.40	1636.78	1637.84	-1.06	2	163	176	K	TNLMVEEVFFSIAR	D	0	-	56.0
198	chr1.LjT29L18.70.nd	535.98	1069.94	1070.63	-0.70	2	12	22	K	LLLIGDSGVGK	S	0	-	70.8
		658.42	1314.82	1315.65	-0.83	2	60	70	K	LQIWDTAGQER	F	0	-	47.8
198	LjSGA_017346.1	535.98	1069.94	1070.63	-0.70	2	18	28	K	LLLIGDSGVGK	S	0	-	70.8
		658.42	1314.82	1315.65	-0.83	2	66	76	K	LQIWDTAGQER	F	0	-	47.8
198	LjSGA_013646.2	535.98	1069.94	1070.63	-0.70	2	18	28	K	LLLIGDSGVGK	S	0	-	70.8
		658.42	1314.82	1315.65	-0.83	2	66	76	K	LQIWDTAGQER	F	0	-	47.8
199	LjSGA_039694.1	652.96	1303.91	1304.68	-0.77	2	77	89	R	ETADALISTGLSK	L	0	-	68.2
200	LjT06B16.110.nc	701.37	1400.73	1400.64	0.10	2	186	199	K	EVGADAVSHGCTGK	G	0	Propionamide (C)	59.3
		819.99	1637.97	1638.89	-0.93	2	314	329	R	LSPASLLAELNEIGGR	H	0	-	90.9
201	chr4.CM0007.620.nd	585.45	1168.88	1169.60	-0.72	2	33	43	K	EDNVTLGPAVR	D	0	-	59.9
		714.92	1427.82	1428.71	-0.89	2	150	162	R	IEDVTPIPSDSTR	R	0	-	67.1
201	LjT35M05.50.nd	585.45	1168.88	1169.60	-0.72	2	26	36	K	EDNVTLGPAVR	D	0	-	59.9
		714.92	1427.82	1428.71	-0.89	2	143	155	R	IEDVTPIPSDSTR	R	0	-	67.1
202	chr4.CM0617.490.nd	820.52	1639.03	1638.88	0.15	2	79	93	R	GLLPPTVSTQELQEK	K	0	-	27.4
		770.42	1538.82	1538.68	0.14	2	21	35	R	STVGGGVEDVYGEDR	A	0	-	116.3
203	LjSGA_038270.1	900.42	1798.83	1799.99	-1.16	2	88	105	R	EVGDGTTSSVVIVAAELLK	R	0	-	77.4

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
204	chr4.CM0173.280.nc	623.95	1245.88	1246.59	-0.71	2	88	97	K	FADLTNYEFK	S	0	-	67.4
		430.00	857.99	858.48	-0.49	2	137	145	R	TSGLVTPVK	D	0	-	66.4
205	LjT42M11.210.nc	971.02	1940.03	1939.88	0.15	2	206	224	K	AIGSGSEGADSSLQEQYNK	E	0	-	72.1
		531.91	1061.80	1062.51	-0.71	2	50	59	R	GVNTFSPEGR	L	0	-	49.1
		700.44	1398.86	1398.76	0.10	2	93	105	R	ITSPLLEPSSVEK	I	0	-	49.1
		412.96	823.90	824.45	-0.55	2	126	132	R	TLVEHAR	V	0	-	27.7
206	chr4.CM0087.390.nc	804.52	1607.02	1606.82	0.20	2	281	294	K	DKVSPQQVSDYTLK	L	1	-	50.7
		748.93	1495.85	1495.66	0.18	2	70	83	R	GILAMDESNAATCGK	R	0	Oxidation (M); Propionamide (C)	90.6
207	chr1.LjT141I3.60.nd	701.37	1400.73	1400.64	0.10	2	184	197	K	EVGADAVSHGCTGK	G	0	Propionamide (C)	59.3
		847.99	1693.97	1693.87	0.10	2	347	362	R	GVYETPGGTILFDAVR	D	0	-	88.6
208	LjSGA_019550.1	837.88	1673.74	1674.72	-0.98	2	241	256	K	ATAGDTHLGGEDFDNR	M	0	-	72.6
		829.96	1657.91	1657.90	0.01	2	189	204	R	IINEPTAAGLAYGLQK	K	0	-	26.0
		893.97	1785.93	1786.00	-0.07	2	189	205	R	IINEPTAAGLAYGLQKK	S	1	-	39.2
		718.95	1435.89	1436.73	-0.84	2	366	377	K	VQELLQDFFNGK	E	0	-	44.0
209	chr1.CM0147.760.nc	539.59	1615.75	1616.82	-1.06	3	285	300	K	AFDLASKPEGAGTPTR	D	0	-	63.1
		693.45	1384.89	1384.78	0.11	2	246	257	R	ELIIGKDEILK	T	1	-	25.4
		804.97	1607.93	1607.78	0.15	2	104	118	K	QTIGASDDVYVGDIR	D	0	-	68.7
		412.45	822.88	823.42	-0.54	2	88	94	R	SSQYIAR	G	0	-	53.2
		508.95	1015.89	1016.56	-0.67	2	65	75	R	STVLVTGAGGR	T	0	-	32.7
210	chr4.CM0288.640.nc	536.93	1071.85	1072.53	-0.68	2	104	112	K	EEPIVEETK	E	0	-	46.2
		737.95	1473.88	1473.68	0.19	2	113	126	K	ETAATEAAPVEEEK	S	0	-	70.2
211	LjSGA_011044.2	948.52	1895.02	1896.02	-1.00	2	373	391	K	EAQEGVAIEIAEAVVGALK	G	0	-	82.7
		757.98	1513.95	1514.87	-0.91	2	425	440	K	LAVQLVSGGSGITSVK	V	0	-	44.3
		966.10	1930.19	1930.03	0.16	2	355	372	K	LVQHENVITVPHLGASTK	E	0	-	29.9
		535.44	1068.87	1069.51	-0.64	2	298	306	K	VFNDETFAK	M	0	-	49.3
212	LjSGA_010022.2	795.40	1588.78	1589.83	-1.05	2	123	136	K	GIQESVEALQFLEK	E	0	-	67.2
		735.43	1468.84	1468.75	0.09	2	185	196	K	WSQDFINHPVVK	E	0	-	58.1
		462.43	922.86	923.47	-0.62	2	213	221	R	YAASINASK	L	0	-	50.8
213	LjT41B11.10.nd	615.66	1229.31	1229.52	-0.21	2	81	91	K	FSDASVQSDMK	L	0	Oxidation (M)	63.0
		402.98	803.94	803.44	0.50	2	507	513	K	ITITNDK	G	0	-	41.3
		545.43	1088.84	1088.53	0.31	2	837	845	K	LLDDIEESR	F	0	-	23.9
		841.00	1679.99	1679.83	0.17	2	145	159	K	NAVVTVPAYFNDSQR	Q	0	-	60.8
		831.50	1660.98	1660.84	0.14	2	60	74	K	NQVTINPTNTVFDAK	R	0	-	32.3
214	chr1.CM0133.1430.nc	647.45	1292.89	1293.68	-0.79	2	153	164	R	EIAEAYLGTTVK	N	0	-	32.0
		841.00	1679.99	1679.83	0.17	2	165	179	K	NAVISVPAYFNDSQR	Q	0	-	48.3
		743.94	1485.86	1486.69	-0.84	2	60	72	R	TTPSYVAFTDIER	L	0	-	54.9
215	chr1.CM0033.430.nc	567.01	1132.00	1132.69	-0.68	2	118	128	K	VSGVSLALFK	E	0	-	81.6
216	chr4.CM1616.30.nc	660.78	1319.54	1319.71	-0.17	2	117	127	R	EQLTQLVQYAK	D	0	-	69.1
		661.28	1320.54	1320.71	-0.17	2	186	197	K	QLLFSDGFPVAK	D	0	-	54.2
217	LjSGA_041684.1	936.97	1871.93	1872.98	-1.05	2	172	189	K	VNQIGTVTESIQAALDSK	T	0	-	98.7
		403.52	805.02	805.44	-0.43	2	235	240	K	YNQLLR	I	0	-	44.9

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
218	LjSGA_122913.1	689.52	1377.03	1377.80	-0.77	2	101	113	K	SPDAPVIGLILQR	S	0	-	50.6
		865.98	1729.95	1730.92	-0.97	2	138	154	K	VVPLFAGGLDFSGPVEK	F	0	-	80.9
219	LjSGA_147294.1	630.95	1259.89	1260.69	-0.80	2	38	49	K	NTVESITGIISK	T	0	-	68.6
220	chr1.CM0410.90.nc	475.98	949.94	950.43	-0.49	2	42	50	R	GEISSSES	L	0	-	47.1
		701.52	1401.03	1401.76	-0.73	2	17	29	R	IAQIPVSEGYLGR	V	0	-	46.6
		626.54	1251.07	1251.72	-0.65	2	51	62	R	LIESPAPGIISR	R	0	-	66.5
221	chr1.CM0016.120.nc	569.91	1137.81	1138.55	-0.74	2	149	159	K	DAAESTLAAYK	S	0	-	66.6
		594.94	1187.87	1188.65	-0.78	2	222	231	K	DSTLMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	222	231	K	DSTLMQLLR	D	0	Oxidation (M)	56.3
		458.96	915.91	916.52	-0.61	2	68	75	R	IISIEQK	E	0	-	23.4
		408.44	814.87	815.41	-0.54	2	17	23	K	LAEQAE	Y	0	-	31.2
		514.94	1027.87	1028.55	-0.68	2	114	124	R	LIPAAASGDSK	V	0	-	55.2
		683.34	1364.67	1365.55	-0.88	2	24	33	R	YEEMVEFMEK	L	0	2 Oxidation (M)	22.4
221	LjT06N06.430.nd	569.91	1137.81	1138.55	-0.74	2	149	159	K	DAAESTLAAYK	S	0	-	66.6
		458.96	915.91	916.52	-0.61	2	68	75	R	IISIEQK	E	0	-	23.4
		408.44	814.87	815.41	-0.54	2	17	23	K	LAEQAE	Y	0	-	31.2
		514.94	1027.87	1028.55	-0.68	2	114	124	R	LIPAAASGDSK	V	0	-	55.2
		683.34	1364.67	1365.55	-0.88	2	24	33	R	YEEMVEFMEK	L	0	2 Oxidation (M)	22.4
221	LjT09J10.70.nc	569.91	1137.81	1138.55	-0.74	2	99	109	K	DAAESTLAAYK	S	0	-	66.6
		458.96	915.91	916.52	-0.61	2	18	25	R	IISIEQK	E	0	-	23.4
221	chr1.CM0982.360.nd	594.94	1187.87	1188.65	-0.78	2	20	29	K	DSTLMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	20	29	K	DSTLMQLLR	D	0	Oxidation (M)	56.3
221	LjT46P06.260.nd	594.94	1187.87	1188.65	-0.78	2	19	28	K	DSTLMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	19	28	K	DSTLMQLLR	D	0	Oxidation (M)	56.3
221	LjSGA_024472.2	594.94	1187.87	1188.65	-0.78	2	128	137	K	DSTLMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	128	137	K	DSTLMQLLR	D	0	Oxidation (M)	56.3
221	LjSGA_087842.1	594.94	1187.87	1188.65	-0.78	2	20	29	K	DSTLMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	20	29	K	DSTLMQLLR	D	0	Oxidation (M)	56.3
221	LjSGA_104179.1	594.94	1187.87	1188.65	-0.78	2	19	28	K	DSTLMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	19	28	K	DSTLMQLLR	D	0	Oxidation (M)	56.3
222	chr1.CM0171.170.nc	719.46	1436.90	1436.75	0.15	2	54	66	R	ALVVHELEDDLK	G	0	-	29.3
		706.92	1411.83	1411.68	0.15	2	67	81	K	GGHELSTGNAGGR	L	0	-	55.7
		562.84	1123.66	1123.53	0.13	2	10	19	K	THGAPDEIR	H	0	-	50.2
222	chr3.CM0396.590.nc	719.46	1436.90	1436.75	0.15	2	161	173	R	ALVVHELEDDLK	G	0	-	29.3
		706.92	1411.83	1411.68	0.15	2	174	188	K	GGHELSTGNAGGR	L	0	-	55.7
		562.84	1123.66	1123.53	0.13	2	115	124	K	THGAPDEIR	H	0	-	50.2
222	chr1.CM0033.280.nc	719.46	1436.90	1436.75	0.15	2	54	66	R	ALVVHELEDDLK	G	0	-	29.3
		562.84	1123.66	1123.53	0.13	2	10	19	K	THGAPDEIR	H	0	-	50.2
223	LjSGA_013718.1	671.51	1341.00	1341.75	-0.76	2	168	179	R	LVVDLPLPSK	G	0	-	71.4
		967.53	1933.05	1932.91	0.14	2	152	167	K	NSMIDIHTFNQSQYPR	L	0	-	29.7
224	chr2.CM0191.630.nc	685.43	1368.86	1368.74	0.12	2	2	15	M	APVAAASDSIKPR	D	0	-	62.2

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		786.49	1570.96	1570.83	0.13	2	222	236	R	GRPSTIVDKDEGLGK	F	1	-	31.0
		534.56	1067.10	1067.73	-0.63	2	372	381	R	ILVTLLGVLK	Q	0	-	66.5
224	chr6.LjT17I05.60.nd	534.56	1067.10	1067.73	-0.63	2	23	32	R	ILVTLLGVLK	R	0	-	66.5
225	LjSGA_082478.1	481.94	961.87	962.48	-0.61	2	96	104	R	GDFRIDGR	Y	0	-	58.6
		812.43	1622.84	1623.86	-1.02	2	80	95	K	IIGATNPAQSEPGTIR	G	0	-	46.0
		584.64	1750.89	1751.95	-1.07	3	79	95	R	KIIGATNPAQSEPGTIR	G	1	-	30.3
		611.95	1221.88	1222.64	-0.76	2	30	40	K	LLTVESSFAEK	H	0	-	62.0
226	LjSGA_005533.1	552.95	1103.89	1104.55	-0.66	2	116	126	K	VIGNTGSNSTR	E	0	-	83.6
227	chr1.CM0591.260.nd	522.92	1043.83	1044.52	-0.69	2	43	53	K	LVAASGEAGDR	V	0	-	85.7
		577.93	1153.85	1154.60	-0.75	2	54	62	R	VQFTEYIQK	N	0	-	20.5
228	chr3.CM0116.300.nc	775.01	1548.01	1547.90	0.10	2	75	89	K	EVLAVPIAPNVSLAR	Q	0	-	50.7
		569.36	1136.70	1136.63	0.07	2	198	207	K	LLNLHVSADR	N	0	-	55.7
229	LjT24M21.140.nd	493.47	984.92	985.58	-0.66	2	237	245	K	ATLQLAEIK	H	0	-	53.2
		535.92	1069.82	1070.54	-0.71	2	208	216	R	NAELDPEKR	L	1	-	47.6
		507.94	1013.87	1014.55	-0.67	2	105	114	K	NLAGDVGTR	T	0	-	40.5
		877.86	1753.70	1754.86	-1.17	2	122	136	K	STPFQPYSEVFGLR	F	0	-	71.2
		433.92	865.83	866.40	-0.57	2	115	121	R	TEFEDVK	S	0	-	31.1
229	LjT24M21.110.nd	493.47	984.92	985.58	-0.66	2	70	78	K	ATLQLAEIK	H	0	-	53.2
229	LjSGA_018808.1	535.92	1069.82	1070.54	-0.71	2	207	215	R	NAELDPEKR	L	1	-	47.6
230	chr4.LjT06I07.80.nd	853.92	1705.83	1706.86	-1.02	2	78	98	R	VGGAAAAGGAAPAAAPAAEK	K	0	-	62.4
231	LjSGA_121474.1	672.89	1343.77	1343.60	0.17	2	12	23	K	GEDPYDDAVVHK	L	0	-	27.2
		647.94	1293.86	1294.67	-0.80	2	1	11	-	ISEEEISFLTK	G	0	-	69.3
231	LjSGA_131611.1	672.89	1343.77	1343.60	0.17	2	25	36	K	GEDPYDDAVVHK	L	0	-	27.2
		647.94	1293.86	1294.67	-0.80	2	14	24	K	ISEEEISFLTK	G	0	-	69.3
231	LjSGA_043018.2	647.94	1293.86	1294.67	-0.80	2	10	20	K	ISEEEISFLTK	G	0	-	69.3
232	chr6.CM0114.320.nc	817.98	1633.94	1633.82	0.12	2	32	46	R	ISQEVLDALGEEFK	G	0	-	36.2
		877.52	1753.03	1752.90	0.13	2	118	133	K	KGDNDLPGLTDVEKPR	M	1	-	93.7
232	LjT31M07.110.nd	817.98	1633.94	1633.82	0.12	2	8	22	R	ISQEVLDALGEEFK	G	0	-	36.2
		877.52	1753.03	1752.90	0.13	2	94	109	K	KGDNDLPGLTDVEKPR	M	1	-	93.7
233	LjSGA_064073.1	477.97	953.92	954.51	-0.59	2	101	108	K	EVPLQDVR	L	0	-	35.5
		1135.47	2268.92	2270.10	-1.18	2	141	162	K	NAGLPTGTPYGGWEGADIELR	G	0	-	90.1
234	chr3.CM0106.120.nd	965.54	1929.07	1928.95	0.12	2	132	149	K	LTIVSDSCHSGGLIEEAK	E	0	Propionamide (C)	25.5
		936.02	1870.02	1869.90	0.12	2	72	89	R	SAESGDVLVVHYSGHGTR	L	0	-	43.3
		656.51	1311.01	1311.80	-0.79	2	231	242	R	SLPLSTLIDILK	Q	0	-	52.3
235	chr2.CM0788.10.nc	642.48	1282.94	1283.62	-0.68	2	250	260	K	EEEEEVAPKPK	A	0	-	57.8
		617.01	1232.00	1232.65	-0.65	2	347	357	K	MLVIGSEPPPK	V	0	Oxidation (M)	37.9
		599.51	1197.01	1197.64	-0.62	2	211	222	K	QAEAVPAVQSAK	K	0	-	51.7
		515.99	1029.96	1030.49	-0.53	2	388	396	K	VDINDEAQK	E	0	-	51.7
235	chr4.CM0042.1550.nc	642.48	1282.94	1283.62	-0.68	2	247	257	K	EEEEEVAPKPK	A	0	-	57.8

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		617.01	1232.00	1232.65	-0.65	2	344	354	K	MLVIGSEPPFK	V	0	Oxidation (M)	37.9
		599.51	1197.01	1197.64	-0.62	2	208	219	K	QAEAVPAVQSAK	K	0	-	51.7
		515.99	1029.96	1030.49	-0.53	2	385	393	K	VDINDEAQK	E	0	-	51.7
236	LjSGA_067100.1	683.40	1364.78	1365.67	-0.89	2	87	99	K	FDVGNVVMVTGGR	N	0	Oxidation (M)	50.5
		634.41	1266.80	1267.62	-0.82	2	47	57	K	GIPYLNTYDGR	T	0	-	43.7
		429.95	857.88	858.44	-0.56	2	74	80	K	LDLQENK	I	0	-	20.2
		474.47	946.92	947.54	-0.62	2	134	142	R	LGNVFTIGK	G	0	-	53.0
		465.46	928.91	929.52	-0.61	2	158	165	K	LSIIEEAR	K	0	-	46.7
236	LjSGA_044802.1	683.40	1364.78	1365.67	-0.89	2	59	71	K	FDVGNVVMVTGGR	N	0	Oxidation (M)	50.5
		634.41	1266.80	1267.62	-0.82	2	19	29	K	GIPYLNTYDGR	T	0	-	43.7
		465.46	928.91	929.52	-0.61	2	130	137	K	LSIIEEAR	K	0	-	46.7
237	LjSGA_053319.1	960.82	1919.62	1919.88	-0.26	2	108	127	K	SLAADESQNGNSASLSGQK	I	0	-	95.5
238	chr1.CM0800.280.nd	775.02	1548.03	1547.86	0.17	2	63	76	K	ADHELPLILSAELK	I	0	-	24.7
		957.44	1912.87	1914.03	-1.16	2	77	96	K	IAGSSILVSDLAVDSTAPAK	T	0	-	79.4
239	chr3.CM0080.50.nd	622.48	1242.94	1242.71	0.23	2	272	283	K	VLLNGMTLIGR	S	0	-	79.7
240	LjSGA_077260.1	622.48	1242.94	1242.71	0.23	2	94	105	K	VILNGMTLIGR	S	0	-	79.7
241	LjT41F16.210.nd	664.44	1326.86	1327.71	-0.84	2	151	163	K	LGADGSAQLLDIR	A	0	-	94.7
242	chr3.CM0136.230.nd	569.46	1136.91	1137.57	-0.66	2	289	299	K	ASIADFVSSNK	L	0	-	52.9
		713.40	1424.79	1425.61	-0.82	2	561	573	K	ESQSSSTDITKDEL	-	1	-	38.2
		524.01	1046.00	1046.61	-0.61	2	300	308	K	LPLVTFTFR	E	0	-	38.7
		686.42	1370.83	1371.62	-0.79	2	420	432	K	SDPVETNDGDVK	I	0	-	44.8
		589.45	1176.89	1177.57	-0.68	2	379	390	K	VVAFAGNDGSK	F	0	-	53.5
243	chr6.CM0037.760.nc	681.98	1361.95	1362.73	-0.78	2	66	77	K	LQAGYLFPEVAR	R	0	-	56.3
		661.28	1320.54	1320.71	-0.17	2	320	331	K	QLLFSDGFPAK	D	0	-	54.2
243	chr4.CM1616.50.nc	681.98	1361.95	1362.73	-0.78	2	68	79	K	LQAGYLFPEVAR	R	0	-	56.3
244	LjSGA_070717.1	711.42	1420.83	1420.72	0.10	2	169	180	R	ASALIQHEWNPR	T	0	-	63.5
		708.42	1414.82	1415.75	-0.93	2	183	196	R	VSLVGEVDTGAIEK	S	0	-	60.6
245	LjSGA_074884.1	506.05	1010.08	1010.65	-0.57	2	127	135	R	IKPVLTVNK	M	0	-	38.4
		712.45	1422.88	1423.68	-0.79	2	220	231	R	LWGENFFDPATK	K	0	-	43.5
		1033.43	2064.84	2066.00	-1.16	2	327	344	R	VENLYEGPLDDQYATAIR	N	0	-	68.3
246	chr4.CM0026.460.nc	623.95	1245.89	1245.64	0.25	2	1	10	-	MADLLEWPKK	D	1	Oxidation (M)	20.2
		560.95	1119.88	1120.62	-0.74	2	245	255	R	QPGPIPLNTK	V	0	-	35.2
		756.92	1511.83	1512.81	-0.99	2	227	241	K	SAEVVNVAQELGGK	I	0	-	91.6
247	LjSGA_100703.1.1	581.94	1161.87	1162.59	-0.73	2	175	186	R	GSASVGQSTLTR	F	0	-	32.5
		708.44	1414.87	1415.75	-0.88	2	16	28	R	LEIQAIADDITSK	Y	0	-	89.8
247	LjSGA_106942.1.1	581.94	1161.87	1162.59	-0.73	2	187	198	R	GSASVGQSTLTR	F	0	-	32.5
		708.44	1414.87	1415.75	-0.88	2	28	40	R	LEIQAIADDITSK	Y	0	-	89.8
247	LjSGA_103041.1	708.44	1414.87	1415.75	-0.88	2	12	24	R	LEIQAIADDITSK	Y	0	-	89.8
248	chr4.CM1616.360.nc	627.42	1252.82	1253.59	-0.78	2	288	298	K	VSTEFNDFPAK	A	0	-	64.1
		923.36	1844.71	1845.90	-1.20	2	317	331	K	YGVVEIFDQTLEYLK	T	0	-	58.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
249	LjSGA_071976.1.1	784.44	1566.86	1567.86	-1.00	2	74	88	R	TALSHVDNLITGVTK	G	0	-	58.3
		449.46	896.92	897.49	-0.58	2	24	31	K	VIEVEGPR	G	0	-	46.3
250	LjT08D05.60.nd	660.44	1318.87	1319.71	-0.84	2	245	256	K	LGDLSQTQIFAK	I	0	-	75.1
251	chr5.CM0299.350.nc	517.96	1033.90	1034.53	-0.64	2	30	38	K	IMDIASLEK	F	0	Oxidation (M)	37.4
		599.44	1196.86	1197.59	-0.73	2	66	76	K	ITVTSDSNFSK	R	0	-	70.9
		779.34	1556.66	1557.61	-0.95	2	112	124	R	YFNIAENEGEEED	-	0	-	36.8
251	chr5.LjT38I13.150.nd	517.96	1033.90	1034.53	-0.64	2	25	33	K	IMDIASLEK	F	0	Oxidation (M)	37.4
		599.44	1196.86	1197.59	-0.73	2	61	71	K	ITVTSDSNFSK	R	0	-	70.9
		779.34	1556.66	1557.61	-0.95	2	107	119	R	YFNIAENEGEEED	-	0	-	36.8
252	LjSGA_126077.1	645.93	1289.85	1290.61	-0.76	2	54	65	K	LNTDESPSTATR	Y	0	-	68.7
253	chr5.CM0357.630.nc	790.01	1578.00	1577.86	0.14	2	200	213	K	ATTGIYPLQNVFVR	K	0	-	50.6
		840.46	1678.91	1678.75	0.15	2	228	242	K	LMEVHGDYSEDVGTK	V	0	-	47.2
		999.58	1997.14	1996.96	0.18	2	243	261	K	VDRPADETVAEETPEIVGA	-	0	-	45.9
253	LjSGA_038721.1	840.46	1678.91	1678.75	0.15	2	110	124	K	LMEVHGDYSEDVGTK	V	0	-	47.2
254	chr4.CM0042.1960.nc	764.93	1527.84	1528.82	-0.99	2	413	427	R	FLIAGGGAPEIELSR	Q	0	-	91.0
		665.41	1328.81	1329.65	-0.85	2	385	396	R	GSNQLVLDEAER	S	0	-	40.2
254	chr4.CM0432.120.nd	764.93	1527.84	1528.82	-0.99	2	410	424	R	FLIAGGGAPEIELSR	Q	0	-	91.0
		665.41	1328.81	1329.65	-0.85	2	382	393	R	GSNQLVLDEAER	S	0	-	40.2
255	chr3.CM0216.760.nc	748.93	1495.85	1495.66	0.18	2	70	83	R	GILAMDESNAICGK	R	0	Oxidation (M); Propionamide (C)	90.6
		663.87	1325.72	1325.57	0.15	2	380	391	K	YNGDGESEAAK	E	1	-	40.6
256	LjSGA_025401.2	690.38	1378.74	1378.65	0.09	2	30	41	R	ANERDEGFSLNK	E	1	-	44.6
		534.33	1066.65	1066.58	0.07	2	97	106	K	AVQDTVVHAK	D	0	-	47.4
		653.83	1305.65	1305.55	0.10	2	130	140	K	MGEYTDYGVQK	A	0	Oxidation (M)	56.6
257	chr1.LjT14I13.210.nd	837.88	1673.74	1673.74	0.00	2	229	244	K	ATAGNTHLGGEDFDNR	M	0	-	70.8
		664.92	1327.83	1327.62	0.21	2	310	319	R	FEELNINMFR	E	0	Oxidation (M)	42.3
258	LjSGA_000267.1	456.48	910.95	911.46	-0.51	2	87	94	R	AMHAVIDR	Q	0	-	42.3
		464.47	926.93	927.46	-0.53	2	87	94	R	AMHAVIDR	Q	0	Oxidation (M)	54.6
		511.95	1021.89	1022.43	-0.54	2	142	149	R	DDFVEQDR	S	0	-	58.2
259	chr1.CM0248.160.nc	599.95	1197.89	1198.66	-0.77	2	84	94	K	ALEQLQDAIAK	S	0	-	63.2
		508.41	1014.81	1015.49	-0.67	2	235	242	K	YVSEVYEK	E	0	-	35.0
260	chr4.CM0044.530.nc	759.43	1516.84	1517.85	-1.01	2	46	59	K	IFQGGQLLSLSLDK	V	0	-	74.3
		572.42	1142.83	1143.59	-0.76	2	173	183	K	NAESVGVFPFK	N	0	-	53.0
261	LjSGA_021575.2	847.99	1693.97	1693.87	0.10	2	54	69	R	GVYETPGGTILFDAVR	D	0	-	88.6
		819.99	1637.97	1636.93	1.04	2	19	34	K	LSPGNLVAKLNEIGGR	H	1	-	25.0
262	chr1.CM0378.320.nd	724.45	1446.88	1447.68	-0.80	2	11	26	K	TPSGEGSTTSAPSAK	A	0	-	88.6
263	chr1.CM0098.210.nc	613.46	1224.91	1225.63	-0.72	2	454	464	K	AFVSEYAVNVK	E	0	-	29.5
		709.43	1416.84	1417.70	-0.86	2	243	254	K	DLFQMVDLNP	F	0	-	77.1
		522.51	1043.00	1043.62	-0.62	2	196	204	R	KIETILEAK	D	1	-	47.3

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
264	LjT18K22.30.nc	854.52	1707.02	1706.91	0.11	2	203	218	K	EGVIQHSSTINNLGIGR	S	0	-	47.9
		402.98	803.95	804.47	-0.53	2	196	202	R	GLFIDK	E	0	-	23.3
		867.39	1732.76	1733.88	-1.12	2	161	177	K	SGGLGDLNYPVSDVTK	S	0	-	56.2
		750.93	1499.85	1500.83	-0.98	2	182	195	K	SYGVLPDQGIALR	G	0	-	42.3
265	chr6.CM0114.310.nc	632.37	1262.72	1262.64	0.09	2	180	192	K	TGEVAGSATETLK	G	0	-	87.6
266	LjSGA_015672.1	701.41	1400.80	1401.73	-0.93	2	105	116	K	VIACIGETLEQR	E	0	Propionamide (C)	63.9
267	LjSGA_016889.1	616.18	1230.35	1230.55	-0.19	2	312	323	R	NAGPSALDSER	R	0	-	61.2
		598.36	1194.71	1194.62	0.09	2	469	480	R	TLTNVGAAGTYK	V	0	-	60.3
267	chr2.CM0783.60.nd	598.36	1194.71	1194.62	0.09	2	683	694	R	TLTNVGAAGTYK	V	0	-	60.3
268	chr1.CM0023.150.nc	540.93	1079.84	1080.51	-0.66	2	393	402	R	AVDDGVNTYK	A	0	-	47.8
		895.03	1788.05	1787.91	0.14	2	257	272	K	GTVLIHSAEQLENYSK	T	0	-	33.4
		798.42	1594.82	1595.80	-0.99	2	241	256	K	VAVFVSGVDTSATDTK	G	0	-	67.7
269	LjSGA_026224.1	680.41	1358.80	1358.78	0.02	2	268	278	K	LLLQQIDEIFK	E	0	-	72.1
270	chr5.CM0040.320.nc	535.46	1068.90	1069.59	-0.68	2	204	213	K	ALQAGDQLVR	V	0	-	71.3
		739.95	1477.88	1478.81	-0.93	2	183	196	R	AVPTLPINLEDAAR	S	0	-	49.2
271	LjSGA_117719.1	748.34	1494.66	1494.85	-0.19	2	79	92	K	VVQTQAPVQLGSLR	A	0	-	64.7
272	chr2.CM0608.160.nd	495.43	988.85	989.46	-0.61	2	8	17	R	ADPASGYPR	T	0	-	62.0
273	chr1.CM0442.310.nd	507.95	1013.89	1014.57	-0.68	2	16	26	K	LVIVGDGGTGK	T	0	-	85.5
		614.41	1226.80	1227.61	-0.81	2	146	155	K	NLQYYEISAK	S	0	-	27.0
273	chr1.CM0442.350.nd	507.95	1013.89	1014.57	-0.68	2	16	26	K	LVIVGDGGTGK	T	0	-	85.5
		614.41	1226.80	1227.61	-0.81	2	146	155	K	NLQYYEISAK	S	0	-	27.0
273	LjSGA_031947.1	507.95	1013.89	1014.57	-0.68	2	15	25	K	LVIVGDGGTGK	T	0	-	85.5
		614.41	1226.80	1227.61	-0.81	2	145	154	K	NLQYYEISAK	S	0	-	27.0
274	chr2.CM0021.160.nc	839.44	1676.87	1677.87	-0.99	2	379	394	R	DVGAVSQQLYTALTR	L	0	-	84.2
275	chr5.CM0077.680.nc	638.76	1275.51	1275.68	-0.18	2	193	204	R	AIASWNIDANFLK	V	0	-	74.7
		579.50	1156.99	1157.64	-0.65	2	176	187	K	GVLLYPPPGTGK	T	0	-	31.8
		581.44	1160.87	1161.58	-0.71	2	341	351	K	LAEGFNGADLR	N	0	-	38.3
276	chr4.CM0182.340.nd	503.48	1004.94	1005.56	-0.63	2	91	98	R	FPFLLVDR	V	0	-	45.6
		729.96	1457.90	1458.81	-0.91	2	99	112	R	VIEYNPGVSAVAIK	N	0	-	51.4
		823.44	1644.86	1645.88	-1.02	2	71	84	R	YPAFPTVLIDINQIR	N	0	-	49.5
276	chr4.CM0182.40.nc	503.48	1004.94	1005.56	-0.63	2	91	98	R	FPFLLVDR	V	0	-	45.6
		729.96	1457.90	1458.81	-0.91	2	99	112	R	VIEYNPGVSAVAIK	N	0	-	51.4
		823.44	1644.86	1645.88	-1.02	2	71	84	R	YPAFPTVLIDINQIR	N	0	-	49.5
277	chr3.CM0070.370.nc	880.89	1759.76	1760.81	-1.05	2	77	91	K	AMGIMNSFINDIFEK	L	0	2 Oxidation (M)	79.6
		590.88	1179.75	1179.62	0.13	2	66	76	K	QVHPDIGSSK	A	0	-	36.4
277	chr3.LjT39G24.210.nd	880.89	1759.76	1760.81	-1.05	2	83	97	K	AMGIMNSFINDIFEK	L	0	2 Oxidation (M)	79.6
		590.88	1179.75	1179.62	0.13	2	72	82	K	QVHPDIGSSK	A	0	-	36.4
277	chr3.LjT39G24.30.nd	880.89	1759.76	1760.81	-1.05	2	78	92	K	AMGIMNSFINDIFEK	L	0	2 Oxidation (M)	79.6

Continues...

Supplemental Table S2.11: (*green_LotusAA GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		590.88	1179.75	1179.62	0.13	2	67	77	K	QVHPDIGISSK	A	0	-	36.4
277	LjSGA_022700.1	880.89	1759.76	1760.81	-1.05	2	76	90	K	AMGIMNSFINDIFEK	L	0	2 Oxidation (M)	79.6
		590.88	1179.75	1179.62	0.13	2	65	75	K	QVHPDIGISSK	A	0	-	36.4
278	chr1.CM0150.640.nd	694.43	1386.85	1387.62	-0.78	2	271	284	R	GDSNEVGPSVDNAK	A	0	-	64.1
		666.48	1330.95	1331.70	-0.75	2	138	151	R	NVQSALTSASLGK	I	0	-	56.3
279	LjSGA_033928.1	584.44	1166.87	1167.55	-0.68	2	53	65	R	YASAGGGSVNASK	E	0	-	82.9
280	chr5.CM0239.440.nd	533.45	1064.88	1065.50	-0.62	2	277	286	K	EFVAASGEEK	K	0	-	32.6
		925.43	1848.84	1849.91	-1.07	2	120	137	R	TAEALAEFVNTEGGTNVK	I	0	-	64.2
281	chr5.CM0335.10.nc	601.92	1201.83	1202.59	-0.76	2	199	211	R	GSGGASLNVEQGK	T	0	-	67.1
282	LjSGA_023994.2	532.42	1062.83	1063.51	-0.69	2	226	236	K	STIASASQDGK	V	0	-	57.0
282	LjSGA_045237.1	532.42	1062.83	1063.51	-0.69	2	239	249	K	STIASASQDGK	V	0	-	57.0
283	LjSGA_046369.1	664.92	1327.83	1328.61	-0.78	2	229	238	R	FEELNMDLFR	R	0	Oxidation (M)	57.0
		615.66	1229.31	1229.52	-0.21	2	2	12	K	FSDASVQSDMK	L	0	Oxidation (M)	63.0
284	LjSGA_094099.1	723.39	1444.77	1445.69	-0.93	2	245	258	K	DAGINCVTVGSSPR	F	0	Propionamide (C)	80.7
		448.43	894.85	895.43	-0.58	2	116	123	K	FSESIDK	I	0	-	32.6
285	chr2.CM0031.300.nc	711.93	1421.85	1422.64	-0.79	2	211	222	R	GQESENYQEAIR	V	0	-	65.6
		604.01	1206.01	1206.74	-0.73	2	200	210	K	IPLQAIVNALR	G	0	-	48.8
		539.51	1077.00	1077.62	-0.62	2	136	145	K	TLFTIGSLAR	N	0	-	25.8
		634.94	1267.87	1268.57	-0.70	2	446	456	K	TSNYGNEPMLK	N	0	Oxidation (M)	24.6
286	LjSGA_075461.1	690.46	1378.91	1379.67	-0.76	2	41	53	R	LFNETSEALGGSR	A	0	-	79.8
287	chr1.CM0318.110.nd	449.49	896.97	897.49	-0.53	2	109	117	K	IPQGGELGK	F	0	-	47.5
		670.77	1339.52	1339.69	-0.17	2	70	80	K	SLTWLDLNHNK	I	0	-	58.2
288	LjSGA_006403.1	750.49	1498.96	1499.93	-0.97	2	233	246	K	LVVYPLSLLGVSIIK	A	0	-	51.3
289	chr3.CM0091.440.nd	603.90	1205.78	1206.55	-0.77	2	298	308	K	AGEADEPSIYR	I	0	-	55.4
		629.97	1257.93	1258.75	-0.82	2	29	39	R	ILVLDDDFALK	S	0	-	62.5
		703.25	1404.48	1404.72	-0.24	2	197	210	K	VLSASPTAYSANPK	S	0	-	29.1
290	chr6.LjT02P05.170.nd	647.90	1293.79	1294.60	-0.81	2	128	139	R	AVSTEEGEQFAK	E	0	-	60.7
		624.93	1247.85	1248.63	-0.79	2	152	162	K	TAQNVEEAFIK	T	0	-	54.2
291	LjSGA_017763.1	834.97	1667.93	1668.93	-1.00	2	60	74	K	QTSPQIIIVDLLDISK	K	0	-	77.4
292	LjSGA_063269.1	621.47	1240.92	1241.69	-0.77	2	22	33	K	ALTDGDSIIPK	V	0	-	39.0
		712.41	1422.80	1423.66	-0.86	2	146	158	K	AVEGYVLANPDYN	-	0	-	31.9
		580.92	1159.82	1160.52	-0.70	2	124	134	K	GDASPSEEEK	A	0	-	43.5
		542.47	1082.92	1083.59	-0.67	2	104	115	K	LVAGPDGGSIK	L	0	-	64.9
293	LjSGA_001057.3	552.91	1103.81	1104.54	-0.74	2	88	97	R	VQTSADDEVTR	I	0	-	71.2
293	LjSGA_008141.1	552.91	1103.81	1104.54	-0.74	2	122	131	R	VQTSADDEVTR	I	0	-	71.2
294	LjT16G18.110.nd	448.47	894.93	895.48	-0.56	2	51	58	R	IVMGLYK	T	0	Oxidation (M)	37.5
		584.43	1166.85	1167.58	-0.73	2	37	46	K	VFFDVEIDGK	A	0	-	67.3

Continues...

Supplemental Table S2.11: (*green_LotusAA GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
295	chr6.CM0314.590.nc	576.85	1151.69	1151.56	0.13	2	7	17	K	IHEAAADPNK	V	0	-	54.4
		1091.21	2180.41	2180.14	0.27	2	243	262	K	IPAEITMAALEPIKDNEEAVK	A	1	-	21.2
		622.43	1242.85	1243.64	-0.79	2	29	39	K	TEDGVVNLLER	M	0	-	50.2
		535.37	1068.73	1068.60	0.12	2	313	322	R	TRPANAIQAK	E	0	-	41.2
296	chr6.CM0037.810.nc	439.50	876.98	876.47	0.51	2	216	224	K	GLISCVTGK	G	0	-	22.0
		621.86	1241.71	1241.62	0.09	2	452	462	R	GPDPHFPFGIK	D	0	-	39.7
		652.97	1303.93	1304.60	-0.67	2	47	57	K	VQACSQEEVNK	V	0	Propionamide (C)	66.7
297	chr1.LjT43O05.80.nd	561.42	1120.82	1121.51	-0.69	2	131	140	R	GVMISDNQSR	F	0	Oxidation (M)	59.2
		529.49	1056.96	1057.61	-0.65	2	230	239	R	IIGVDLVSSR	F	0	-	46.1
		692.36	1382.70	1382.58	0.12	2	115	125	K	SEESNMCDLLR	I	0	Oxidation (M); Propionamide (C)	39.5
298	chr1.CM0050.40.nc	735.96	1469.90	1470.86	-0.95	2	67	81	R	GFIFGPPIALAIGAK	F	0	-	60.6
298	chr1.LjT45O14.130.nd	735.96	1469.90	1470.86	-0.95	2	67	81	R	GFIFGPPIALAIGAK	F	0	-	60.6
299	LjB01J01.10.nc	934.51	1867.00	1866.86	0.13	2	94	110	K	AEANNYDSTYGEPVPK	E	0	-	24.0
		906.83	1811.65	1812.84	-1.19	2	144	159	R	DGPQLYMVPEPGVSYSR	Y	0	Oxidation (M)	41.1
		664.87	1327.72	1327.63	0.09	2	73	86	R	HSGMAVAGLAADGR	Q	0	Oxidation (M)	40.8
		534.44	1066.86	1067.57	-0.71	2	21	29	R	VFQIEYAAK	A	0	-	44.1
300	LjSGA_048933.1	751.50	1500.98	1500.83	0.15	2	31	43	K	HPEIDVPNLQVIK	L	0	-	36.5
		829.47	1656.93	1657.93	-1.00	2	77	91	R	TYLNLPSEIVPATLK	K	0	-	52.4
300	chr4.CM0501.190.nd	829.47	1656.93	1657.93	-1.00	2	100	114	R	TYLNLPSEIVPATLK	K	0	-	52.4
301	LjSGA_077870.1	662.41	1322.80	1323.55	-0.75	2	98	108	K	EAEEMAEDKK	V	1	Oxidation (M)	74.8
302	chr1.LjT48M07.70.nc	665.44	1328.86	1329.71	-0.86	2	6	18	R	SGIAEDVTQLIGK	T	0	-	74.7
303	chr4.CM0617.300.nd	421.50	840.98	841.50	-0.52	2	87	95	K	KGPGGVTVK	K	1	-	34.8
		553.45	1104.88	1105.57	-0.68	2	122	131	R	LG DYLV EQGL	-	0	-	32.5
		716.44	1430.86	1431.75	-0.89	2	72	84	K	YMQVQGEPAVIR	G	0	-	41.1
		724.43	1446.85	1447.75	-0.90	2	72	84	K	YMQVQGEPAVIR	G	0	Oxidation (M)	41.4
303	chr2.CM0783.270.nd	421.50	840.98	841.50	-0.52	2	87	95	K	KGPGGVTVK	K	1	-	34.8
		716.44	1430.86	1431.75	-0.89	2	72	84	K	YMQVQGEPAVIR	G	0	-	41.1
		724.43	1446.85	1447.75	-0.90	2	72	84	K	YMQVQGEPAVIR	G	0	Oxidation (M)	41.4
304	chr4.CM0025.300.nc	493.99	985.97	986.58	-0.61	2	100	108	R	GLISEIISR	F	0	-	44.1
		535.49	1068.96	1069.61	-0.65	2	170	179	R	KLIGATDPQK	S	1	-	57.9
		471.48	940.94	941.52	-0.58	2	171	179	K	LIGATDPQK	S	0	-	31.9
		608.27	1821.79	1822.91	-1.12	3	196	212	R	NIIHGS DGPETAKDEIK	L	1	-	42.2
304	chr2.CM0060.440.nc	493.99	985.97	986.58	-0.61	2	102	110	R	GLISEIISR	F	0	-	44.1
		535.49	1068.96	1069.61	-0.65	2	172	181	R	KLIGATDPQK	S	1	-	57.9
		471.48	940.94	941.52	-0.58	2	173	181	K	LIGATDPQK	S	0	-	31.9
305	LjSGA_085597.1	455.97	909.93	910.40	-0.48	2	49	57	R	DGGS DYLGK	G	0	-	57.8
		469.02	936.02	936.51	-0.50	2	134	142	K	HIANLAGNK	T	0	-	40.7
306	LjT22I05.200.nd	739.46	1476.91	1477.78	-0.87	2	143	155	K	EYLP IGVGLADFNK	L	0	-	64.8
		564.05	1126.08	1126.67	-0.59	2	167	176	R	KIIQPSSNLK	N	1	-	30.9
		727.49	1452.97	1452.83	0.14	2	116	128	R	TEEGKPLVLNVVR	K	0	-	38.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
307	chr5.CM0077.700.nc	828.93	1655.85	1656.87	-1.02	2	529	543	R	NLIVVFEELGGNPEK	I	0	-	73.6
		625.94	1249.87	1250.64	-0.77	2	347	357	R	SFTFNGPVNLR	A	0	-	22.4
308	CM0319.130.nd	516.94	1031.87	1031.47	0.39	2	613	621	K	GRNQGEESR	R	1	-	52.1
309	chr3.CM0792.20.nd	692.97	1383.92	1384.75	-0.83	2	19	30	K	TALNWAVDNLLR	N	0	-	60.7
310	LjB03P03.140.nd	873.51	1745.00	1744.85	0.15	2	387	401	K	FLQDGDDEVILTGHCK	G	0	Propionamide (C)	39.8
		545.50	1088.98	1089.60	-0.63	2	93	102	K	LLSATESTLR	D	0	-	66.6
311	chr2.CM0695.320.nd	734.85	1467.68	1468.61	-0.93	2	301	314	K	GGETSSQDATMTER	A	0	-	72.7
312	LjSGA_019091.2	634.94	1267.87	1268.71	-0.83	2	76	88	K	VDAPVVVVGTGASR	G	0	-	72.7
313	LjSGA_039741.1	679.03	1356.05	1356.80	-0.75	2	99	110	R	ILLGDLQTPFIK	Y	0	-	49.1
		588.52	1175.02	1175.68	-0.66	2	181	190	K	TLDIPIYITK	V	0	-	23.5
		559.02	1116.02	1116.63	-0.61	2	90	98	R	VVIFDLQQR	I	0	-	47.9
314	LjSGA_114323.1	749.42	1496.82	1497.78	-0.97	2	48	60	R	SIGISNYDIFLTR	D	0	-	72.1
315	LjT16G18.150.nd	624.38	1246.75	1247.55	-0.79	2	107	118	K	MEAEGNQSGTPK	S	0	-	69.8
316	chr6.CM0679.170.nd	529.78	1057.54	1057.47	0.07	2	23	30	K	FDNLYGCR	H	0	Propionamide (C)	27.2
		424.03	846.04	845.54	0.50	2	220	226	K	KVYVLPK	H	1	-	30.0
		404.54	807.06	807.50	-0.43	2	232	239	K	VAALHLGK	L	0	-	22.9
		567.51	1133.01	1133.61	-0.59	2	49	60	K	VAVVAGYGDVGK	G	0	-	72.0
													-	
317	chr1.CM0064.390.nc	729.40	1456.78	1457.71	-0.93	2	342	356	R	TTGPVEASQPGTTGR	L	0	-	71.7
318	LjSGA_088248.1	851.50	1700.99	1700.88	0.12	2	49	64	K	ILDDAMAGDNVGLLLR	G	0	Oxidation (M)	29.7
		572.00	1141.98	1142.63	-0.65	2	23	33	K	VGDTVEIVGVR	E	0	-	65.5
		740.41	1478.81	1478.69	0.12	2	126	138	K	VTAIMNDKDEESK	M	1	-	40.4
319	chr1.CM0371.130.nc	503.95	1005.88	1006.45	-0.57	2	97	105	K	EDAANNFAR	G	0	-	66.6
		698.93	1395.85	1395.75	0.10	2	85	96	R	QLFHPEQLISCK	E	0	-	26.5
		846.50	1690.98	1690.86	0.11	2	216	229	R	SLDIERPTYTNLNR	L	0	-	40.0
320	chr2.CM0168.320.nc	624.96	1247.90	1248.67	-0.78	2	49	61	K	GGLSVGDVAALYK	Y	0	-	27.9
		495.44	988.87	989.52	-0.65	2	4	13	K	GPGLFSDIGK	K	0	-	65.4
		666.46	1330.91	1330.80	0.11	2	237	248	K	LGALLQHEIIPK	S	0	-	37.0
		446.93	891.85	892.43	-0.58	2	98	105	K	LPDYNSGK	L	0	-	22.6
		458.96	915.91	916.50	-0.59	2	196	204	K	SAAVAEITR	K	0	-	38.9
													-	
321	LjSGA_145133.1	784.97	1567.92	1567.74	0.19	2	30	44	K	LQEVASGASEYSAEK	A	0	-	71.0
322	chr1.CM0012.470.nc	535.98	1069.94	1070.63	-0.70	2	14	24	K	ILLIGDSGVGK	S	0	-	70.8
323	LjSGA_038243.1	860.33	1718.65	1717.90	0.75	2	53	67	R	LLDVVYNASNNELV	T	0	-	52.6
		773.43	1544.85	1544.72	0.12	2	137	150	R	TLDSHIEEQFGGGR	L	0	-	47.2
323	LjSGA_040678.1	860.33	1718.65	1717.90	0.75	2	51	65	R	LLDVVYNASNNELV	T	0	-	52.6
324	LjSGA_054553.2.1	662.41	1322.81	1322.71	0.10	2	9	20	K	KGEIYLADVSTK	L	1	-	69.9
325	chr2.CM0608.40.nd	695.98	1389.95	1390.79	-0.84	2	69	81	K	LSQLVNSAPPPIR	L	0	-	69.8
326	LjSGA_038169.1	657.97	1313.92	1314.68	-0.76	2	168	178	K	LIQDTENDVLR	F	0	-	69.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		716.46	1430.90	1431.72	-0.83	2	1	13	-	SFLPSETPEGLQK	L	0	-	33.1
327	chr6.CM0055.10.nd	580.45	1158.89	1159.57	-0.68	2	605	614	K	EIEDAVSELR	T	0	-	59.8
		451.50	900.99	901.52	-0.53	2	456	463	R	NTTIPTKK	S	1	-	46.1
328	chr6.CM0679.120.nd	628.54	1255.06	1255.78	-0.71	2	368	379	K	LVAILESLLGTK	A	0	-	69.1
329	LjSGA_019672.2	715.95	1429.88	1430.74	-0.87	2	320	333	R	AGNASLEEVVMALK	C	0	-	46.5
		647.39	1292.78	1293.55	-0.78	2	89	101	R	DGEQSPGASMTSK	E	0	-	45.7
		743.96	1485.90	1486.80	-0.90	2	113	127	K	LGVDIIIEAGFPAASK	D	0	-	36.5
330	LjSGA_081530.1	718.25	1434.49	1434.66	-0.17	2	118	129	K	KYDEIDAAPEER	A	1	-	68.7
331	chr6.CM0139.780.nd	535.00	1067.98	1068.53	-0.55	2	242	251	K	TPATNQQQPR	A	0	-	68.3
332	chr4.CM0119.50.nd	508.95	1015.89	1015.52	0.37	2	164	174	R	AMIGQVAGGGR	T	0	-	57.1
		516.43	1030.85	1031.52	-0.67	2	164	174	R	AMIGQVAGGGR	T	0	Oxidation (M)	23.7
		625.98	1249.95	1250.77	-0.82	2	94	105	K	ATLVVGNVLPPIR	S	0	-	49.1
332	LjSGA_122226.1	508.95	1015.89	1015.52	0.37	2	165	175	R	AMIGQVAGGGR	T	0	-	57.1
		516.43	1030.85	1031.52	-0.67	2	165	175	R	AMIGQVAGGGR	T	0	Oxidation (M)	23.7
		625.98	1249.95	1250.77	-0.82	2	95	106	K	ATLVVGNVLPPIR	S	0	-	49.1
332	LjT17O07.90.nd	508.95	1015.89	1015.52	0.37	2	164	174	R	AMIGQVAGGGR	T	0	-	57.1
		516.43	1030.85	1031.52	-0.67	2	164	174	R	AMIGQVAGGGR	T	0	Oxidation (M)	23.7
332	LjT48K17.180.nd	508.95	1015.89	1015.52	0.37	2	62	72	R	AMIGQVAGGGR	T	0	-	57.1
		516.43	1030.85	1031.52	-0.67	2	62	72	R	AMIGQVAGGGR	T	0	Oxidation (M)	23.7
332	LjT48K17.130.nd	625.98	1249.95	1250.77	-0.82	2	94	105	K	ATLVVGNVLPPIR	S	0	-	49.1
333	LjT43D04.90.nc	746.89	1491.76	1492.74	-0.98	2	169	182	K	VYLSAASSENSPEVK	D	0	-	68.1
334	LjT13C08.100.nc	482.45	962.89	963.48	-0.60	2	97	104	K	CGVNIPIYK	I	0	Propionamide (C)	25.2
		573.45	1144.88	1145.58	-0.71	2	85	96	R	FNAGNAASLP GK	C	0	-	52.0
		611.43	1220.84	1221.60	-0.76	2	105	115	K	ISTSTNCANIK	-	0	Propionamide (C)	56.4
335	LjSGA_041825.1.1	768.91	1535.81	1536.81	-1.01	2	187	200	R	LAQSEADILHEAIK	D	0	-	21.9
		609.46	1216.91	1217.71	-0.80	2	167	177	R	QLLVGLVSSFR	Y	0	-	61.2
336	chr2.CM0783.340.nd	457.97	913.93	914.49	-0.56	2	46	54	K	AGEIPGIMK	D	0	-	20.7
		716.44	1430.86	1431.75	-0.89	2	74	86	K	YMQVIGQEPGAVIR	G	0	-	41.1
		724.43	1446.85	1447.75	-0.90	2	74	86	K	YMQVIGQEPGAVIR	G	0	Oxidation (M)	41.4
337	LjSGA_017574.2	1129.02	2256.02	2257.20	-1.17	2	200	221	K	LVVGFINSLVGPESEELAAASR	L	0	-	67.1
338	LjSGA_085428.1	645.97	1289.92	1290.68	-0.76	2	131	142	R	ISSSQIVDFPAK	L	0	-	66.9
339	chr1.CM0206.150.nd	580.47	1158.92	1159.66	-0.74	2	23	33	K	ILFLGLDNACK	T	0	-	66.4
339	chr4.CM0429.130.nd	580.47	1158.92	1159.66	-0.74	2	23	33	K	ILFLGLDNACK	T	0	-	66.4
339	CM0385.100.nd	580.47	1158.92	1159.66	-0.74	2	23	33	K	ILFLGLDNACK	T	0	-	66.4
340	LjT07P16.160.nd	663.98	1325.94	1326.74	-0.80	2	117	128	K	LPTDEALLS QIK	D	0	-	25.9
		567.46	1132.91	1133.58	-0.67	2	19	28	K	TPPQQAQTIR	K	0	-	40.4
		424.47	846.93	847.47	-0.53	2	42	49	K	VVEVSTSK	T	0	-	50.6

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
341	chr5.LjT02I10.300.nd	531.91	1061.80	1062.51	-0.71	2	62	71	R	GWNTFSPEGR	L	0	-	49.1
		700.44	1398.86	1398.76	0.10	2	105	117	R	ITSPLEPSSVEK	I	0	-	49.1
		599.99	1197.97	1197.65	0.31	2	244	252	R	LLLYPFYNR	L	0	-	23.3
		412.96	823.90	824.45	-0.55	2	138	144	R	TLVEHAR	V	0	-	27.7
342	LjSGA_071971.1	812.39	2434.14	2434.46	-0.32	3	23	46	K	ALGVNTVPVLVGPVSYLLLSKPAK	G	0	-	66.2
		510.98	1019.94	1020.54	-0.60	2	226	234	K	SWLAFAAQK	V	0	-	28.2
343	LjSGA_068268.1	734.97	1467.92	1468.81	-0.89	2	120	132	K	SPLSVIILDDIER	L	0	-	66.0
344	LjT30M06.90.nd	620.00	1237.99	1238.69	-0.70	2	37	46	K	TKDDILLFFK	L	1	-	55.7
		635.48	1268.95	1269.66	-0.71	2	184	195	K	VAQQLGLDDPSK	I	0	-	44.2
344	chr2.CM0545.290.nc	620.00	1237.99	1238.69	-0.70	2	688	697	K	TKDDILLFFK	L	1	-	55.7
345	chr1.LjT01D01.60.nd	608.48	1214.95	1215.71	-0.76	2	38	49	K	LSAAIASILETK	L	0	-	65.9
345	LjSGA_079444.1	608.48	1214.95	1215.71	-0.76	2	23	34	K	LSAAIASILETK	L	0	-	65.9
346	chr4.CM0173.30.nd	521.90	1041.79	1042.47	-0.68	2	181	189	K	FSGYELDGR	V	0	-	34.9
		821.87	1641.73	1642.79	-1.07	2	162	176	R	GFGFVIMSTAEDLEK	A	0	-	65.6
347	LjT04E07.20.nc	861.53	1721.04	1720.92	0.12	2	197	212	K	EGVIQHSTINNLAIGR	S	0	-	25.6
		402.98	803.95	804.47	-0.53	2	190	196	R	GLFIIDK	E	0	-	23.3
		867.39	1732.76	1733.88	-1.12	2	155	171	K	SGGLGDLNYPVSDVTK	S	0	-	56.2
		750.93	1499.85	1500.83	-0.98	2	176	189	K	SYGVLIPDQGIALR	G	0	-	42.3
348	chr1.CM0433.180.nd	495.29	988.57	988.52	0.05	2	182	189	R	SIKEEIDR	V	1	-	59.0
349	chr4.CM0680.130.nc	503.97	1005.92	1006.52	-0.60	2	96	105	R	LATSGANFAR	A	0	-	65.1
350	chr1.CM0233.110.nc	667.94	1333.87	1334.69	-0.82	2	511	523	K	AIFASGSPFPDPVK	Y	0	-	59.2
		834.95	1667.88	1668.91	-1.03	2	123	137	R	GLLPFAVFTQELQEK	R	0	-	34.0
350	LjSGA_137596.1	667.94	1333.87	1334.69	-0.82	2	71	83	K	AIFASGSPFPDPVK	Y	0	-	59.2
351	LjSGA_012802.2	715.42	1428.83	1429.74	-0.91	2	72	83	K	QSNILEDLETLR	L	0	-	64.6
353	chr1.CM0206.230.nc	759.92	1517.83	1518.79	-0.96	2	74	87	K	LVSYGPEVTAQVEK	G	0	-	36.8
		740.91	1479.81	1480.74	-0.94	2	131	143	R	SFPVSAFEIVEEK	S	0	-	49.2
		769.95	1537.89	1537.78	0.10	2	150	165	K	SKNHEVVG DG VGGGVK	E	1	-	35.5
354	LjSGA_005489.3	557.43	1112.84	1113.54	-0.70	2	162	172	R	AAGDNNPQLSK	E	0	-	63.8
355	LjSGA_060719.2	505.45	1008.88	1009.48	-0.60	2	27	35	R	GTQSVFEFSR	E	0	-	63.5
356	chr2.CM0102.150.nd	643.48	1284.94	1285.75	-0.81	2	177	188	K	LTVDLVLASLK	S	0	-	63.2
357	chr4.CM0617.240.nd	743.90	1485.79	1486.74	-0.95	2	163	177	R	EVEAIGGNVQASASR	E	0	-	63.1
358	LjSGA_016231.2	542.40	1082.78	1083.48	-0.69	2	112	121	R	TCCTYAAGNR	F	0	Propionamide (C)	62.8
359	LjSGA_034228.1	700.46	1398.91	1399.74	-0.82	2	111	122	K	ELESICNPPIAK	M	0	Propionamide (C)	47.8
		402.98	803.94	803.44	0.50	2	14	20	K	ITITNDK	G	0	-	41.3
		687.71	1373.40	1373.60	-0.20	2	53	63	K	NALENYAYNMR	N	0	Oxidation (M)	39.4
360	chr1.CM0122.460.nc	636.00	1269.98	1270.76	-0.78	2	161	171	K	IFLIPVSDVIR	V	0	-	62.3

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
361	chr4.CM0042.1530.nc	577.46	1152.91	1153.61	-0.70	2	308	318	K	NAPGVVVIDDR	E	0	-	61.8
362	LjSGA_056310.1	570.99	1139.98	1140.65	-0.68	2	55	64	R	NILELAAELR	V	0	-	61.7
363	LjSGA_051623.1	421.50	840.99	841.48	-0.49	2	63	69	K	VDRSLPR	G	1	-	44.9
364	LjT48C16.170.nd	665.44	1328.86	1329.72	-0.85	2	107	117	R	ELYPTLQLPEK	C	0	-	38.7
		780.45	1558.88	1559.88	-1.00	2	137	150	K	SLGIEYIPLEVSLK	E	0	-	52.0
365	chr6.CM0066.640.nc	861.54	1721.07	1720.85	0.21	2	245	261	K	GFLSIGSSSITSTSSYK	F	0	-	37.2
		658.91	1315.80	1315.64	0.16	2	66	78	K	SGLSIGSGNYYAK	M	0	-	28.0
		686.48	1370.95	1370.78	0.17	2	298	310	K	VPTIIDSCTVITR	L	0	-	53.7
365	chr3.CM0127.710.nc	686.48	1370.95	1370.78	0.17	2	233	245	K	VPTIIDSCTVITR	L	0	-	53.7
366	LjSGA_052954.1	660.45	1318.89	1319.65	-0.75	2	8	19	R	FSQGLAQDPTTR	R	0	-	53.2
366	LjSGA_090599.1	660.45	1318.89	1319.65	-0.75	2	8	19	R	FSQGLAQDPTTR	R	0	-	53.2
366	LjSGA_102170.1	660.45	1318.89	1319.65	-0.75	2	8	19	R	FSQGLAQDPTTR	R	0	-	53.2
367	chr5.CM0077.20.nd	855.99	1709.97	1709.76	0.20	2	4	18	R	NQYDVTDTWSPAGR	L	0	-	61.4
		436.96	871.91	871.49	0.43	2	31	39	K	QGSAAIGLR	S	0	-	29.3
368	LjSGA_030023.1.2	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_039485.1	764.43	1526.84	1527.83	-0.99	2	122	135	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_040951.0.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_041952.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_055307.1	764.43	1526.84	1527.83	-0.99	2	105	118	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_059014.1	764.43	1526.84	1527.83	-0.99	2	122	135	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_080429.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_091127.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_094940.1	764.43	1526.84	1527.83	-0.99	2	28	41	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_103684.1	764.43	1526.84	1527.83	-0.99	2	27	40	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_107226.0.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	D	0	-	61.0
368	LjSGA_112701.1	764.43	1526.84	1527.83	-0.99	2	130	143	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_116308.2	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_118901.1	764.43	1526.84	1527.83	-0.99	2	138	151	R	DPNLAEFIAGQLK	N	0	-	61.0
368	LjSGA_128247.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQLK	N	0	-	61.0
369	LjSGA_035136.1	764.43	1526.84	1527.83	-0.99	2	123	136	R	DPNLAEFIAGQIK	K	0	-	61.0
370	chr1.CM0017.490.nc	812.01	1622.00	1621.87	0.13	2	198	215	K	AGSGVATLGLPDSPGVPK	A	0	-	45.8
		656.79	1311.56	1311.74	-0.18	2	73	85	K	SVGGQPILIDSVK	G	0	-	41.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
371	chr4.CM0126.670.nc	542.96	1083.91	1084.62	-0.71	2	277	285	K	EPPELLPIK	E	0	-	33.5
		616.41	1230.80	1231.59	-0.79	2	170	180	R	MPISSDLSNFR	N	0	Oxidation (M)	60.8
372	LjSGA_038659.1	651.97	1301.93	1302.74	-0.81	2	67	77	R	IILLDSPLEYK	K	0	-	60.7
373	chr1.CM0593.380.nc	578.50	1154.98	1155.67	-0.68	2	260	269	R	EVGLTFHLLK	D	0	-	28.4
		563.01	1124.00	1124.64	-0.65	2	95	104	R	QDLVVVEVPK	L	0	-	61.6
374	chr3.CM0091.660.nd	763.01	1524.00	1524.81	-0.81	2	38	49	K	RVLTYMLQNP	C	1	-	22.7
		598.36	1194.71	1194.62	0.09	2	670	681	R	TLTNVGAAGTYK	V	0	-	60.3
375	chr1.CM0284.440.nc	703.35	1404.69	1404.59	0.10	2	213	224	K	GGNDHEIYESER	T	0	-	48.4
		749.95	1497.89	1497.77	0.12	2	225	238	R	TIGHTVTSPEDTIK	Q	0	-	38.2
376	chr4.CM0042.1600.nc	564.50	1126.99	1127.67	-0.68	2	56	65	K	AFEPILLGR	H	0	-	60.2
377	chr1.CM0147.900.nc	727.33	1452.65	1453.58	-0.93	2	437	450	R	AAIDSSSDTDDSR	T	0	-	60.1
378	chr6.LjT30N23.130.nd	729.89	1457.76	1458.67	-0.92	2	255	266	K	IEEEEEETKPQV	-	0	-	59.6
379	chr2.LjT01H08.60.nc	568.95	1135.89	1136.57	-0.68	2	259	268	R	EDGGYEVIIK	A	1	-	56.6
		540.97	1079.93	1080.58	-0.65	2	39	49	R	TLPGPVSDPAK	L	0	-	38.3
381	chr1.CM0105.1320.nd	611.92	1221.83	1222.58	-0.75	2	173	183	K	VLSPYSSSEDAR	G	0	-	58.8
382	LjSGA_041906.1	620.92	1239.82	1240.59	-0.77	2	22	31	K	TSLMNQYVNR	K	0	Oxidation (M)	29.6
		528.98	1055.94	1056.62	-0.68	2	11	21	K	VIIIGDSGVGK	T	0	-	61.4
383	LjSGA_009908.1	602.94	1203.87	1204.60	-0.74	2	175	186	R	VIGSGTNLDSSR	F	0	-	57.5
384	LjT32D02.120.nc	845.46	1688.90	1689.88	-0.98	2	62	76	R	LEGLLNLDVTPYTDK	F	0	-	57.5
		760.49	1518.97	1518.84	0.13	2	97	110	R	TISKPVSHPSSELPK	W	0	-	21.1
385	chr5.CM0052.420.nd	479.97	957.93	958.51	-0.57	2	15	23	R	VLNTNVDGK	Q	0	-	57.1
385	LjSGA_085279.1	479.97	957.93	958.51	-0.57	2	14	22	R	VLNTNVDGK	Q	0	-	57.1
386	chr3.CM0111.260.nc	594.94	1187.87	1188.65	-0.78	2	220	229	K	DSTLIMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	220	229	K	DSTLIMQLLR	D	0	Oxidation (M)	56.3
		458.96	915.91	916.52	-0.61	2	66	73	R	ILSSIEQK	E	0	-	23.4
387	chr1.LjB18K24.40.nd	524.93	1047.85	1048.53	-0.69	2	123	131	R	FIDQGSNLR	G	0	-	56.3
387	chr1.CM0544.600.nd	524.93	1047.85	1048.53	-0.69	2	69	77	R	FIDQGSNLR	G	0	-	56.3
387	chr5.CM0089.680.nd	524.93	1047.85	1048.53	-0.69	2	123	131	R	FIDQGSNLR	S	0	-	56.3
388	LjT35C01.110.nd	589.38	1176.75	1177.53	-0.78	2	3	12	K	YSQEPDNPTK	S	0	-	48.0
389	LjT30L14.20.nd	479.98	957.94	958.45	-0.51	2	247	254	R	DENFGHLK	S	0	-	21.5
		565.51	1129.01	1129.67	-0.66	2	44	54	R	SVALQLISATK	A	0	-	56.4
390	chr1.CM0171.780.nd	491.45	980.88	981.53	-0.65	2	91	98	R	LFNYIQGK	N	0	-	56.1
391	chr4.CM0119.370.nc	720.92	1439.82	1440.75	-0.93	2	121	134	R	EGQSIGVIPEGIDK	N	0	-	56.0
392	chr6.CM0302.80.nc	583.90	1165.78	1166.55	-0.77	2	12	22	R	EAISGIMTDSK	E	0	Oxidation (M)	56.0

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
393	LjT01G11.120.nd	631.95	1261.88	1262.66	-0.79	2	48	59	K	GKDFAEIIASGR	E	1	-	56.0
394	chr5.LjT24B10.140.nc	569.94	1137.87	1138.60	-0.73	2	129	138	R	NVVFDFITGK	G	0	-	56.0
395	LjSGA_054224.1	451.01	900.01	900.48	-0.47	2	53	60	K	ATQNQLAR	G	0	-	50.2
396	LjSGA_018602.1	731.37	1460.73	1460.69	0.05	2	34	48	R	SGVQNGATLETGGDR	L	0	-	55.8
397	chr2.CM0124.90.nc	742.46	1482.91	1483.76	-0.86	2	432	445	K	GVVDSNDLPLNVSR	E	0	-	55.6
		486.52	971.03	971.58	-0.55	2	215	223	R	VVVSTKSPR	S	1	-	20.1
398	chr4.LjT13D08.30.nd	658.42	1314.82	1315.65	-0.83	2	60	70	R	LQLWDTAGQER	F	0	-	47.8
399	LjB01J01.30.nc	535.82	1069.62	1069.57	0.06	2	53	62	K	VPDDLLEAAK	A	0	-	55.3
400	chr2.CM0695.90.nd	789.48	1576.95	1577.83	-0.88	2	810	823	R	SNLVGMGIPLCFK	S	0	Oxidation (M); Propionamide (C)	26.1
		558.50	1114.99	1115.62	-0.63	2	472	483	K	TS LAPGSGVVTK	Y	0		54.2
401	chr3.CM0792.110.nd	630.89	1259.77	1260.58	-0.82	2	134	146	R	AVSEDDGGALAEK	E	0	-	45.8
		528.98	1055.94	1056.62	-0.68	2	15	25	K	IVLIGDSGVCK	S	0	-	48.4
401	LjSGA_058377.2	528.98	1055.94	1056.62	-0.68	2	15	25	K	IVLIGDSGVCK	S	0	-	48.4
402	chr1.CM0094.310.nc	673.49	1344.97	1345.72	-0.75	2	125	136	K	GEVSPYLAELLR	L	0	-	46.8
		707.02	1412.03	1412.82	-0.79	2	668	681	R	TNVALTLLEAGLAK	L	0	-	39.8
402	chr1.CM0094.340.nc	673.49	1344.97	1345.72	-0.75	2	125	136	K	GEVSPYLAELLR	L	0	-	46.8
		707.02	1412.03	1412.82	-0.79	2	668	681	R	TNVALTLLEAGLAK	L	0	-	39.8
402	chr1.CM0094.360.nc	673.49	1344.97	1345.72	-0.75	2	125	136	K	GEVSPYLAELLR	L	0	-	46.8
		707.02	1412.03	1412.82	-0.79	2	668	681	R	TNVALTLLEAGLAK	L	0	-	39.8
403	chr1.CM0109.360.nc	549.84	1097.67	1097.56	0.11	2	51	60	R	GYHAVAPDLR	G	0	-	50.7
		723.89	1445.77	1445.60	0.16	2	143	153	R	HAYGDDYYICR	F	0	Propionamide (C)	20.1
		527.87	1053.72	1053.59	0.13	2	42	50	R	HQILTLSSR	G	0		42.3
404	chr2.CM0272.170.nc	859.47	1716.92	1716.78	0.15	2	191	204	K	IPCFDELEQNPDAR	F	0	Propionamide (C)	55.0
405	chr1.LjT14I13.300.nd	574.97	1147.93	1148.56	-0.63	2	175	185	R	SVGISDDEISK	F	0	-	55.0
405	LjSGA_031174.2.1	574.97	1147.93	1148.56	-0.63	2	37	47	R	SVGISDDEISK	F	0	-	55.0
406	LjSGA_036172.1	687.43	1372.85	1373.70	-0.85	2	48	59	R	EGDILTLESER	E	0	-	55.0
407	LjSGA_003098.1	716.47	1430.93	1430.81	0.12	2	31	43	K	TPLPDIVTIHTPK	E	0	-	54.8
407	LjSGA_118471.1	716.47	1430.93	1430.81	0.12	2	66	78	K	TPLPDIVTIHTPK	E	0	-	54.8
408	LjSGA_129660.2	401.03	800.04	799.52	0.52	2	10	16	K	KGIEIIK	N	1	-	54.8
409	LjSGA_108878.1	508.96	1015.91	1016.55	-0.64	2	9	18	K	LGSQGLEVSK	L	0	-	54.7
410	LjSGA_037888.1	655.45	1308.89	1309.61	-0.73	2	202	213	R	SALSEFSADEVR	S	0	-	54.6
411	chr6.CM0041.320.nd	653.90	1305.79	1306.60	-0.81	2	38	49	R	ASLEQDDSSLR	Q	0	-	54.5
412	chr5.LjT41L03.150.nd	685.97	1369.92	1370.79	-0.87	2	472	484	K	IIAGADFIVIPSR	F	0	-	54.3
		629.97	1257.93	1257.74	0.19	2	587	597	R	LLVVKLEMGK	R	1	-	22.5

Continues...

Supplemental Table S2.11: (*green_LotusAA GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		549.98	1097.95	1098.65	-0.70	2	400	409	R	NIPLIGFIGR	L	0	-	27.9
413	chr4.CM0007.860.nd	670.99	1339.97	1340.73	-0.76	2	83	95	K	LLAGESGITPIDR	F	0	-	54.3
414	chr1.CM0544.500.nd	792.48	1582.95	1582.78	0.17	2	175	189	K	EGSSIINTTSVNAYK	G	0	-	30.8
		658.91	1315.81	1315.68	0.14	2	190	201	K	GHPTLLDYTATK	G	0	-	43.0
414	LjSGA_029600.1	792.48	1582.95	1582.78	0.17	2	19	33	K	EGSSIINTTSVNAYK	G	0	-	30.8
		658.91	1315.81	1315.68	0.14	2	34	45	K	GHPTLLDYTATK	G	0	-	43.0
415	LjSGA_036526.1.1	666.44	1330.86	1331.60	-0.74	2	63	76	R	DPNSGQLGGTGDSK	Q	0	-	54.0
416	LjSGA_017485.1	916.52	1831.03	1830.92	0.11	2	115	131	K	TLEESNLSNDEVVALAK	E	0	-	53.9
417	LjSGA_062145.1	567.45	1132.88	1133.55	-0.66	2	102	110	R	RFDDPQTQK	E	1	-	43.6
		487.46	972.91	973.48	-0.57	2	52	60	K	VIENSEGAR	T	0	-	46.3
418	LjSGA_093090.1	717.41	1432.80	1433.70	-0.90	2	11	23	R	LTPDYDALDVANK	I	0	-	53.8
419	chr3.CM0711.10.nd	746.95	1491.88	1492.77	-0.89	2	208	219	K	VVFVPWVETDFR	T	0	-	53.7
420	chr6.CM0066.230.nc	719.93	1437.84	1438.72	-0.88	2	83	94	R	IFFIAWSPDTSR	V	0	-	53.3
421	chr6.CM0057.310.nd	494.45	986.89	987.51	-0.62	2	30	37	K	LWATNEVR	A	0	-	38.8
		781.42	1560.82	1560.81	0.00	2	55	68	K	SNGQVLAINEIFEK	N	0	-	53.3
421	LjT35M05.20.nd	494.45	986.89	987.51	-0.62	2	26	33	K	LWATNEVR	A	0	-	38.8
		781.42	1560.82	1560.81	0.00	2	51	64	K	SNGQVLAINEIFEK	N	0	-	53.3
422	LjSGA_034891.1	641.38	1280.74	1281.57	-0.83	2	145	155	K	YEDQVDSIGEK	A	0	-	53.2
423	CM0385.180.nd	611.98	1221.95	1222.70	-0.76	2	75	85	R	LVVNNIAIEVPR	L	0	-	53.2
424	chr2.CM0008.650.nc	587.48	1172.95	1172.60	0.34	2	123	133	K	IAADSDAIELR	S	0	-	53.1
425	LjT30N04.290.nd	638.96	1913.87	1915.02	-1.15	3	52	68	K	AHGLAPEIPEDLYHLIK	K	0	-	32.2
		691.49	1380.98	1380.85	0.13	2	18	30	K	KGLTPSQIGVILR	D	1	-	47.1
426	chr5.CM0019.20.nd	903.97	1805.93	1806.94	-1.01	2	460	475	K	LGTVEVQDLPPFDTVK	V	0	-	49.8
		621.97	1241.92	1242.61	-0.69	2	910	921	K	NTAGIEPEDVAK	R	0	-	34.9
427	CM1729.60.nc	623.47	1244.92	1245.65	-0.73	2	682	693	R	EELGTGLLTGEK	V	0	-	52.8
		531.99	1061.97	1062.60	-0.62	2	192	200	R	FEILEAITK	L	0	-	28.1
428	LjSGA_014026.1	860.33	1718.65	1717.90	0.75	2	53	67	R	ILDVVYNASNNEIVR	T	0	-	52.6
429	chr5.CM0200.440.nc	788.43	1574.85	1575.85	-1.01	2	585	598	K	IGDIPAVEEFVFLK	L	0	-	29.0
		587.48	1172.95	1172.66	0.29	2	95	104	K	ISLCDALIVR	S	0	Propionamide (C)	20.5
		501.46	1000.90	1001.51	-0.61	2	171	180	R	NVAQADASVK	A	0	-	51.5
430	chr5.CM0052.270.nd	767.91	1533.80	1533.67	0.13	2	295	308	K	AGDESHSAITEFDR	T	0	-	52.5
430	chr5.CM0052.280.nd	767.91	1533.80	1533.67	0.13	2	289	302	K	AGDESHSAITEFDR	T	0	-	52.5
431	LjSGA_124612.1	420.00	837.98	838.47	-0.49	2	113	120	K	VAPATQPR	A	0	-	52.5
431	LjSGA_125379.2	420.00	837.98	838.47	-0.49	2	243	250	K	VAPATQPR	A	0	-	52.5

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
431	LjSGA_127553.2	420.00	837.98	838.47	-0.49	2	216	223	K	VAPATQPR	A	0	-	52.5
431	LjSGA_128526.2	420.00	837.98	838.47	-0.49	2	154	161	K	VAPATQPR	A	0	-	52.5
433	chr5.CM0211.170.nc	823.44	1644.86	1645.90	-1.04	2	235	251	R	LVAAIDGLPDPGGPQVK	D	0	-	52.3
434	chr4.CM0739.260.nd	479.48	956.95	957.55	-0.60	2	4	12	R	VSVLNDALK	S	0	-	52.3
434	LjT32D02.180.nc	479.48	956.95	957.55	-0.60	2	4	12	R	VSVLNDALK	S	0	-	52.3
435	chr6.CM0679.70.nc	580.04	1158.07	1158.68	-0.61	2	107	117	R	FLIAPSLVSGR	I	0	-	52.2
436	LjSGA_022701.1	586.91	1171.80	1172.57	-0.76	2	9	19	R	GLAANEDDLQK	A	0	-	37.4
		692.46	1382.91	1383.82	-0.91	2	73	84	R	LLPITLGQVFQR	I	0	-	43.2
437	LjSGA_029241.1	463.46	924.91	925.52	-0.61	2	153	161	R	ILPDGVNAK	L	0	-	31.4
		611.37	1220.72	1220.64	0.08	2	162	172	K	LLGCHGPLAMR	Q	0	Propionamide (C)	51.1
438	chr6.CM0118.520.nd	743.91	1485.80	1485.75	0.05	2	40	52	R	TTPSYVAFTDTKR	L	1	-	52.0
439	LjSGA_148679.1	744.77	1487.52	1487.76	-0.24	2	63	76	R	AEDLTAINTQSAVR	I	0	-	52.0
440	chr3.LjT02L14.180.nd	479.98	957.94	958.45	-0.51	2	14	21	R	DENFGHLK	S	0	-	21.5
		567.46	1132.90	1133.55	-0.65	2	304	313	R	DTMNINALAR	N	0	Oxidation (M)	51.9
442	chr5.LjT08O17.200.nd	757.41	1512.80	1513.80	-1.00	2	36	49	K	GNVKPEDVLETISK	S	0	-	27.9
		698.87	1395.73	1396.65	-0.92	2	17	28	K	MEGVESFNIDLK	E	0	Oxidation (M)	49.8
443	chr1.LjT43O05.70.nd	761.97	1521.92	1521.78	0.14	2	139	151	K	FITHTVSFSEINK	A	0	-	38.2
		529.49	1056.96	1057.61	-0.65	2	13	22	R	IIGVDLVSSR	F	0	-	46.1
444	LjSGA_030247.1	549.96	1097.90	1098.56	-0.65	2	39	49	R	TLAGPVDDPSK	L	0	-	51.7
445	chr1.CM0016.130.nc	614.94	1227.86	1228.62	-0.76	2	40	50	K	EVAPPEETVVEK	T	0	-	50.0
		562.99	1123.97	1124.68	-0.71	2	24	33	K	VVVEKPVEVK	E	0	-	32.7
446	LjSGA_017894.1.1	702.94	1403.87	1404.80	-0.93	2	10	21	R	SINTLFLTELVR	G	0	-	51.7
447	LjSGA_015801.1	810.95	1619.89	1620.92	-1.03	2	214	229	K	NLPLVGEVGLGADLVR	L	0	-	51.6
447	LjSGA_115896.1	810.95	1619.89	1620.92	-1.03	2	75	90	K	NLPLVGEVGLGADLVR	L	0	-	51.6
448	chr4.CM0307.70.nc	799.95	1597.88	1597.77	0.11	2	61	74	K	DLLDGTQVQFMSTK	L	0	Oxidation (M)	39.5
		646.87	1291.73	1291.58	0.15	2	360	370	K	SYQQAGYDAVR	K	0	-	39.1
449	LjSGA_116769.1	636.00	1269.98	1270.68	-0.69	2	266	276	R	LMLLPMPEVGR	C	0	Oxidation (M)	51.4
450	chr3.LjT03D10.60.nd	585.43	1168.85	1169.60	-0.75	2	131	140	K	FLDGIYVSEK	G	0	-	51.2
		473.95	945.89	946.49	-0.60	2	113	120	R	SCALINQK	C	0	Propionamide (C)	27.5
450	LjSGA_071678.1	585.43	1168.85	1169.60	-0.75	2	48	57	K	FLDGIYVSEK	G	0	-	51.2
		473.95	945.89	946.49	-0.60	2	30	37	R	SCALINQK	W	0	Propionamide (C)	27.5
450	chr3.CM0160.930.nd	585.43	1168.85	1169.60	-0.75	2	129	138	K	FLDGIYVSEK	G	0	-	51.2
		473.95	945.89	946.49	-0.60	2	111	118	R	SCALINQK	C	0	Propionamide (C)	27.5
451	LjT31F05.60.nd	591.92	1181.82	1182.53	-0.72	2	361	369	R	EYDINVCTLR	V	0	Propionamide (C)	23.6
		616.41	1230.80	1231.59	-0.79	2	372	382	R	MPISSDLSNPR	N	0	Oxidation (M)	60.8

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		857.93	2570.77	2571.35	-0.58	3	394	416	K	VVNIPNSMTILDELLPISIEMAK	R	0	2 Oxidation (M)	20.9
452	LjT33L17.40.nc	523.99	1045.97	1046.60	-0.63	2	130	138	R	FALLVEDLK	V	0	-	51.0
453	LjSGA_091288.1	839.56	1677.11	1676.96	0.15	2	267	281	K	GGLSIIRPPLEQEIR	E	0	-	29.7
		466.31	930.60	930.54	0.07	2	243	250	K	VKEDLSK	L	1	-	42.2
454	chr1.CM0192.420.nd	535.48	1068.95	1069.60	-0.65	2	120	128	R	ALHNLFSIR	I	0	-	35.8
		508.98	1015.95	1016.57	-0.62	2	352	359	R	LPITWYPK	D	0	-	48.3
455	LjSGA_068738.1	721.51	1441.01	1441.81	-0.81	2	13	27	R	AAVAALSQVLTAEK	K	0	-	50.6
455	LjSGA_146350.1	721.51	1441.01	1441.81	-0.81	2	62	76	R	AAVAALSQVLTAEK	-	0	-	50.6
456	LjSGA_082502.1	672.95	1343.89	1344.74	-0.86	2	32	43	R	KVDMLDAVSLVR	S	1	-	45.9
		680.94	1359.87	1360.74	-0.87	2	32	43	R	KVDMLDAVSLVR	S	1	Oxidation (M)	28.0
457	LjSGA_031155.1	568.39	1134.76	1135.50	-0.74	2	90	98	K	CNMQIDPTK	Y	0	Oxidation (M); Propionamide (C)	34.7
		553.96	1105.91	1106.63	-0.72	2	101	111	K	SISGFGVLLK	E	0	-	39.8
		501.94	1001.87	1002.52	-0.66	2	189	197	R	VQTQPGFAR	G	0	-	39.2
458	LjSGA_008384.1	580.71	1159.41	1159.61	-0.20	2	47	56	K	LLSDDVDQKK	F	1	-	50.2
459	chr1.CM0150.610.nd	664.99	1327.97	1328.73	-0.76	2	133	144	R	ITDGTLLAQIER	Y	0	-	38.4
		622.52	1243.02	1243.78	-0.75	2	344	355	R	SIATLAITTLK	T	0	-	46.2
459	LjSGA_026406.2	622.52	1243.02	1243.78	-0.75	2	140	151	R	SIATLAITTLK	T	0	-	46.2
461	chr1.CM0029.40.nc	415.48	828.94	828.47	0.47	2	71	78	R	AIGVEVNK	Q	0	-	40.7
		466.47	930.92	931.53	-0.61	2	121	129	K	AKGEVISTK	R	1	-	41.3
		468.44	934.87	935.47	-0.60	2	36	43	R	IGDYVDVR	V	0	-	42.2
462	LjSGA_026492.1	866.42	1730.82	1731.87	-1.05	2	62	77	K	EGDQVLLPEYGGSQIK	L	0	-	31.7
		507.48	1012.95	1013.58	-0.63	2	23	32	K	TSGGILLPEK	S	0	-	31.2
		427.99	853.96	854.50	-0.54	2	41	49	K	VIAVPGSR	D	0	-	49.5
463	LjSGA_051144.1	829.96	1657.91	1657.90	0.01	2	59	74	R	IINEPTAAGLAYGLQK	K	0	-	26.0
		893.97	1785.93	1786.00	-0.07	2	59	75	R	IINEPTAAGLAYGLQKK	S	1	-	39.2
		718.95	1435.89	1435.75	0.14	2	235	246	K	VQQLLQDFFNGK	E	0	-	49.7
464	LjSGA_087577.1	730.40	1458.79	1458.67	0.11	2	129	141	K	AEYDESGPSIVHR	-	0	-	28.9
		573.98	1145.94	1146.60	-0.66	2	85	95	K	EITALAPSSMK	I	0	-	32.3
		581.97	1161.93	1162.59	-0.66	2	85	95	K	EITALAPSSMK	I	0	Oxidation (M)	48.7
465	chr1.LjT29N14.160.nd	496.98	991.94	992.55	-0.61	2	132	139	R	ITDLQIYK	X	0	-	52.5
		496.98	991.94	991.57	0.37	2	132	139	R	ITNLQIYK	X	0	-	28.2
466	chr3.CM0590.750.nc	647.43	1292.84	1293.68	-0.84	2	127	136	R	VDFKEPVWFK	A	1	-	50.6
466	LjSGA_009322.1	647.43	1292.84	1293.68	-0.84	2	128	137	R	VDFKEPVWFK	A	1	-	50.6
467	chr2.CM0153.150.nd	502.01	1002.00	1002.57	-0.58	2	46	54	R	TPLFLGLDK	I	0	-	48.7
467	LjSGA_042867.1	502.01	1002.00	1002.57	-0.58	2	107	115	R	TPLFLGLDK	S	0	-	48.7
467	LjSGA_134435.1	502.01	1002.00	1002.57	-0.58	2	43	51	R	TPLFLGLDK	I	0	-	48.7
468	LjT39N06.220.nd	431.48	860.94	860.43	0.51	2	509	515	R	GQMAWIR	X	0	-	48.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
469	chr5.CM0040.270.nc	563.98 650.97	1125.94 1299.92	1126.62 1299.65	-0.68 0.27	2 2	295 171	304 181	K K	APLLVGCDIR TFASWGIDYLK	A Y	0 0	Propionamide (C) -	21.8 46.2
469	LjSGA_047213.1	650.97	1299.92	1299.65	0.27	2	56	66	K	TFASWGIDYLK	Y	0	-	46.2
470	LjSGA_031900.1	458.96 408.44 530.93 810.47 683.34	915.91 814.87 1059.84 1618.92 1364.67	916.52 815.41 1060.54 1618.77 1365.55	-0.61 -0.54 -0.70 0.15 -0.88	2 2 2 2 2	68 17 114 34 24	75 23 124 48 33	R K R K R	IISIEQK LAEQAER LIPSASSGDSK VSAAADTEELTVEER YEEMVEFMEK	E Y V N V	0 0 0 0 0	- - - - 2 Oxidation (M)	23.4 31.2 37.8 38.7 22.4
471	chr3.CM0160.1010.nc	528.98	1055.94	1056.62	-0.68	2	14	24	K	LVLIGDSGVGK	S	0	-	48.4
471	LjT39G17.10.nc	528.98	1055.94	1056.62	-0.68	2	16	26	K	LVLIGDSGVGK	S	0	-	48.4
471	LjSGA_036175.1.1	528.98	1055.94	1056.62	-0.68	2	16	26	K	LVLIGDSGVGK	S	0	-	48.4
472	LjSGA_032513.2	528.98	1055.94	1056.62	-0.68	2	1	11	-	LVLIGDSGVGK	S	0	-	48.4
473	chr1.CM0098.40.nd	794.92	1587.82	1588.86	-1.04	2	28	41	R	LGVQLQTIATDFQR	I	0	-	48.3
474	LjSGA_120105.0.1	401.46 608.42	800.91 1214.82	801.43 1215.62	-0.53 -0.80	2 2	104 56	110 65	K K	NTLAEVR WQVEAISDIR	F V	0 0	- -	39.9 48.2
475	LjSGA_018437.1	702.41 606.96	1402.81 1211.90	1403.67 1212.65	-0.86 -0.75	2 2	115 39	125 50	K R	LEPAEFDEWIR SLGGNPTQAQLK	E S	0 0	- -	41.6 34.3
476	LjSGA_008385.1	534.66 580.71	1067.30 1159.41	1067.49 1159.61	-0.18 -0.20	2 2	71 118	79 127	K K	GIQTSEDYR LLSDDVDQKK	F F	0 1	- -	30.5 50.2
478	LjSGA_014341.1	580.45 878.49 893.46 457.99	1158.89 1754.96 1784.91 913.96	1158.64 1754.95 1784.96 914.43	0.25 0.01 -0.05 -0.47	2 2 2 2	426 621 621 496	435 634 634 502	K K K R	LQLSDVCILR LRSLLYLTVNYACR LRSLLYLTVNYTCR SHWACRR	H L L R	0 1 1 1	- Propionamide (C) Propionamide (C) -	20.8 47.4 27.9 21.8
479	chr6.LjT28D11.70.nc	545.51	1089.01	1089.62	-0.61	2	134	143	K	SLFTIGSLPR	N	0	-	47.3
480	chr3.CM0460.50.nc	587.02	1172.02	1172.69	-0.67	2	656	665	R	LYLINSPPVVR	A	0	-	47.2
481	LjSGA_066832.1	594.44	1186.87	1187.65	-0.78	2	25	35	R	TVIINSEGVTR	N	0	-	47.2
482	LjSGA_038377.1.1	645.44	1288.86	1289.63	-0.77	2	111	120	K	MNLNCPRI SR	V	1	Oxidation (M); Propionamide (C)	47.0
482	LjSGA_097533.1	645.44	1288.86	1289.63	-0.77	2	259	268	K	MNLNCPRI SR	V	1	Oxidation (M); Propionamide (C)	47.0
483	chr3.CM0261.320.nd	642.46 633.99	1282.91 1265.97	1283.70 1265.72	-0.79 0.24	2 2	248 248	257 257	R R	LDNLLNLWLQR LPNLLNLWLQR	E E	0 0	- -	31.0 47.0
484	LjSGA_013606.1	718.52	1435.02	1435.86	-0.84	2	91	104	K	VIVLPVIGDDLGVK	I	0	-	46.9
485	LjSGA_026337.1	436.96 480.97	871.90 959.92	872.44 960.51	-0.53 -0.59	2 2	116 54	123 63	R R	DLQVAGR GGLGVGAFQR	I I	0 0	- -	34.1 46.8
486	chr2.CM0021.670.nc	560.88	1119.76	1120.41	-0.66	2	158	166	K	FCCEEDAAH	-	0	Propionamide (C)	46.8
487	LjSGA_086102.1	593.44	1184.86	1185.62	-0.76	2	51	62	K	EAGVTTVESPAK	I	0	-	46.7

Continues...

Supplemental Table S2.11: (green_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
488	LjSGA_013409.1	719.00	1435.99	1436.90	-0.91	2	169	182	R	SNIVGLPASLLLLK	E	0	-	46.7
488	LjSGA_094337.1	719.00	1435.99	1436.90	-0.91	2	10	23	R	SNIVGLPASLLLLK	E	0	-	46.7
489	chr1.CM0378.170.nd	588.98	1175.94	1176.64	-0.70	2	186	196	R	YAILAEDGVVK	L	0	-	46.7
490	LjSGA_044439.1	619.47	1236.92	1237.71	-0.79	2	3	13	R	ILGLNASYFLK	T	0	-	46.6
491	LjSGA_011958.1	647.94	1293.87	1294.62	-0.74	2	140	150	R	SEFLSTVENNR	S	0	-	46.6
492	LjSGA_065625.1	810.44	1618.87	1619.77	-0.90	2	11	25	K	SGGFDEILTDQPVDK	K	0	-	46.5
493	chr5.LjT39E05.230.nd	539.95	1077.88	1078.57	-0.68	2	279	287	R	TNQFLES�K	A	0	-	46.2
494	chr6.CM0066.70.nd	528.94	1055.87	1056.56	-0.69	2	105	115	K	AATAPANSLNK	E	0	-	46.2
495	LjSGA_046433.1	795.00	1587.99	1588.92	-0.93	2	105	119	R	LSHEALAPLVEVALK	L	0	-	46.1
497	chr4.CM0234.330.nd	525.44	1048.86	1049.54	-0.68	2	48	56	R	ASIQEEFVK	S	0	-	46.1
498	chr1.CM0147.490.nc	829.96	1657.91	1657.90	0.01	2	178	193	R	IINEPTAAGLAYGIQK	K	0	-	26.0
		893.97	1785.93	1786.00	-0.07	2	178	194	R	IINEPTAAGLAYGIQKK	S	1	-	39.2
		451.50	900.99	901.52	-0.53	2	425	432	R	NTTIPTKK	K	1	-	46.1
499	LjT09O11.20.nd	585.47	1168.92	1169.64	-0.72	2	507	518	R	VPAVNAVNSTAK	S	0	-	46.0
500	chr4.CM0006.640.nd	704.41	1406.80	1407.60	-0.80	2	1423	1435	R	DSEDNADDSVTIK	S	0	-	45.8
		590.56	1179.10	1179.76	-0.65	2	798	808	R	LVSIILNLALPK	S	0	-	22.6
		531.94	1061.86	1062.59	-0.73	2	877	885	R	VVLLMEGFR	A	0	-	25.9
501	chr1.CM0318.590.nd	632.37	1262.72	1263.64	-0.92	2	193	204	R	GIGPCYASKVNR	N	1	-	25.4
		489.45	976.89	977.48	-0.58	2	47	56	K	LTAADSSASR	I	0	-	45.8
502	chr5.CM0260.200.nc	596.48	1190.95	1191.69	-0.74	2	261	270	K	FLYPLELGIK	E	0	-	45.8
503	chr4.CM0429.360.nc	551.52	1101.03	1101.66	-0.64	2	269	278	K	DLLSTLLSLK	D	0	-	45.8
504	LjSGA_015992.1	753.96	1505.91	1506.75	-0.84	2	597	608	R	DLFINQMNLLDR	A	0	Oxidation (M)	21.2
		650.51	1299.01	1299.74	-0.73	2	261	273	R	GPQIVSSIISTAK	Q	0	-	45.8
505	LjSGA_014973.1	414.98	827.95	828.47	-0.52	2	328	334	K	ALIELDR	L	0	-	45.7
506	chr5.CM0095.260.nd	505.46	1008.91	1008.55	0.36	2	370	377	R	ISKEEYLK	S	1	-	45.7
		515.48	1028.95	1029.51	-0.56	2	421	429	R	TRDDPELGK	M	1	-	28.5
507	LjSGA_007953.1	594.94	1187.87	1188.65	-0.78	2	219	228	K	DSTLIMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	219	228	K	DSTLIMQLLR	D	0	Oxidation (M)	56.3
		458.96	915.91	916.52	-0.61	2	65	72	R	ILSSIEQK	E	0	-	23.4
		408.44	814.87	815.41	-0.54	2	16	22	K	LAEQAEK	Y	0	-	31.2
		893.57	892.57	892.50	0.06	1	46	53	R	NLLSVGYK	N	0	-	20.4
507	chr2.CM0120.430.nc	594.94	1187.87	1188.65	-0.78	2	219	228	K	DSTLIMQLLR	D	0	-	35.7
		602.94	1203.87	1204.65	-0.78	2	219	228	K	DSTLIMQLLR	D	0	Oxidation (M)	56.3
		408.44	814.87	815.41	-0.54	2	16	22	K	LAEQAEK	Y	0	-	31.2
		893.57	892.57	892.50	0.06	1	46	53	R	NLLSVGYK	N	0	-	20.4
507	chr4.CM0229.540.nc	594.94	1187.87	1188.65	-0.78	2	219	228	K	DSTLIMQLLR	D	0	-	35.7

Continues...

Supplemental Table S2.11: (*green_LotusAA GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		602.94	1203.87	1204.65	-0.78	2	219	228	K	DSTLIMQLLR	D	0	Oxidation (M)	56.3
		893.57	892.57	892.50	0.06	1	46	53	R	NLLSVGVYK	N	0	-	20.4
508	LjSGA_065280.2	693.94	1385.87	1386.80	-0.92	2	113	125	R	LIETLSTPSVLSK	R	0	-	45.6
509	LjSGA_121030.1	477.42	952.82	953.44	-0.61	2	79	86	R	NFGFNEAR	K	0	-	45.6
510	LjSGA_038851.1	703.00	1403.98	1403.80	0.18	2	75	86	K	KLDVLSNEVFIK	A	1	-	45.6
511	chr3.CM0396.200.nc	480.47	958.93	959.47	-0.54	2	250	258	K	LVDGGESQR	T	0	-	40.8
		873.01	1744.00	1743.85	0.15	2	310	326	K	VSGEQAPETPTLDVSSK	E	0	-	36.7
511	LjSGA_006242.1	480.47	958.93	959.47	-0.54	2	26	34	K	LVDGGESQR	T	0	-	40.8
512	chr6.CM0055.1140.nd	582.45	1162.88	1163.60	-0.72	2	44	53	K	DPGQKPFTFK	I	0	-	36.2
		705.89	1409.77	1409.66	0.11	2	32	43	K	NGDLSQQFWSTK	D	0	-	38.2
512	chr6.CM0055.920.nc	582.45	1162.88	1163.60	-0.72	2	44	53	K	DPGQKPFTFK	I	0	-	36.2
		705.89	1409.77	1409.66	0.11	2	32	43	K	NGDLSQQFWSTK	D	0	-	38.2
513	chr1.CM0318.10.nd	667.46	1332.91	1333.71	-0.80	2	91	102	R	VIDLYSSPDVVK	Q	0	-	45.3
513	chr6.CM0037.1210.nd	667.46	1332.91	1333.71	-0.80	2	91	102	R	VIDLYSSPDVVK	Q	0	-	45.3
514	LjSGA_102150.1	835.95	1669.88	1668.92	0.96	2	112	126	K	LLGSEELSPELEIK	D	0	-	45.2
515	LjSGA_016798.1	790.01	1578.01	1578.92	-0.91	2	96	110	R	AVPLALGLLCISNPK	V	0	Propionamide (C)	45.0
		525.45	1048.88	1049.52	-0.63	2	111	119	K	VNVMDTLR	L	0	Oxidation (M)	22.1
516	LjSGA_053764.1	550.50	1098.99	1099.65	-0.65	2	47	56	K	IGVLTVELEK	T	0	-	45.0
517	LjSGA_148099.1	403.52	805.02	805.44	-0.43	2	18	23	K	YNQLIR	I	0	-	44.9
519	chr2.CM0323.110.nc	544.49	1086.97	1087.62	-0.66	2	515	524	K	LSELLGSLTR	K	0	-	44.7
519	chr6.CM0836.570.nd	544.49	1086.97	1087.62	-0.66	2	489	498	K	LSELLGSLTR	K	0	-	44.7
519	LjSGA_143024.1	544.49	1086.97	1087.62	-0.66	2	147	156	K	LSELLGSLTR	N	0	-	44.7
520	chr6.CM0037.1610.nc	887.91	1773.80	1774.97	-1.17	2	100	116	K	SSSVPSLLVPFLVESSK	V	0	-	44.3
521	LjSGA_013043.2	544.96	1087.91	1088.58	-0.68	2	68	77	K	DSQLLSVATR	K	0	-	44.2
		552.96	1103.90	1104.60	-0.70	2	68	77	K	MSQLLSVATR	K	0	-	36.3
		544.49	1086.97	1087.60	-0.63	2	68	77	K	NSQLLSVATR	K	0	-	30.2
522	LjSGA_010753.1	642.89	1283.77	1284.64	-0.88	2	100	110	K	FILMVGAYEDK	I	0	-	45.9
523	LjSGA_024368.1	771.93	1541.84	1542.86	-1.02	2	89	102	K	FNPLWNSLVLGGVK	N	0	-	43.9
525	LjSGA_024132.1	626.98	1251.94	1252.76	-0.82	2	39	48	R	ECLPLILILR	N	0	Propionamide (C)	31.9
		634.41	1266.80	1267.62	-0.82	2	134	144	K	GIPYLNITYDGR	T	0	-	43.7
526	chr1.CM0133.1010.nc	580.45	1158.89	1159.61	-0.72	2	20	28	K	WGKWWSEIR	L	1	-	43.5
526	chr2.CM0018.340.nd	580.45	1158.89	1159.61	-0.72	2	24	32	K	WGKWWSEIR	V	1	-	43.5
526	chr2.CM0018.470.nd	580.45	1158.89	1159.61	-0.72	2	27	35	K	WGKWWSEIR	E	1	-	43.5
526	chr2.CM0018.610.nd	580.45	1158.89	1159.61	-0.72	2	32	40	K	WGKWWSEIR	E	1	-	43.5

Continues...

Supplemental Table S2.11: (*green_LotusAA GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
526	chr5.CM0040.1050.nd	580.45	1158.89	1159.61	-0.72	2	47	55	K	WGKWVSEIR	L	1	-	43.5
527	LjT46P06.210.nd	636.93	1271.84	1272.72	-0.88	2	257	266	K	LCLLEKQLSR	C	1	Propionamide (C)	43.2
528	chr5.LjT48O19.170.nd	736.90	1471.79	1471.69	0.10	2	10	22	K	LTNGTVFDSSFER	N	0	-	42.9
529	chr5.CM0260.520.nd	713.50	1424.98	1425.86	-0.87	2	52	64	R	LNIAQVLTVISQK	Q	0	-	42.8
530	chr6.CM0885.50.nc	513.94	1025.86	1026.53	-0.67	2	129	137	K	SDVVIETHK	E	0	-	37.6
		842.87	1683.72	1684.82	-1.09	2	129	143	K	SDVVIETHKEELTG	-	1	-	27.2
531	LjSGA_040309.1	433.47	864.92	865.45	-0.54	2	28	35	R	VFDVTTGK	S	0	-	42.8
532	chr1.CM0094.150.nc	579.97	1157.92	1158.59	-0.66	2	522	532	K	AIDLIDEAGSR	A	0	-	42.7
532	LjSGA_033557.1	579.97	1157.92	1158.59	-0.66	2	45	55	K	AIDLIDEAGSR	V	0	-	42.7
532	chr4.CM0175.340.nc	579.97	1157.92	1158.59	-0.66	2	484	494	K	AIDLIDEAGSR	V	0	-	42.7
533	chr4.CM0042.940.nc	878.56	1755.10	1754.92	0.19	2	30	46	R	IDTTPIDGQKPGTSGLR	K	0	-	42.3
534	chr2.CM0249.1110.nc	697.89	1393.76	1393.69	0.07	2	108	119	R	FLPSEFGLDVDR	H	0	-	42.2
535	LjT25G12.90.nc	490.93	979.84	980.49	-0.65	2	187	195	K	TVFASATER	D	0	-	42.2
536	chr3.CM0574.200.nd	476.45	950.90	951.50	-0.61	2	41	49	K	VSPNVDPK	T	0	-	42.2
537	LjSGA_020183.1	670.44	1338.87	1339.76	-0.89	2	9	20	K	LLGAWQSPVTLR	A	0	-	42.1
537	LjSGA_054228.1	670.44	1338.87	1339.76	-0.89	2	13	24	K	LLGAWQSPVTLR	A	0	-	42.1
538	LjSGA_024816.2	633.47	1264.92	1265.67	-0.74	2	53	62	K	LYYAEPELLR	H	0	-	42.1
539	chr1.LjT04O06.30.nc	634.01	1266.00	1265.83	0.17	2	90	100	R	LPLLILSLKEK	E	1	-	42.1
540	LjSGA_025007.1	401.03	800.04	800.46	-0.43	2	111	117	K	ELGEILK	G	0	-	42.1
541	LjSGA_104128.1	674.47	1346.92	1346.67	0.24	2	18	29	R	VTGDFPDQIIDK	T	0	-	42.0
542	chr3.CM0127.200.nc	642.41	1282.81	1283.65	-0.83	2	255	266	R	EIAHTISNSANK	V	0	-	42.0
543	LjSGA_074342.1	473.44	944.86	945.48	-0.62	2	1	8	-	IDNNETLK	V	0	-	42.0
544	LjSGA_025475.1.1	448.48	894.95	895.52	-0.57	2	53	61	R	AGVVPVQAR	R	0	-	41.9
545	chr1.CM0012.430.nc	649.90	1297.78	1298.63	-0.86	2	32	41	K	TFDVCFQQLK	A	0	Propionamide (C)	41.7
546	LjSGA_138374.1	488.97	975.93	976.49	-0.56	2	98	105	K	LATEELCK	H	0	Propionamide (C)	41.7
547	chr1.CM0001.430.nc	655.41	1308.80	1309.60	-0.80	2	252	262	K	DQNVMAVEFNK	Q	0	Oxidation (M)	41.6
548	LjSGA_038689.1	590.89	1179.76	1179.62	0.14	2	9	18	K	DINALEQHIK	N	0	-	41.6
549	chr3.CM0005.500.nc	479.94	957.87	958.50	-0.62	2	191	199	K	AEVIDDVAK	F	0	-	28.7
		860.50	1718.98	1718.87	0.11	2	126	142	K	EVAGDAPLFTTSDLGVK	K	0	-	41.4
550	LjSGA_036265.1	491.47	980.93	980.57	0.36	2	55	62	K	EIKVIDHK	K	1	-	41.0

Continues...

Supplemental Table S2.11: (*green_LotusAA GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
550	LjSGA_092476.1	491.47	980.93	980.57	0.36	2	55	62	K	EIKVIDHK	K	1	-	41.0

Supplemental Table S2.12: The complete list of the 18 peptides identified in the “green_LotusNT” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.2. The observed mass (*D*), expected mass (*D*), calculated mass (*D*), delta (*D*), charge, start position (*Start*), end position (*End*), amino acid (AA) residue before the peptide (*Residue before*), the peptide AA sequence (*Peptide*), the AA residue after the peptide (*Residue after*), miss cleavage, modification, and MOWSE score (*Score*) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	chr6.CM0679.100.nd	843.38	1684.75	1685.79	-1.04	2	6	21	K	SLEDAFSSFGTVAEAR	V	0	-	118.0
2	LjSGA_039741.1	657.93	1313.85	1314.57	-0.71	2	432	443	R	GMFDGAFDNIGR	G	0	Oxidation (M)	60.5
		804.98	1607.95	1608.84	-0.89	2	392	407	R	LAAELGDNVPSLPEGK	V	0	-	74.2
3	LjSGA_057408.1	768.77	1535.52	1535.74	-0.23	2	51	64	R	NGHVEIIANDQGNR	I	0	-	52.8
		537.45	1072.89	1073.53	-0.64	2	85	93	K	NQFAVNPER	T	0	-	45.5
4	LjSGA_031454.1	783.44	1564.86	1565.73	-0.87	2	151	163	K	EQMTPLSEFEDKL	-	1	-	44.5
		791.42	1580.82	1581.72	-0.90	2	151	163	K	EQMTPLSEFEDKL	-	1	Oxidation (M)	52.8
5	chr3.CM0164.170.nd	773.85	1545.68	1545.65	0.03	2	578	589	R	TRDEEEEEQPR	F	1	-	57.4
6	LjSGA_013193.1	910.92	1819.83	1820.95	-1.12	2	106	123	R	IGVGVTSQAQSIFDALSK	-	0	-	89.4
7	chr4.CM0500.250.nd	934.33	1866.64	1867.78	-1.14	2	150	168	K	GSSNVGDGLGGFEDSAEGR	D	0	-	87.0
8	chr1.CM0012.440.nc	732.45	1462.88	1462.77	0.11	2	1	14	-	GPEFATIINSVTSK	K	0	-	76.3
9	LjSGA_059009.1	749.87	1497.73	1498.72	-0.99	2	51	62	R	AYEEIYQEDLVK	R	0	-	59.5
		630.91	1259.80	1259.66	0.14	2	64	74	R	LESEIKGDLEK	A	1	-	49.8
10	LjSGA_011073.1	723.91	1445.80	1446.71	-0.91	2	61	74	R	TQLNSLQESSGGAR	I	0	-	71.3
11	LjSGA_111606.1	718.41	1434.80	1435.71	-0.91	2	74	86	R	SVQQEGLFWGASK	L	0	-	67.1
12	LjT32C22.20.nd	604.44	1206.86	1206.61	0.25	2	556	567	R	VSAANGRPNPQ	-	0	-	65.2
13	LjSGA_020590.0.1	546.49	1090.97	1091.67	-0.70	2	4	13	R	VVDLIVHVAK	S	0	-	43.4
14	LjSGA_066691.0.1	557.97	1113.92	1114.66	-0.74	2	65	75	R	GTLEVVLVSAK	G	0	-	47.4

Supplemental Table S2.13: The complete list of the 39 peptides identified in the “green_NCBInr” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.3. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	gi 1076373	676.41	1350.81	1350.69	0.11	2	1	13	-	AYGEAANVFGKPK	T	0	-	85.8
		675.93	1349.84	1349.75	0.10	2	1	13	-	AYGKAANVFGKPK	T	1	-	86.6
2	gi 11023055	1127.35	2252.69	2253.15	-0.46	2	345	364	R	MPTFFETFPVVLVDGNGIVR	A	0	Oxidation (M)	99.7
		803.89	2408.64	2409.25	-0.61	3	344	364	R	RMPTFFETFPVVLVDGNGIVR	A	1	Oxidation (M)	33.3
2	gi 37721488	1127.35	2252.69	2253.15	-0.46	2	349	368	R	MPTFFETFPVVLVDGNGIVR	A	0	Oxidation (M)	99.7
		803.89	2408.64	2409.25	-0.61	3	348	368	R	RMPTFFETFPVVLVDGNGIVR	A	1	Oxidation (M)	33.3
3	gi 7230391	774.96	2321.85	2322.18	-0.32	3	392	411	K	MIPTKPMVVETFSQYPPLGR	F	0	2 Oxidation (M)	49.8
		769.62	2305.85	2306.18	-0.33	3	392	411	K	MIPTKPMVVETFSQYPPLGR	F	0	Oxidation (M)	77.2
3	gi 48527431	774.96	2321.85	2322.18	-0.32	3	392	411	K	MIPTKPMVVETFSQYPPLGR	F	0	2 Oxidation (M)	49.8
		769.62	2305.85	2306.18	-0.33	3	392	411	K	MIPTKPMVVETFSQYPPLGR	F	0	Oxidation (M)	77.2
3	gi 89275337	774.96	2321.85	2322.18	-0.32	3	203	222	K	MIPTKPMVVETFSQYPPLGR	F	0	2 Oxidation (M)	49.8
		769.62	2305.85	2306.18	-0.33	3	203	222	K	MIPTKPMVVETFSQYPPLGR	F	0	Oxidation (M)	77.2
4	gi 22330456	660.95	1319.89	1319.73	0.16	2	94	108	K	APGGAPANVAVGIAR	L	0	-	58.6
		725.01	1448.00	1447.83	0.17	2	93	108	K	KAPGGAPANVAVGIAR	L	1	-	60.1
4	gi 23476263	660.95	1319.89	1319.73	0.16	2	83	97	K	APGGAPANVAVGIAR	L	0	-	58.6
		725.01	1448.00	1447.83	0.17	2	82	97	K	KAPGGAPANVAVGIAR	L	1	-	60.1
4	gi 51535181	660.95	1319.89	1319.73	0.16	2	119	133	K	APGGAPANVAVGIAR	L	0	-	58.6
		725.01	1448.00	1447.83	0.17	2	118	133	K	KAPGGAPANVAVGIAR	L	1	-	60.1
4	gi 113595266	660.95	1319.89	1319.73	0.16	2	107	121	K	APGGAPANVAVGIAR	L	0	-	58.6
		725.01	1448.00	1447.83	0.17	2	106	121	K	KAPGGAPANVAVGIAR	L	1	-	60.1
5	Unknown/dead	633.36	1264.70	1264.63	0.07	2	1	11	-	TNAENEFVTIK	K	0	-	66.8
6	gi 5924375	1022.93	2043.84	2044.10	-0.25	2	285	303	R	LSIATFQNPAPNATVYPLK	I	0	-	76.4
6	gi 51039637	1022.93	2043.84	2044.10	-0.25	2	288	306	R	LSIATFQNPAPNATVYPLK	I	0	-	76.4
6	gi 51556895	1022.93	2043.84	2044.10	-0.25	2	289	307	R	LSIATFQNPAPNATVYPLK	I	0	-	76.4
7	gi 20146556	769.55	2305.62	2306.17	-0.54	3	372	393	R	EVAFAAQFGSNLDAATQALLNR	G	0	-	59.9
7	gi 20146600	769.55	2305.62	2306.17	-0.54	3	372	393	R	EVAFAAQFGSNLDAATQALLNR	G	0	-	59.9
8	gi 16588840	749.85	1497.69	1498.66	-0.97	2	129	141	R	YDMSVEAAELAR	R	0	Oxidation (M)	73.7
9	gi 51039632	846.87	1691.72	1692.85	-1.13	2	2	16	M	ATEEVLVEITYPSK	I	0	-	66.9
10	gi 62183962	642.96	1925.85	1925.10	0.75	3	246	264	K	IMTAAQLVKPVSLELGK	S	0	-	60.1
10	gi 86156419	642.96	1925.85	1925.10	0.75	3	89	107	K	IMTAAQLVKPVSLELGK	S	0	-	60.1
10	Unknown/dead	642.96	1925.85	1925.10	0.75	3	246	264	K	IMTAAQLVKPVSLELGK	S	0	-	60.1

Continues...

Supplemental Table S2.13: (*green_NCBInr GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
10	gi 113205159	642.96	1925.85	1925.10	0.75	3	291	309	K	IMTAAQLVKPVSLELGK	S	0	-	60.1
11	gi 2708324	858.22	2571.63	2571.28	0.35	3	42	65	K	VIELDLESDGSAIQAALEWTGQR	T	0	-	58.1
12	gi 6911142	616.44	1230.87	1231.58	-0.71	2	88	102	R	SGSGGGGGGGFRGPR	R	1	-	47.7
12	gi 6911146	616.44	1230.87	1231.58	-0.71	2	88	102	R	SGSGGGGGGGFRGPR	R	1	-	47.7
13	gi 113565257	616.86	1231.70	1232.50	-0.80	2	116	130	R	SGSGGGGGGGDDLDR	S	0	-	51.0
15	gi 20146580	769.55	2305.63	2306.19	-0.56	3	372	393	R	EVAAFQFGSDLDAATQALLIR	G	0	-	47.5
16	gi 27461579	769.55	2305.62	2305.13	0.49	3	369	390	R	EPAAFQFGSDLDAATQALLNR	G	0	-	45.4
17	gi 14334219	832.98	1663.95	1664.93	-0.98	2	57	72	K	IIIEGPITVAPQATVK	Q	0	-	44.1

Supplemental Table S2.14: The complete list of the 47 peptides identified in the “green_SPROT” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.4. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	METE_ARATH	713.71	2138.10	2139.26	-1.15	3	146	166	K	ALGVDTPVPLVGPVSYLLLSK	A	0	-	73.3
1	METE_MESCR	713.71	2138.10	2139.26	-1.15	3	146	166	K	ALGVDTPVPLVGPVSYLLLSK	Q	0	-	73.3
2	TBA_DAUCA	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA_PRUDU	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA_WHEAT	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA1_ANEPH	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA1_ELEIN	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA1_GOSHI	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA1_MAIZE	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA1_PEA	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA2_ARATH	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA2_GOSHI	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA2_HORVU	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA2_MAIZE	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA2_ORYSA	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA3_HORVU	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA3_MAIZE	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA4_GOSHI	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
2	TBA6_ARATH	736.99	1471.97	1472.86	-0.89	2	230	243	R	LVSQVISSLTASLR	F	0	-	90.6
3	ATPB_SCHSP	800.29	2397.84	2398.24	-0.40	3	53	73	R	DTVGQQINVTCKVQQLGNRR	V	1	Propionamide (C)	75.2
4	MDAR_PEA	754.43	1506.85	1507.74	-0.89	2	146	158	R	EVDDADKLYEAIK	R	1	-	73.9
5	PSA6_ORYSA	642.90	1925.68	1925.97	-0.29	3	229	245	R	ALTTEEDQHLTAISER	D	0	-	71.2
		622.90	1243.79	1243.72	0.06	2	31	43	K	AVKSAGVTSIGVR	G	1	-	20.2
6	PSAE_SPIOL	1113.85	2225.68	2226.04	-0.36	2	106	125	K	VNYANVSTNNYALDEIQEVA	-	0	-	58.7
7	EFTU_ARATH	841.54	1681.07	1680.94	0.12	2	342	357	K	ILDEALAGDNVGLLLR	G	0	-	56.0
7	EFTU1_SOYBN	841.54	1681.07	1680.94	0.12	2	345	360	K	ILDEALAGDNVGLLLR	G	0	-	56.0
7	EFTU2_SOYBN	841.54	1681.07	1680.94	0.12	2	345	360	K	ILDEALAGDNVGLLLR	G	0	-	56.0

Continues...

Supplemental Table S2.14: (*green_SPROT GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
8	TBA1_CHLVU	736.99	1471.97	1470.88	1.09	2	230	243	R	LIAQVISSLTASLR	F	0	-	50.1
8	TBA1_CHLRE	736.99	1471.97	1470.88	1.09	2	230	243	R	LIAQVISSLTASLR	F	0	-	50.1
8	TBA1_VOLCA	736.99	1471.97	1470.88	1.09	2	230	243	R	LIAQVISSLTASLR	F	0	-	50.1
8	TBA2_CHLRE	736.99	1471.97	1470.88	1.09	2	230	243	R	LIAQVISSLTASLR	F	0	-	50.1
9	RL40_BRARA	614.97	1227.92	1228.68	-0.76	2	1	11	-	IIEPSLMALAR	K	0	Oxidation (M)	49.8
9	RL40_NICSY	614.97	1227.92	1228.68	-0.76	2	1	11	-	IIEPSLMALAR	K	0	Oxidation (M)	49.8
10	EF1A_MAIZE	912.19	2733.55	2733.32	0.23	3	181	204	K	VGYNPDKIHFPISGFEGDNMIER	S	1	-	49.5
11	MDARS_CUCSA	743.42	1484.83	1484.72	0.11	2	63	76	R	LPGFHVCVSGGGER	L	0	Propionamide (C)	48.0
11	MDAR_SOLLC	743.42	1484.83	1484.72	0.11	2	63	76	R	LPGFHVCVSGGGER	Q	0	Propionamide (C)	48.0
12	SUCA2_ARATH	703.93	2108.77	2109.12	-0.35	3	269	289	K	ENGTDKPVVAFIAGLTAPPGR	R	0	-	44.2
13	UGPA_HORVU	820.95	1639.89	1640.88	-0.99	2	391	405	R	VKPSNPSELGPEFK	K	0	-	41.6
14	BADH_ARATH	652.42	1302.83	1303.71	-0.88	2	333	344	R	LGPVVSKGQYEK	I	1	-	41.5
15	TKTC_CRAPL	801.77	1601.52	1601.77	-0.25	2	198	212	K	ALPTYTPENPGDATR	N	0	-	36.9
16	CB2A_SPIOL	1176.19	3525.56	3525.76	-0.20	3	178	212	R	IAGGPLGEVVDPLYPGGSFDPLGLADDPEAFaelK	V	0	-	34.2
16	CB2G_SOLLC	1176.19	3525.56	3525.76	-0.20	3	178	212	R	IAGGPLGEVVDPLYPGGSFDPLGLADDPEAFaelK	V	0	-	34.2
16	CB21_MAIZE	1176.19	3525.56	3525.76	-0.20	3	173	207	R	IAGGPLGEVVDPLYPGGSFDPLGLADDPEAFaelK	V	0	-	34.2
16	CB22_ORYSA	1176.19	3525.56	3525.76	-0.20	3	172	206	R	IAGGPLGEVVDPLYPGGSFDPLGLADDPEAFaelK	V	0	-	34.2
16	CB22_PEA	1176.19	3525.56	3525.76	-0.20	3	180	214	R	IAGGPLGEVVDPLYPGGSFDPLGLADDPEAFaelK	V	0	-	34.2
16	CB28_PEA	1176.19	3525.56	3525.76	-0.20	3	179	213	R	IAGGPLGEVVDPLYPGGSFDPLGLADDPEAFaelK	V	0	-	34.2
18	ALF2_PEA	722.59	2164.74	2164.03	0.71	3	150	169	K	IGANEPSEHSIHENAYGLAR	Y	0	-	32.2

Supplemental Table S2.15: The complete list of the 157 peptides identified in the “green_lotusEST_TIGR” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.5. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	TC9431	938.98	1875.94	1875.71	0.23	2	116	133	R	ESEEEGSSSSSSSESSR	R	0	-	107.3
2	TC14090	577.85	1153.69	1153.56	0.13	2	373	383	K	ANSEATLGTYK	G	0	-	76.9
		538.27	1611.80	1612.77	-0.97	3	384	399	K	GDSQLGEGASESLHVK	D	0	-	53.7
		1110.18	2218.34	2218.07	0.27	2	152	174	K	GTVELAGTDGETTTQGLDGLGAR	C	0	-	65.9
		1084.17	2166.32	2166.07	0.25	2	194	213	K	IGNPESELSEIHENAYGLAR	Y	0	-	48.6
		730.02	1458.02	1457.75	0.27	2	85	97	R	LASINVENVETNR	R	0	-	67.9
		1281.29	2560.57	2560.26	0.31	2	149	174	K	VDKGTVELAGTDGETTTQGLDGLGAR	C	1	-	47.9
		668.95	1335.88	1335.71	0.16	2	283	294	K	VTPEVVAEHTVR	A	0	-	48.4
		916.42	1830.82	1831.91	-1.09	2	53	69	K	YHDELIANAAYIGTPGK	G	0	-	104.1
3	TC19114	926.38	1850.75	1851.94	-1.19	2	69	84	K	FDVNSLFSVVDNIVER	S	0	-	82.1
		997.83	1993.64	1993.97	-0.33	2	88	106	R	IADNVVQSGHSGSPEQTDIK	T	0	-	71.7
		775.44	1548.87	1549.78	-0.91	2	107	120	K	TPSANFTSPLCTLK	Q	0	Propionamide (C)	87.4
4	TC18091	867.39	1732.76	1733.88	-1.12	2	122	136	K	DVQVLESDSDFIIVSR	Y	0	-	83.8
5	TC8325	533.45	1064.88	1065.50	-0.62	2	304	312	K	ETMEIVSNK	E	0	Oxidation (M)	32.4
		790.47	1578.93	1579.86	-0.93	2	313	327	K	EVIANVQDPIGVQAK	K	0	-	65.1
		892.36	1782.71	1783.77	-1.06	2	230	244	R	TTNDINDSWESMISR	A	0	Oxidation (M)	68.6
		827.46	1652.91	1652.72	0.19	2	177	190	K	YDNCNNDGSKPTVR	Y	0	Propionamide (C)	88.3
6	TC14411	493.32	984.63	984.52	0.11	2	223	231	R	EIHGTSITK	K	0	-	24.5
		574.45	1146.89	1147.65	-0.76	2	319	328	K	FLLTLGKED	-	1	-	30.2
		880.03	1758.04	1757.84	0.20	2	144	159	K	HSLEEDVAAHTSGHLR	Q	0	-	119.4
		512.94	1535.79	1536.81	-1.02	3	180	193	K	LAQSEAEILHEAVK	E	0	-	58.0
		591.87	1181.73	1181.60	0.12	2	300	310	R	NSVHLEDAVAK	E	0	-	48.4
		511.43	1020.84	1021.51	-0.67	2	171	179	R	YVGEEINAK	L	0	-	43.7
7	TC7865	425.99	849.97	850.41	-0.44	2	174	180	K	AEEVFEK	T	0	-	30.2
		460.01	918.01	918.48	-0.48	2	276	284	R	ATDIMIAK	V	0	-	49.7
		931.42	1860.82	1861.99	-1.17	2	399	415	R	FVFPETNTGIIVLAEGR	L	0	-	76.3
		660.25	1318.49	1318.70	-0.21	2	220	232	R	LVGVSEETITGVK	R	0	-	66.6
		618.37	1234.73	1234.63	0.10	2	37	47	K	VKDLSQADFGR	L	1	-	25.5
8	TC8215	787.99	1573.97	1573.82	0.15	2	231	245	K	DALAECDKITLETAK	L	1	-	43.9
		856.69	1711.37	1711.65	-0.28	2	70	84	R	DMGYNVSMADSTSR	W	0	3 Oxidation (M)	31.2
		837.38	1672.75	1673.76	-1.00	2	249	262	R	EDYLAQNAFTPYDK	F	0	-	58.9
		731.92	1461.82	1461.70	0.12	2	319	332	K	FEDPAEGESALVAK	F	0	-	55.4
		780.94	1559.86	1560.79	-0.93	2	40	54	R	TTLVANTSNMPVAAR	E	0	Oxidation (M)	73.0
9	TC8009	485.47	968.92	969.49	-0.57	2	215	224	R	AHASTEGVAK	Y	0	-	51.4
		702.77	1403.54	1403.73	-0.19	2	238	250	K	ELDYLVGAVSNPK	K	0	-	60.7
		419.95	837.89	838.38	-0.49	2	336	343	K	FSADANSK	T	0	-	28.6
		762.56	1523.10	1522.90	0.20	2	321	335	K	GVALLLPDVTVDIAK	F	0	-	26.1
		537.88	1073.75	1073.62	0.12	2	251	261	K	KPFAAIVGSGK	V	0	-	28.2
		644.95	1931.84	1932.97	-1.13	3	197	214	K	LASLADLYVNDAFGTAAH	A	0	-	52.6

Continues...

Supplemental Table S2.15: (*green_lotusEST_TIGR* GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		607.00	1817.98	1819.06	-1.08	3	165	181	K	LVAQIPEGGVILENVR	F	0	-	57.4
		1021.60	2041.18	2041.00	0.18	2	83	100	R	VDLNVPLDDNLNITDDTR	V	0	-	51.8
		733.31	1464.61	1464.82	-0.21	2	225	237	K	YLKPAVAGFLMQK	E	0	-	24.0
10	TC16258	803.48	1604.94	1604.83	0.11	2	3	17	K	VATPAQAQEVHADLR	K	0	-	71.0
		867.53	1733.05	1732.92	0.13	2	3	18	K	VATPAQAQEVHADLRK	W	1	-	66.2
		842.48	1682.95	1682.84	0.11	2	19	33	K	WIHDNVSAEVASTVR	I	0	-	39.3
11	TC7926	500.47	998.92	999.50	-0.57	2	270	279	R	AHASTEGVTK	Y	0	-	54.0
		696.29	1390.57	1390.73	-0.17	2	293	305	K	ELDYLVGAVSTPK	R	0	-	54.3
		644.95	1931.84	1932.97	-1.13	3	252	269	K	LASLADLYVNDAFGTAHR	A	0	-	52.6
		882.51	1763.00	1764.01	-1.01	2	220	236	K	LVASLPDGGVLLLENVR	F	0	-	21.4
		551.86	1101.71	1101.63	0.08	2	306	316	K	RPFAAIVGGSK	V	0	-	34.8
		732.34	1462.66	1462.85	-0.20	2	280	292	K	YLKPSVAGFLLQK	E	0	-	44.4
		508.01	1014.00	1014.59	-0.58	2	189	197	K	YSLAPLVPR	L	0	-	53.2
12	TC14283	747.89	1493.77	1494.75	-0.98	2	86	97	K	ITQLTDNVYVCR	S	0	Propionamide (C)	55.0
		774.41	1546.80	1547.80	-1.00	2	144	157	K	NFLETGLIVGGWDK	Y	0	-	57.5
		770.36	1538.71	1539.72	-1.01	2	98	112	R	SGSAADSQVVS DYVR	Y	0	-	82.0
13	TC8165	842.36	1682.71	1683.81	-1.10	2	226	241	K	GNAYAQVAIGTDDVYK	S	0	-	73.9
		782.47	1562.92	1562.79	0.13	2	242	256	K	SAELVNLATQEFGGK	I	0	-	81.6
14	TC8727	782.40	1562.78	1563.79	-1.01	2	146	159	K	GFPTQDIEVNIGK	Q	0	-	60.6
		627.67	1880.00	1881.00	-1.01	3	68	82	K	IVWIPIVEEWNQDLK	N	0	-	53.3
		482.95	963.88	964.49	-0.61	2	14	22	K	TPIDGATK	T	0	-	52.6
15	TC8258	617.88	1233.75	1233.60	0.15	2	77	87	K	APSEEFVNVR	W	0	-	75.1
		590.93	1179.85	1180.60	-0.75	2	66	76	K	DDVTVAALSK	A	0	-	46.5
16	TC10840	456.99	911.97	912.54	-0.57	2	31	39	R	GLVGEIIGR	F	0	-	45.5
		728.40	1454.78	1455.70	-0.91	2	127	140	R	NVIHGSDSVESANK	E	0	-	93.4
17	TC9761	757.44	1512.88	1512.73	0.14	2	63	74	K	AYEELYQEDIK	R	0	-	52.3
		821.50	1640.98	1640.83	0.15	2	62	74	R	KAYEELYQEDIK	R	1	-	42.3
		807.46	1612.91	1612.77	0.14	2	143	157	R	SLEEDVAAHTTGDLR	Q	0	-	96.7
18	TC14102	670.25	1338.48	1338.67	-0.18	2	120	132	K	FAQYTGANAIAGR	H	0	-	85.2
19	CN825001	493.95	985.89	986.50	-0.61	2	191	199	K	EVGQDIQAK	A	0	-	21.5
		577.42	1152.82	1153.54	-0.72	2	171	181	R	MADVAGYVGQK	T	0	Oxidation (M)	51.0
		694.40	1386.79	1386.67	0.12	2	155	168	R	QSQGTGPGQLES AK	R	0	-	54.8
		595.92	1189.82	1190.57	-0.75	2	43	52	R	YETGVNPQQR	Y	0	-	32.2
		682.38	1362.75	1362.63	0.12	2	53	63	R	YETGVNYPQHR	Y	0	-	55.5
20	TC9795	620.87	1239.72	1239.62	0.10	2	173	183	K	MKETAEAF LGK	K	1	Oxidation (M)	48.0
		775.43	1548.85	1549.81	-0.96	2	159	172	K	VFSPEEVSAMILTK	M	0	-	66.4
		783.45	1564.89	1565.80	-0.91	2	159	172	K	VFSPEEVSAMILTK	M	0	Oxidation (M)	55.9
21	TC9755	751.45	1500.89	1500.79	0.10	2	203	216	K	ASSVAQVVNTLQER	G	0	-	59.5
		806.53	1611.05	1611.89	-0.84	2	26	41	K	IVNTGTVLQVGDGIAR	I	0	-	70.1
		803.98	1605.94	1605.84	0.11	2	467	480	K	TNKPQFNEISSTK	T	0	-	31.7
22	TC8048	578.43	1154.85	1155.60	-0.75	2	58	67	R	HITIFSP EGR	L	0	-	36.1
		850.04	1698.07	1697.94	0.14	2	106	120	K	LLDQTSVSHLFPITK	Y	0	-	24.1
		1022.08	2042.15	2041.98	0.17	2	275	292	R	VLSTDEIDEHLTAISERD	-	1	-	65.2

Continues...

Supplemental Table S2.15: (*green_lotusEST_TIGR* GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		734.39	1466.78	1467.74	-0.96	2	121	134	K	YLGLLATGMTADAR	T	0	Oxidation (M)	52.9
23	TC16731	742.94	1483.86	1484.78	-0.92	2	65	78	K	GNVQPDTVLQTVSK	T	0	-	51.6
		690.44	1378.87	1379.68	-0.81	2	46	57	K	LEGVESYDIDLK	E	0	-	66.3
24	TC9709	637.40	1272.78	1273.59	-0.82	2	35	45	K	LLDNASDDFHK	A	0	-	51.9
		591.87	1181.73	1181.60	0.12	2	102	112	R	NSVHLEDAVAK	E	0	-	48.4
25	TC14129	664.92	1327.83	1328.66	-0.83	2	281	293	R	KFVESAASSFSVA	-	1	-	73.4
		1064.11	2126.21	2126.02	0.19	2	242	262	R	TADGDEGKGHIITATVNDGK	L	1	-	44.0
26	CN825207	868.41	1734.80	1735.95	-1.15	2	131	146	R	VALSSIQPNNLEPLNK	I	0	-	64.7
27	TC14826	885.91	1769.80	1770.96	-1.16	2	254	270	K	TVDSLLITAIEGVPELK	A	0	-	72.5
		648.41	1294.81	1295.67	-0.86	2	191	202	R	VNQSVYIGTSTK	V	0	-	44.5
28	TC14233	663.42	1324.83	1324.71	0.12	2	124	136	R	SVHDVVLVGGSTR	I	0	-	59.7
28	TC14234	663.42	1324.83	1324.71	0.12	2	117	129	K	SVHDVVLVGGSTR	I	0	-	59.7
29	TC14860	717.43	1432.84	1432.74	0.10	2	268	281	R	EAGTTLAVVSEQTK	A	0	-	83.5
		536.86	1071.70	1071.63	0.07	2	154	163	K	KIVGTLINEAK	V	1	-	32.8
30	TC16128	636.44	1270.87	1271.64	-0.77	2	115	127	K	GTGSVVAVDQDPK	T	0	-	82.7
31	TC8046	885.30	1768.58	1769.75	-1.16	2	83	100	R	STASSSSSSANMASQDPR	I	0	-	49.9
		893.29	1784.57	1785.74	-1.18	2	83	100	R	STASSSSSSANMASQDPR	I	0	Oxidation (M)	61.3
32	TC11167	783.37	1564.73	1565.76	-1.03	2	92	105	K	DDFFDALISAPVEK	A	0	-	81.9
33	TC14170	588.62	1762.82	1763.95	-1.13	3	148	165	R	VAMIGFAASLLGEALTCK	G	0	Oxidation (M)	27.7
		785.39	1568.77	1569.77	-0.99	2	124	139	K	VEDGVFGTSGGIGFTK	Q	0	-	79.8
34	TC14768	842.52	1683.03	1682.90	0.13	2	176	190	K	DVELVMTQATVPRPK	A	0	-	51.9
		850.52	1699.04	1698.90	0.14	2	176	190	K	DVELVMTQATVPRPK	A	0	Oxidation (M)	53.2
35	TC14111	831.45	1660.89	1661.83	-0.94	2	97	110	R	DDADFTWEVVKPLK	W	0	-	79.8
36	TC14758	788.35	1574.68	1575.64	-0.97	2	140	159	R	GYGGGGGGYGGGGGGYGGGR	R	0	-	55.2
37	TC18990	648.91	1295.81	1295.71	0.09	2	66	76	K	FSTTPIKDIFK	D	1	-	20.1
		885.43	1768.84	1769.95	-1.11	2	37	54	K	IASGTDIVSAAPNVSLQK	A	0	-	77.9
38	TC8324	812.42	1622.83	1623.90	-1.07	2	383	400	K	VFVGLPTTGAAPAAPAK	A	0	-	65.1
39	TC16164	718.46	1434.90	1434.72	0.18	2	65	79	R	HPSTAATPTPTAGAR	R	0	-	48.3
		750.96	1499.90	1499.71	0.19	2	167	179	R	KLEDDFDAFTATK	S	1	-	55.4
40	TC10602	559.41	1116.81	1117.50	-0.69	2	76	86	R	AQGDADSAIDR	L	0	-	59.4
40	TC11545	559.41	1116.81	1117.50	-0.69	2	86	96	R	AQGDADSAIDR	L	0	-	59.4
41	TC14070	868.33	1734.64	1735.75	-1.11	2	328	341	K	LVSWYDNEMGYSTR	V	0	Oxidation (M)	63.4
42	TC8011	693.42	1384.83	1384.74	0.10	2	182	193	R	HIIGEKDEFIGK	K	1	-	48.5
		833.48	1664.95	1664.84	0.11	2	288	304	R	IYGGSVNGGNSSELAK	K	0	-	47.0
43	TC14938	747.49	1492.96	1493.88	-0.93	2	61	75	R	VNTVLGSVAPPLTVK	L	0	-	70.5

Continues...

Supplemental Table S2.15: (*green_lotusEST_TIGR* GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
44	TC8718	787.89	1573.76	1574.78	-1.02	2	188	202	K	SATEVIGSSFFYTSVK	N	0	-	68.0
45	TC14174	773.85	1545.68	1546.68	-1.01	2	473	485	R	AAEDPEFETFFYTK	N	0	-	51.5
		748.40	1494.78	1495.70	-0.92	2	848	861	R	SPTGEVIFGGETMR	F	0	Oxidation (M)	42.3
46	TC16511	605.34	1208.67	1208.61	0.07	2	57	67	K	HATYVPHTAGR	Y	0	-	43.3
46	TC16742	605.34	1208.67	1208.61	0.07	2	72	82	K	HATYVPHTAGR	Y	0	-	43.3
47	TC8440	608.99	1215.96	1216.59	-0.64	2	71	83	K	ATGSAAEVASEPK	D	0	-	64.7
48	TC8596	672.97	1343.92	1344.80	-0.88	2	53	64	R	AELGLLVLYLNK	A	0	-	62.0
49	TC16605	827.48	1652.94	1653.93	-0.99	2	177	191	K	IVVTDPDVLNLLTR	E	0	-	61.9
50	TC14545	556.34	1110.66	1110.58	0.08	2	128	137	R	GEGKPPHYVK	V	0	-	34.6
		631.44	1260.86	1261.69	-0.83	2	51	61	K	VYITVQLPDSK	D	0	-	60.6
51	TC13498	665.39	1328.76	1329.62	-0.86	2	102	114	R	ASMGYISSQSVK	K	0	Oxidation (M)	61.3
52	TC16034	801.94	1601.86	1602.83	-0.96	2	80	94	R	NSPIDFELGSGGVK	G	0	-	61.3
53	TC16259	807.44	1612.86	1613.94	-1.08	2	24	38	R	LSPTVIQSLSTLSR	L	0	-	60.6
54	BP043716	894.96	1787.91	1788.93	-1.03	2	148	164	K	EPMPFIPVAIGLLDSSGK	D	0	Oxidation (M)	59.6
55	TC9804	642.91	1283.80	1284.61	-0.81	2	72	83	K	VVNFSGSESFR	I	0	-	59.5
56	TC9618	615.94	1229.86	1230.62	-0.76	2	94	104	R	AAEDTYHIK	K	0	-	58.5
57	TC9100	674.37	1346.73	1347.62	-0.89	2	166	179	K	DTPAVSSSDSPSKA	-	1	-	58.2
57	BP055887	674.37	1346.73	1347.62	-0.89	2	105	118	K	DTPAVSSSDSPSKA	-	1	-	58.2
58	TC9294	721.99	1441.96	1442.76	-0.80	2	113	125	R	LLETSPTIENQAK	Q	0	-	50.0
59	TC16914	917.89	1833.77	1834.92	-1.15	2	24	40	K	TILSSETMDIPDGVTIK	V	0	Oxidation (M)	57.1
60	AV776844	742.47	1482.92	1483.84	-0.92	2	69	82	K	LVIPAINAFNDGIK	F	0	-	47.7
61	TC14220	467.94	933.87	934.46	-0.59	2	59	67	R	EATLSDTAK	A	0	-	36.7
		1001.65	2001.28	2001.04	0.24	2	76	94	K	SLGVTLVAGDLYHDSLK	V	0	-	24.3
		426.46	850.90	851.45	-0.55	2	142	149	R	THAVEPAK	S	0	-	33.1
62	TC9107	724.88	1447.75	1447.66	0.10	2	274	286	R	EVQDHIDYGTSGK	V	0	-	53.1
63	TC7901	914.89	1827.77	1828.86	-1.09	2	71	85	K	TINVPEGFYELYNR	N	0	-	52.7
64	TC17673	731.45	1460.89	1460.78	0.11	2	93	105	R	VPLYIGSVEEVEK	V	0	-	51.5
65	TC10225	662.43	1322.85	1323.67	-0.82	2	139	150	K	LLGIETQAHDDL	-	0	-	48.7
66	TC8223	671.42	1340.82	1341.70	-0.88	2	101	111	K	TIFSFIIPDQK	S	0	-	36.6
67	TC14632	536.93	1071.85	1072.54	-0.69	2	181	190	K	EPEAQLATSK	R	0	-	46.3
68	TC8417	499.95	997.89	998.51	-0.62	2	123	132	K	AVGESVANPR	R	0	-	46.0
69	TC8618	866.37	1730.73	1730.86	-0.14	2	113	128	K	IFNSPNGPNVYEGVPK	D	0	-	44.3

Continues...

Supplemental Table S2.15: (*green_lotusEST_TIGR GeLC-MS/MS Peptides continued*)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
70	TC8712	514.95	1027.89	1028.55	-0.66	2	226	235	K	AIDNAEGLVK	I	0	-	30.4
		574.94	1147.87	1148.61	-0.74	2	111	121	R	TPYTAGLGLEK	I	0	-	41.5
71	TC12003	586.34	1170.66	1170.56	0.09	2	54	64	R	HQGMVMGMGQK	D	0	-	43.1
72	BP070882	788.47	1574.92	1574.78	0.14	2	100	113	K	AIAFDEIDKAPEEK	K	1	-	42.6
73	TC8611	705.93	1409.85	1410.71	-0.86	2	37	49	R	GTSVLEMVTAFEK	A	0	-	41.5
74	TC10826	671.46	1340.90	1340.78	0.12	2	148	159	K	KVNTLIRPDGTYK	K	1	-	41.1
75	TC14770	804.95	1607.89	1608.92	-1.03	2	234	248	K	AIDVIPLLTPAVMEK	I	0	-	40.7
77	TC20208	787.95	1573.89	1574.87	-0.98	2	23	37	K	VFSVPEAAPFTAVLK	F	0	-	39.7

Supplemental Table S2.16: The complete list of the 625 peptides identified in the “mature_LotusAA” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.6. The observed mass (*D*), expected mass (*D*), calculated mass (*D*), delta (*D*), charge, start position (*Start*), end position (*End*), amino acid (*AA*) residue before the peptide (*Residue before*), the peptide *AA* sequence (*Peptide*), the *AA* residue after the peptide (*Residue after*), miss cleavage, modification, and MOWSE score (*Score*) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score		
1	chr5.CM0357.530.nc	612.95	1223.90	1224.68	-0.79	2	216	226	R	AILTIVNPNDR	D	0	-	50.0		
		636.99	1271.97	1272.64	-0.67	2	329	339	K	ASQDQIQLSR	H	0	-	89.8		
		756.46	1510.91	1511.79	-0.89	2	498	510	R	DDNVISQIERPVK	E	0	-	71.8		
		679.00	1355.99	1356.75	-0.76	2	385	396	R	DLDILLSEAQIK	E	0	-	64.5		
		921.86	1841.71	1842.91	-1.19	2	313	328	R	EEQRGEQSQEGVIVK	A	1	-	63.4		
		866.44	1730.87	1731.89	-1.03	2	511	526	K	ELAFPGSAEIESLIK	N	0	-	70.6		
		551.91	1652.70	1653.75	-1.05	3	39	51	R	EQGEDERQPWQPR	R	1	-	29.8		
		851.41	1700.81	1701.64	-0.83	2	125	140	R	ESEEEEGSSSSSESSR	R	0	-	103.8		
		818.84	1635.67	1636.75	-1.08	2	155	167	R	FQTHFENEHCHVR	V	0	-	69.5		
		507.49	1012.97	1013.55	-0.59	2	420	428	R	GELELVAQR	R	0	-	57.5		
		650.95	1299.89	1300.66	-0.77	2	317	328	R	GEQSQEGVIVK	A	0	-	95.6		
		743.82	1485.62	1486.62	-0.99	2	434	445	R	GQEEEQEEEQPR	I	0	-	93.1		
		488.45	974.88	975.53	-0.65	2	372	379	K	LFEITPEK	N	0	-	58.2		
		598.47	1194.93	1195.60	-0.67	2	178	186	K	LFENLQNYR	I	0	-	82.6		
		1191.50	3571.48	3571.77	-0.29	3	261	291	K	LLIPINRPQGYQFFPSSSETQESYLNGFSR	N	0	-	47.5		
		920.36	1838.70	1839.86	-1.16	2	292	307	R	NILEASFNAGYDEIER	V	0	-	108.2		
		408.96	815.90	816.40	-0.50	2	146	151	R	NPFHFR	S	0	-	27.3		
		454.28	1359.82	1360.59	-0.76	3	99	109	R	QSEEEESDRPR	R	0	-	22.4		
		486.99	971.96	972.50	-0.55	2	145	151	R	RNPFHFR	S	1	-	35.7		
		415.44	828.87	829.42	-0.55	2	71	76	R	RPSWER	K	0	-	22.2		
		431.42	860.82	861.43	-0.61	2	353	359	K	SEPFNLR	S	0	-	37.2		
		705.91	1409.81	1410.73	-0.91	2	176	186	R	SKLFENLQNYR	I	1	-	58.8		
		473.96	945.91	946.51	-0.60	2	360	368	R	SSKPISSNK	F	0	-	58.9		
		2	chr5.LjT15N12.90.nc	424.45	846.88	847.42	-0.54	2	415	421	R	ADLYNPR	A	0	-	56.3
				722.94	1443.86	1444.77	-0.91	2	535	548	R	ATPAEVLNNAFGIR	Q	0	-	96.6
				833.76	1665.50	1666.56	-1.06	2	317	329	R	EEDEDEDEDEER	Q	0	-	64.4
				707.88	2120.62	2121.78	-1.17	3	317	334	R	EEDEDEDEDEERQGGGR	G	1	-	25.3
725.33	1448.65			1449.59	-0.94	2	366	376	R	EEEEEEESRR	T	1	-	35.2		
944.37	1886.73			1887.89	-1.15	2	557	573	K	FSGNWGPLVNPDTQSR	S	0	-	103.1		
736.31	2205.91			2206.19	-0.28	3	80	99	K	GLHLPSFTPSQLIMIVQGR	G	0	Oxidation (M)	40.7		
694.93	1387.84			1388.60	-0.76	2	342	351	R	HFEEEEEEER	E	1	-	52.5		
634.21	1899.60			1900.78	-1.18	3	362	375	K	HWQREEEEEEESR	R	1	-	23.7		
617.99	1233.97			1234.65	-0.68	2	405	414	K	IHENINRPSR	A	0	-	31.3		
534.97	1067.92			1068.56	-0.63	2	37	45	R	INVLEPDNR	V	0	-	74.1		
727.49	1452.96			1453.85	-0.89	2	425	437	R	ISDINSLTLPILR	F	0	-	126.2		
543.45	1084.89			1085.51	-0.62	2	257	265	K	QLQSPDDQR	R	0	-	71.7		
621.45	1240.89			1241.61	-0.72	2	257	266	K	QLQSPDDQRR	Q	1	-	22.6		
721.56	2162.66			2162.85	-1.19	3	313	329	R	RPSREDEDEDEDEER	Q	1	-	55.5		
456.40	910.78			911.38	-0.59	2	22	28	R	SFDWSDR	F	0	-	35.8		
1222.10	3663.28			3664.42	-1.14	3	271	302	K	VEGDDLSPISPEADEDEDEDEDEQEQHGR	H	0	-	98.0		
762.27	2283.77			2284.12	-0.35	3	187	206	R	VFYLAGNPAIEHPETQQSQR	Q	0	-	61.1		
3	chr5.LjT15N12.80.nc			424.45	846.88	847.42	-0.54	2	414	420	R	ADLYNPR	A	0	-	56.3
		714.50	1426.99	1427.79	-0.80	2	534	547	R	ATPAQVLNNAFGIR	Q	0	-	91.2		
		833.76	1665.50	1666.56	-1.06	2	317	329	R	EEDEDEDEDEER	Q	0	-	64.4		

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		725.33	1448.65	1449.59	-0.94	2	365	375	R	EEEEEEESRR	T	1	-	35.2
		951.84	1901.67	1901.90	-0.23	2	556	572	K	FSGNWGPLINPDNTQSR	S	0	-	130.3
		1103.92	2205.82	2206.19	-0.37	2	80	99	K	GLHLPSFTSPQLIMVIQGR	G	0	Oxidation (M)	39.1
		694.93	1387.84	1388.60	-0.76	2	341	350	R	HFEEEEEEER	E	1	-	52.5
		634.21	1899.60	1900.78	-1.18	3	361	374	K	HWQREEEEEEEESR	R	1	-	23.7
		617.99	1233.97	1234.65	-0.68	2	404	413	K	IHENINRPSR	A	0	-	31.3
		520.97	1039.92	1040.53	-0.61	2	37	45	R	INALEPDNR	V	0	-	71.7
		727.49	1452.96	1453.85	-0.89	2	424	436	R	ISDINSLTLPILR	F	0	-	126.2
		543.45	1084.89	1085.51	-0.62	2	257	265	K	QLQSPDDQR	R	0	-	71.7
		621.45	1240.89	1241.61	-0.72	2	257	266	K	QLQSPDDQRR	Q	1	-	22.6
		721.56	2161.66	2162.85	-1.19	3	313	329	R	RPSREDEDEDEDEER	Q	1	-	55.5
		1222.10	3663.28	3664.42	-1.14	3	271	302	K	VEGDDLSPISPEAEDDEDEDEDEDQEQR	H	0	-	98.0
		786.94	1571.87	1572.78	-0.91	2	46	59	R	VESEAGLIETWSPR	Q	0	-	91.9
4	chr1.CM0295.260.nd	629.96	1257.90	1258.62	-0.71	2	236	246	K	DEEQDKGAIVR	V	1	-	73.9
		494.97	987.93	988.55	-0.62	2	459	466	R	FNFLVPPR	E	0	-	58.1
		459.44	916.86	917.46	-0.61	2	408	414	K	FNYSISFK	T	0	-	39.0
		1017.91	2033.80	2034.94	-1.14	2	179	194	R	FYLSGNQNEFLQYQR	Q	0	-	108.1
		563.00	1123.98	1124.62	-0.64	2	249	259	K	GGLSVITPPR	Q	0	-	64.2
		597.93	1790.76	1791.70	-0.94	3	265	279	R	GSEEEEEEDDRPSR	H	0	-	47.0
		1126.90	2251.78	2252.05	-0.27	2	46	64	R	IESEAGFIETWNPTNNQFR	C	0	-	93.7
		843.60	2527.78	2528.33	-0.55	3	380	402	R	IPDGELEEGQLVLPQNFAIAAR	S	0	-	84.2
		1297.35	2592.69	2593.28	-0.59	2	424	447	K	LAGAASAFEAQMPLEVIQNSFNLR	D	0	Oxidation (M)	92.8
		520.45	1038.89	1039.58	-0.69	2	37	45	R	LNALKPDNR	I	0	-	85.9
		594.92	1187.83	1188.56	-0.73	2	232	241	K	LQKDEEQDK	G	1	-	40.4
		541.94	1081.86	1082.55	-0.69	2	336	345	K	LSAHEGSINR	N	0	-	83.2
		763.58	2287.71	2288.17	-0.47	3	346	365	R	NAMVVPVPHYNANSIYALR	G	0	Oxidation (M)	113.5
		809.37	1616.72	1617.72	-0.99	2	24	36	R	QQSQQQNECQLR	L	0	-	74.2
		650.22	1947.64	1947.80	-0.17	3	264	279	R	RGSEEEEEEDDRPSR	H	1	-	68.5
		712.87	1423.73	1424.63	-0.91	2	307	319	K	SSSPDFYNPQAGR	I	0	-	75.3
		718.39	1434.76	1435.70	-0.93	2	403	414	R	STSDKFNYSISFK	T	1	-	83.6
		565.39	1128.76	1129.50	-0.75	2	415	423	K	THEMPWMAK	L	0	-	52.0
		581.38	1160.74	1161.49	-0.75	2	415	423	K	THEMPWMAK	L	0	2 Oxidation (M)	24.6
		573.39	1144.76	1145.50	-0.74	2	415	423	K	THEMPWMAK	L	0	Oxidation (M)	31.6</

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		955.86	1909.71	1910.90	-1.19	2	292	307	R	NILEASFNAEYNEIER	V	0	-	105.5
		421.93	841.85	842.41	-0.56	2	144	149	R	NPFFFR	S	0	-	45.5
		699.38	1396.74	1396.66	0.08	2	529	540	R	NSHFANAQPQQR	E	0	-	97.8
		457.47	912.93	913.52	-0.60	2	317	324	R	QEQLIVK	V	0	-	37.2
		514.91	1027.81	1028.49	-0.68	2	85	92	R	RLEDPDER	E	1	-	43.5
		499.93	997.85	998.51	-0.66	2	143	149	R	RNPFFFR	S	1	-	35.3
		705.91	1409.81	1410.73	-0.91	2	176	186	R	SKLFENLQNYR	I	1	-	58.8
		706.40	1410.79	1411.67	-0.88	2	356	367	R	SRDPIYSNEFGK	H	1	-	75.5
		593.46	1184.91	1185.67	-0.77	2	405	415	R	STVILVVNEGR	G	0	-	68.7
		638.46	1274.90	1275.61	-0.71	2	345	355	R	TSSEPEPFNLR	S	0	-	64.2
6	LjSGA_030216.1	629.96	1257.90	1258.62	-0.71	2	59	69	R	DEEQDKGAIVR	V	1	-	73.9
		494.97	987.93	988.55	-0.62	2	282	289	R	FNFLVPPR	E	0	-	58.1
		444.43	886.84	887.45	-0.62	2	231	237	K	FNYYAFK	T	0	-	40.0
		1024.92	2047.83	2048.96	-1.13	2	2	17	R	FYLSGNQEQLFYQQR	Q	0	-	104.9
		563.00	1123.98	1124.62	-0.64	2	72	82	K	GGLSVITPPER	Q	0	-	64.2
		1023.84	3068.50	3069.41	-0.91	3	22	49	R	GREENQGGNIFSGFGGEFLEDALNIDR	N	1	-	82.2
		597.93	1790.76	1791.70	-0.94	3	88	102	R	GSEEEDEEDRPSR	H	0	-	47.0
		877.58	2629.71	2630.34	-0.63	3	247	270	K	LAGATSEIQAMPLEVIQNAFNLER	E	0	Oxidation (M)	71.5
		541.94	1081.86	1082.55	-0.69	2	159	168	K	LSAEHGSILNR	N	0	-	83.2
		763.58	2287.71	2288.17	-0.47	3	169	188	R	NAMVVVPHYNLNANSIIYALR	G	0	Oxidation (M)	113.5
		650.22	1947.64	1947.80	-0.17	3	87	102	R	RGSEEEDEEDRPSR	H	1	-	68.5
		726.38	1450.75	1451.68	-0.92	2	226	237	R	SMSDKFNYYAFK	T	1	Oxidation (M)	54.3
		687.84	1373.66	1374.65	-0.99	2	130	142	K	SSSPDIFNPQAGR	I	0	-	73.8
		597.97	1193.92	1194.60	-0.68	2	145	155	K	TATGDFDFPALR	F	0	-	80.4
		512.41	1022.81	1023.44	-0.63	2	238	246	K	TNDMPTMAK	L	0	Oxidation (M)	35.2
		676.47	1350.93	1351.78	-0.85	2	70	82	R	VKGGLSVITPPER	Q	1	-	66.2
7	LjSGA_133863.1	475.44	948.86	949.43	-0.57	2	87	95	R	ASEMQQATR	E	0	-	48.7
		483.44	964.87	965.42	-0.55	2	87	95	R	ASEMQQATR	E	0	Oxidation (M)	23.9
		566.48	1130.95	1131.59	-0.64	2	30	40	K	DKTAQTAQAAK	E	1	-	66.7
		707.42	1412.82	1413.66	-0.84	2	63	75	K	DKTQQAHAHSTGDR	T	1	-	89.4
		560.45	1118.89	1119.52	-0.63	2	118	128	K	DMAQGATEAVK	S	0	-	49.8
		568.42	1134.83	1135.52	-0.69	2	118	128	K	DMAQGATEAVK	S	0	Oxidation (M)	50.0
		862.42	1722.82	1723.81	-0.99	2	141	155	K	EHVTTTTTTTQDPR	N	0	-	70.8
		1034.86	2067.70	2068.88	-1.18	2	96	115	R	ESAQAGNDNTGGFMQQTGEK	V	0	-	108.4
		1043.32	2084.63	2084.87	-0.24	2	96	115	R	ESAQAGNDNTGGFMQQTGEK	V	0	Oxidation (M)	107.4
		589.44	1176.87	1177.52	-0.66	2	14	24	K	GNQMMGNIGEK	A	0	-	55.3
		605.41	1208.81	1209.51	-0.70	2	14	24	K	GNQMMGNIGEK	A	0	2 Oxidation (M)	75.3
		597.40	1192.79	1193.52	-0.73	2	14	24	K	GNQMMGNIGEK	A	0	Oxidation (M)	54.4
		410.95	819.89	820.41	-0.52	2	129	136	K	STLGMQKQK	D	0	-	36.2
		655.42	1308.83	1309.62	-0.79	2	129	140	K	STLGMQKQKDETK	E	1	Oxidation (M)	60.5
		673.97	1345.93	1346.69	-0.76	2	116	128	K	VKDMAQGATEAVK	S	1	-	78.6
		681.96	1361.91	1362.68	-0.78	2	116	128	K	VKDMAQGATEAVK	S	1	Oxidation (M)	87.2
8	LjSGA_052214.1	817.41	1632.81	1633.87	-1.05	2	238	253	K	AATNVLGLTAAYVGQK	G	0	-	79.6
		460.00	917.99	917.42	0.57	2	13	19	K	AREEEER	S	1	-	25.1
		494.45	986.89	987.52	-0.63	2	208	216	K	DIAADLKDK	A	1	-	43.0
		723.96	1445.90	1446.70	-0.80	2	111	124	K	GQPGYVATETAPEK	N	0	-	63.5
		708.98	1415.94	1416.72	-0.78	2	83	96	K	GQPGYVATVTAPEK	N	0	-	74.5
		739.44	1476.87	1477.70	-0.84	2	139	152	K	GQPGYVATETAPEK	N	0	-	97.7
		474.95	947.89	948.50	-0.61	2	199	207	K	GQGGYVVAK	D	0	-	28.1
		524.48	1046.95	1047.52	-0.57	2	267	277	K	NLASSAGETAK	E	0	-	64.6
		579.45	1156.88	1157.58	-0.70	2	320	330	K	SAAAAQNLEQR	E	0	-	91.1

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		473.99	945.96	946.51	-0.54	2	20	27	R	SRLEEVSK	Y	1	-	40.4
9	LjT46P06.60.nd	837.40	1672.78	1673.79	-1.01	2	75	89	R	ETHELGAQFESIADK	V	0	-	79.0
		566.62	1696.84	1697.87	-1.04	3	125	140	K	FELKPEGNAGLVGPDR	T	0	-	67.3
		475.96	949.91	950.48	-0.57	2	297	305	K	GQQGYVATK	D	0	-	40.7
		578.42	1154.83	1155.52	-0.70	2	328	338	K	GYTAQAAMAK	S	0	Oxidation (M)	41.7
		471.97	941.93	942.51	-0.58	2	671	679	K	IIVAGEGER	E	0	-	46.4
		881.92	1761.82	1762.88	-1.07	2	339	356	K	SAGGTTVQFVGENAVQAK	D	0	-	73.1
		594.93	1187.85	1188.57	-0.72	2	246	256	K	SNDVISAAQER	Y	0	-	57.8
		484.45	966.89	967.49	-0.59	2	230	237	K	SVLEELSK	Y	0	-	42.8
		625.46	1248.91	1249.62	-0.71	2	314	325	K	TAAEYTAAPVAEK	A	0	-	60.7
		588.45	1174.89	1175.60	-0.71	2	153	163	R	VITGGTEDKEK	N	1	-	63.0
		1087.94	3260.81	3261.65	-0.84	3	640	670	K	VQEHGQVQQGEGGVLDIAIGETIVEIAQTTK	I	0	-	108.0
10	chr2.LjT30P12.40.nc	513.43	1024.84	1025.51	-0.68	2	172	180	K	EVGHDIQTK	A	0	-	49.4
		616.44	1230.87	1231.64	-0.77	2	146	156	R	GIVPEQLDYAK	N	0	-	50.1
		614.38	1226.75	1227.53	-0.78	2	159	169	R	MADMADYVGQK	T	0	-	55.1
		630.38	1258.74	1259.52	-0.78	2	159	169	R	MADMADYVGQK	T	0	2 Oxidation (M)	51.4
		622.39	1242.76	1243.52	-0.76	2	159	169	R	MADMADYVGQK	T	0	Oxidation (M)	51.6
		584.95	1167.88	1168.62	-0.74	2	186	195	K	RTPITTHDTK	-	1	-	42.7
		506.93	1011.85	1012.52	-0.67	2	187	195	R	TPITTHDTK	-	0	-	64.3
		803.85	1605.68	1606.75	-1.06	2	29	42	R	YEAGGINFNNQPQR	Y	0	-	93.4
		594.93	1187.85	1188.55	-0.70	2	18	28	R	YETGGANPPQR	Y	0	-	69.2
		743.89	1485.77	1486.68	-0.92	2	43	57	R	YGGGGGFSLLPPER	G	0	-	81.9
11	LjT03L06.120.nd	438.96	875.90	876.48	-0.58	2	125	132	K	ARGDALFK	A	1	-	29.5
		1021.37	2040.73	2041.03	-0.30	2	21	41	K	AVDAIQSVETVEGNGPGTIK	K	0	-	124.2
		450.45	898.88	899.46	-0.58	2	13	20	K	DAEILPK	A	0	-	51.9
		578.91	1155.80	1156.54	-0.73	2	111	121	K	GNAEPNEAEVK	E	0	-	54.5
		1000.22	2997.65	2998.44	-0.79	3	58	84	K	IEAIDEANLVYNSLVGSSEFPENVEK	I	0	-	75.1
		557.41	1112.80	1112.58	0.22	2	91	102	K	LVDGPNNGSIGK	L	0	-	94.3
		418.95	835.89	836.44	-0.55	2	51	57	K	SNYVLNK	I	0	-	32.0
12	chr4.CM0126.1570.nc	733.87	1465.72	1466.61	-0.89	2	202	213	K	DDENVNSQPFMR	W	0	Oxidation (M)	46.5
		510.98	1019.94	1020.52	-0.59	2	33	41	K	DTDILAAFR	V	0	-	57.1
		415.47	828.93	829.43	-0.50	2	440	446	R	EGNEIIR	E	0	-	32.2
		638.00	1273.98	1274.72	-0.74	2	340	350	R	EITLGFVDLLR	D	0	-	71.3
		696.92	1391.82	1392.64	-0.83	2	22	32	K	LTYTTPDYETK	D	0	-	51.1
		732.98	1463.94	1464.75	-0.81	2	147	159	K	TFQGPPHGIQVER	D	0	-	100.0
12	LjSGA_084876.1	733.87	1465.72	1466.61	-0.89	2	65	76	K	DDENVNSQPFMR	W	0	Oxidation (M)	46.5
		415.47	828.93	829.43	-0.50	2	303	309	R	EGNEIIR	E	0	-	32.2
		638.00	1273.98	1274.72	-0.74	2	203	213	R	EITLGFVDLLR	D	0	-	71.3
		732.98	1463.94	1464.75	-0.81	2	10	22	K	TFQGPPHGIQVER	D	0	-	100.0
12	LjSGA_124257.1	733.87	1465.72	1466.61	-0.89	2	138	149	K	DDENVNSQPFMR	W	0	Oxidation (M)	46.5
		638.00	1273.98	1274.72	-0.74	2	276	286	R	EITLGFVDLLR	D	0	-	71.3
		732.98	1463.94	1464.75	-0.81	2	83	95	K	TFQGPPHGIQVER	D	0	-	100.0
12	LjSGA_141109.1	733.87	1465.72	1466.61	-0.89	2	196	207	K	DDENVNSQPFMR	W	0	Oxidation (M)	46.5
		510.98	1019.94	1020.52	-0.59	2	27	35	K	DTDILAAFR	V	0	-	57.1
		696.92	1391.82	1392.64	-0.83	2	16	26	K	LTYTTPDYETK	D	0	-	51.1
		732.98	1463.94	1464.75	-0.81	2	141	153	K	TFQGPPHGIQVER	D	0	-	100.0
12	LjSGA_116237.1	733.87	1465.72	1466.61	-0.89	2	190	201	K	DDENVNSQPFMR	W	0	Oxidation (M)	46.5

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		510.98	1019.94	1020.52	-0.59	2	21	29	K	DTDILAAFR	V	0	-	57.1
		696.92	1391.82	1392.64	-0.83	2	10	20	K	LTYTTPDYETK	D	0	-	51.1
		732.98	1463.94	1464.75	-0.81	2	135	147	K	TFQGPPIHGIQVER	D	0	-	100.0
12	LjSGA_138404.1	510.98	1019.94	1020.52	-0.59	2	33	41	K	DTDILAAFR	V	0	-	57.1
		696.92	1391.82	1392.64	-0.83	2	22	32	K	LTYTTPDYETK	D	0	-	51.1
		732.98	1463.94	1464.75	-0.81	2	147	159	K	TFQGPPIHGIQVER	D	0	-	100.0
12	LjSGA_105267.1	415.47	828.93	829.43	-0.50	2	170	176	R	EGNEIIR	E	0	-	32.2
		638.00	1273.98	1274.72	-0.74	2	70	80	R	EITLGFVDLLR	D	0	-	71.3
12	LjSGA_134471.1	415.47	828.93	829.43	-0.50	2	166	172	R	EGNEIIR	E	0	-	32.2
		638.00	1273.98	1274.72	-0.74	2	66	76	R	EITLGFVDLLR	D	0	-	71.3
12	LjSGA_149364.1	638.00	1273.98	1274.72	-0.74	2	69	79	R	EITLGFVDLLR	D	0	-	71.3
12	LjSGA_113307.1	638.00	1273.98	1274.72	-0.74	2	62	72	R	EITLGFVDLLR	D	0	-	71.3
12	chr3.CM0106.360.nd	696.92	1391.82	1392.64	-0.83	2	22	32	K	LTYTTPDYETK	D	0	-	51.1
12	LjSGA_096321.1	696.92	1391.82	1392.64	-0.83	2	22	32	K	LTYTTPDYETK	E	0	-	51.1
12	LjSGA_102132.1	510.98	1019.94	1020.52	-0.59	2	23	31	K	DTDILAAFR	V	0	-	57.1
12	LjSGA_136714.1	733.87	1465.72	1466.61	-0.89	2	194	205	K	DDENVNSQPFMR	W	0	Oxidation (M)	46.5
		732.98	1463.94	1464.75	-0.81	2	139	151	K	TFQGPPIHGIQVER	D	0	-	100.0
13	chr5.CM0357.340.nc	793.89	1585.77	1586.79	-1.02	2	215	230	K	AATLQDAEGVASAEVR	N	0	-	111.5
		751.92	1501.83	1502.78	-0.95	2	129	143	R	ESAITIGEALAEATAK	T	0	-	70.1
		495.92	989.83	990.46	-0.63	2	78	86	R	EVTDTVIGDR	G	0	-	68.1
		626.45	1250.88	1251.66	-0.78	2	87	98	R	GVTVTETHVPGR	R	0	-	60.9
		529.98	1057.94	1058.60	-0.66	2	199	209	K	LADVLTGATAK	L	0	-	79.5
		540.45	1078.88	1079.55	-0.67	2	68	77	R	NEQAGLVGHR	E	0	-	65.9
		617.60	1849.77	1850.92	-1.16	3	231	251	R	NNPEAGATPGGVAASVAAAAAR	L	0	-	101.1
		569.96	1137.90	1138.61	-0.71	2	8	17	R	RTQPGQDPIK	Y	1	-	54.2
		743.88	742.87	743.36	-0.48	1	2	7	M	SQEQPR	R	0	-	34.5
		491.96	981.90	982.51	-0.61	2	9	17	R	TQPGQDPIK	Y	0	-	29.5
		719.30	2154.88	2156.07	-1.19	3	144	164	K	TVGDKPVDQSDASAIQAAAEVR	A	0	-	67.2
		641.27	1920.79	1921.98	-1.19	3	48	67	R	VLGHTQPGGAAAVMQSAATR	N	0	-	64.0
14	chr6.CM0114.310.nc	537.46	1072.91	1073.50	-0.59	2	136	144	R	AKDYAYDTK	E	1	-	56.7
		619.44	1236.87	1237.56	-0.69	2	74	84	R	AKETMSEGVDR	A	1	Oxidation (M)	61.2
		460.95	919.89	920.40	-0.51	2	109	117	K	DVAGSMADR	A	0	-	37.1
		503.45	1004.88	1005.44	-0.56	2	160	168	R	EGAEWTAADK	T	0	-	47.7
		510.45	1018.89	1019.46	-0.57	2	171	179	R	EGAEWTAEEK	T	0	-	68.2
		605.43	1208.85	1209.53	-0.67	2	54	64	R	GTQAYDPTDSR	R	0	-	81.3
		683.44	1364.87	1365.63	-0.75	2	54	65	R	GTQAYDPTDSRR	D	1	-	32.8
		631.97	1261.92	1262.64	-0.72	2	180	192	K	TGEVAGSATETLK	G	0	-	96.4
		575.46	1148.90	1149.54	-0.64	2	107	117	K	TKDVAGSMADR	A	1	-	43.8
		583.46	1164.90	1165.54	-0.64	2	107	117	K	TKDVAGSMADR	A	1	Oxidation (M)	35.4
15	chr1.CM0544.400.nd	746.96	1491.91	1492.74	-0.84	2	50	62	R	DATTGLHWTNLHK	R	0	-	65.1
		689.07	1376.12	1376.85	-0.73	2	38	49	K	SKPNLLVLPLQR	D	0	-	56.7
16	LjSGA_015149.2	705.40	1408.79	1409.70	-0.91	2	178	190	R	AVGYLGDKTEETK	Q	1	-	53.4
		437.43	872.85	873.42	-0.56	2	22	28	K	DLEEVNR	A	0	-	31.2

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		945.48	1888.94	1889.98	-1.04	2	41	58	R	GVIGSVLQAVQNTYENAK	G	0	-	108.6
		601.98	1201.94	1202.63	-0.69	2	313	323	K	SIVPFGDNNIK	S	0	-	25.8
		587.39	1172.76	1173.51	-0.75	2	104	114	K	SYDTSSATTNK	A	0	-	77.8
		572.89	1143.76	1144.50	-0.74	2	142	152	K	TGEYAGYAGEK	A	0	-	63.4
		604.90	1207.78	1208.57	-0.79	2	119	130	K	VGGESTDFAAQK	A	0	-	68.3
17	chr5.LjT43D06.110.nd	845.94	1689.86	1690.81	-0.95	2	236	250	K	EVSVGFSATTWNTHR	E	0	-	74.9
		739.93	1477.85	1478.73	-0.88	2	48	61	K	FTDDGSLILQGDAK	I	0	-	96.2
		894.43	1786.86	1787.89	-1.04	2	172	187	R	HIGIDVNSVMSMNLVK	W	0	2 Oxidation (M)	56.4
		450.98	899.95	900.49	-0.54	2	141	148	K	NLGILDEK	N	0	-	34.2
		831.66	2491.96	2492.36	-0.40	3	208	230	K	TLSVVVVTHQNGQITTTVAQQIDLK	V	0	-	84.9
18	LjSGA_034221.1	566.97	1131.92	1132.56	-0.64	2	132	142	R	AGEVVESVESK	A	0	-	81.4
		703.44	1404.86	1405.63	-0.77	2	143	155	K	AQEMAQAQSEAR	D	0	Oxidation (M)	104.4
		602.95	1203.89	1204.60	-0.71	2	169	179	R	KTGLDVQSDSR	E	1	-	76.7
		547.32	1638.94	1639.87	-0.93	3	117	131	R	LKPPLQAAETMAQR	A	0	Oxidation (M)	60.7
		538.96	1075.90	1076.51	-0.61	2	170	179	K	TGLDVQSDSR	E	0	-	68.4
19	LjSGA_091288.1	960.35	1918.69	1919.85	-1.16	2	222	239	K	EGGVNMFGGFDSAFLSR	V	0	Oxidation (M)	93.6
		838.94	1675.86	1676.96	-1.10	2	267	281	K	GGLSIIRPPLEQIR	E	0	-	43.7
		465.97	929.92	930.54	-0.62	2	243	250	K	VKEDLISK	L	1	-	52.7
20	chr5.LjT43D06.20.nd	560.49	1118.97	1119.62	-0.64	2	189	198	K	AIIIDYSPTK	T	0	-	75.8
		739.93	1477.85	1478.73	-0.88	2	39	52	K	FTDDGSLILQGDAK	I	0	-	96.2
		894.43	1786.86	1787.89	-1.04	2	163	178	R	HIGIDVNSVMSMNLVK	W	0	2 Oxidation (M)	56.4
		562.02	1122.03	1122.66	-0.64	2	59	69	R	LALPSDPLIGK	T	0	-	58.0
		450.98	899.95	900.49	-0.54	2	132	139	K	NLGILDEK	N	0	-	34.2
21	chr1.LjT38A19.110.nc	516.43	1030.85	1031.52	-0.68	2	13	23	K	ETAANIGASAK	S	0	-	81.4
		799.81	1597.61	1598.70	-1.09	2	126	142	R	VGGNPNATGYGTGTYN	-	0	-	68.1
		444.95	887.88	888.46	-0.57	2	59	66	K	VSQAELDK	L	0	-	48.0
		457.45	912.90	913.49	-0.59	2	40	48	K	VTAGDPVQK	E	0	-	49.0
21	chr5.LjT10N02.50.nd	516.43	1030.85	1031.52	-0.68	2	13	23	K	ETAANIGASAK	S	0	-	81.4
22	LjSGA_145133.1	636.87	1271.73	1272.55	-0.82	2	14	25	K	EASSYASDTSQK	T	0	-	66.9
		912.86	1823.70	1824.87	-1.18	2	28	44	K	EKLQEVASGASEYSAEK	A	1	-	109.3
		476.42	950.82	951.43	-0.61	2	3	11	K	EYAGDAAQK	I	0	-	47.6
		757.39	1512.76	1513.73	-0.97	2	12	25	K	IKEASSYASDTSQK	T	1	-	64.5
		784.37	1566.73	1567.74	-1.00	2	30	44	K	LQEVASGASEYSAEK	A	0	-	67.8
		583.91	1165.81	1166.56	-0.75	2	1	11	-	SKEYAGDAAQK	I	1	-	67.2
23	chr3.LjT02L14.180.nd	673.47	1344.93	1344.73	0.20	2	242	253	K	EGVESTIWLLAK	A	0	-	56.1
		852.51	1703.01	1704.04	-1.04	2	70	85	K	LPLDVISTISPLPVIK	E	0	-	100.1
		679.40	1356.79	1357.56	-0.77	2	109	119	K	SAWMTDEEFAR	E	0	Oxidation (M)	60.9
23	LjT30L14.20.nd	673.47	1344.93	1344.73	0.20	2	475	486	K	EGVESTIWLLAK	A	0	-	56.1
		852.51	1703.01	1704.04	-1.04	2	303	318	K	LPLDVISTISPLPVIK	E	0	-	100.1
		679.40	1356.79	1357.56	-0.77	2	342	352	K	SAWMTDEEFAR	E	0	Oxidation (M)	60.9
23	chr3.CM0115.370.nc	679.40	1356.79	1357.56	-0.77	2	292	302	K	SAWMTDEEFAR	E	0	Oxidation (M)	60.9
23	LjSGA_052903.1	679.40	1356.79	1357.56	-0.77	2	223	233	K	SAWMTDEEFAR	E	0	Oxidation (M)	60.9
24	chr3.CM0246.60.nd	533.98	1065.95	1066.55	-0.59	2	340	348	R	AMEYGIVLR	G	0	Oxidation (M)	43.9
		532.98	1063.94	1064.53	-0.59	2	370	378	K	EGDVFFVPR	Y	0	-	65.9

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		973.94	1945.86	1946.93	-1.07	2	444	461	R	EYVIVPSTWAAPGDEGEK	E	0	-	53.2
		708.39	1414.77	1415.64	-0.87	2	108	119	K	LGFMYGDELSER	R	0	-	51.2
		716.39	1430.76	1431.63	-0.87	2	108	119	K	LGFMYGDELSER	R	0	Oxidation (M)	61.5
		724.44	1446.87	1447.72	-0.85	2	74	85	R	LMHIGFITMEPK	S	0	2 Oxidation (M)	31.3
		716.43	1430.86	1431.73	-0.87	2	74	85	R	LMHIGFITMEPK	S	0	Oxidation (M)	35.8
		779.03	1556.05	1556.90	-0.86	2	404	417	K	NKPQFLVGSVSLLR	T	0	-	62.0
		422.01	842.01	842.47	-0.47	2	437	443	R	RVVDAQR	E	1	-	41.6
		751.45	1500.89	1501.72	-0.83	2	389	402	R	SGPLEFFGFST SAR	K	0	-	56.6
		756.45	1510.88	1511.71	-0.83	2	418	431	R	TMMGPELAATFGVR	E	0	2 Oxidation (M)	67.4
25	LjSGA_025401.2	608.38	1214.75	1215.54	-0.79	2	196	206	K	AGEYTNAAEK	A	0	-	74.9
		601.37	1200.72	1201.53	-0.80	2	218	228	K	AGEYTNAGEK	A	0	-	65.0
		689.88	1377.75	1378.65	-0.90	2	30	41	R	ANERDEGFS LNK	E	1	-	59.1
		533.95	1065.88	1066.58	-0.70	2	97	106	K	AVQDTVVHAK	D	0	-	53.5
		515.94	1029.86	1030.57	-0.71	2	289	299	K	DATVGT LGLK	D	0	-	55.9
		532.41	1062.81	1063.50	-0.69	2	256	266	K	DATVNMA GAAK	D	0	Oxidation (M)	50.2
		430.43	858.85	859.40	-0.55	2	60	66	K	DLEDVNR	A	0	-	39.3
		645.37	1288.73	1289.56	-0.83	2	130	140	K	MGEYTDYGVQK	A	0	-	48.6
		653.35	1304.69	1305.55	-0.86	2	130	140	K	MGEYTDYGVQK	A	0	Oxidation (M)	55.8
		463.41	924.81	925.41	-0.60	2	113	120	K	SYETGDVR	G	0	-	42.0
		616.37	1230.72	1231.54	-0.82	2	152	162	K	TGEYADYASQK	A	0	-	59.6
		616.93	1231.84	1232.52	-0.68	2	174	184	K	TGEYTDYAADK	A	0	-	43.5
26	chr3.LjT02L14.10.nd	739.42	1476.82	1477.66	-0.84	2	650	661	K	DYVSLYPPSDEK	L	0	-	42.2
		673.46	1344.91	1345.69	-0.78	2	495	506	K	EGVESSQWLLAK	A	0	-	70.4
		664.46	1326.91	1327.69	-0.79	2	371	382	R	EMLAGVNPVIR	C	0	Oxidation (M)	63.5
		644.91	1287.80	1288.60	-0.80	2	779	789	R	HASDELYLGER	D	0	-	38.9
		639.47	1276.92	1277.65	-0.73	2	740	750	K	KGTPEYDELVK	S	1	-	46.5
		765.94	1529.87	1530.75	-0.88	2	662	673	K	LQQDSELQAWWK	E	0	-	56.9
		679.40	1356.79	1357.56	-0.77	2	360	370	K	SAWMTDEEFAR	E	0	Oxidation (M)	60.9
		564.50	1126.99	1127.59	-0.59	2	272	281	K	SSDFLVVGLK	S	0	-	55.5
26	chr3.CM0115.330.nc	644.91	1287.80	1288.60	-0.80	2	788	798	R	HASDELYLGER	D	0	-	38.9
		679.40	1356.79	1357.56	-0.77	2	368	378	K	SAWMTDEEFAR	E	0	Oxidation (M)	60.9
27	chr1.CM0544.500.nd	791.89	1581.77	1582.78	-1.01	2	175	189	K	EGSSIINTTSVNAYK	G	0	-	78.1
		658.43	1314.84	1315.68	-0.83	2	190	201	K	GHPTLLDYTATK	G	0	-	51.1
		472.50	942.98	943.57	-0.59	2	210	218	R	GLSLQLVSK	G	0	-	40.6
		614.95	1227.88	1228.68	-0.80	2	44	56	K	IALITGGDSGIGR	A	0	-	71.5
		982.43	1962.84	1963.09	-0.25	2	222	240	R	VNGVAPGPIWTP LIPASFK	E	0	-	54.0
		596.42	1190.83	1191.59	-0.76	2	116	126	R	VVDEAVNAYGR	I	0	-	66.4
27	LjSGA_029600.1	791.89	1581.77	1582.78	-1.01	2	19	33	K	EGSSIINTTSVNAYK	G	0	-	78.1
		658.43	1314.84	1315.68	-0.83	2	34	45	K	GHPTLLDYTATK	G	0	-	51.1
		472.50	942.98	943.57	-0.59	2	54	62	R	GLSLQLVSK	G	0	-	40.6
27	LjSGA_014692.1	614.95	1227.88	1228.68	-0.80	2	169	181	K	IALITGGDSGIGR	A	0	-	71.5
		596.42	1190.83	1191.59	-0.76	2	241	251	R	VVDEAVNAYGR	I	0	-	66.4
28	chr1.CM0032.460.nc	741.04	1480.06	1480.90	-0.84	2	88	102	R	ASITPGTVLILLAGR	F	0	-	95.0
		735.03	1468.04	1468.87	-0.83	2	113	126	R	QLPSGLLVTPGPK	I	0	-	90.0
		885.99	1769.97	1770.96	-0.99	2	198	214	K	TVDSALLTAIESVPDLK	S	0	-	68.6
29	LjSGA_092567.1	530.94	1059.86	1060.54	-0.68	2	102	111	K	AAIKEESEGK	L	1	-	62.2
		717.41	1432.80	1433.75	-0.95	2	43	57	R	AASFNIIPSSTGA AK	A	0	-	33.5

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		1016.48	2030.94	2031.12	-0.18	2	10	28	R	FGIVKGLMTTVHSITATQK	T	1	-	69.6
		749.44	1496.86	1497.84	-0.98	2	77	90	R	VPTVDVSVVDLTVR	L	0	-	94.8
29	LjSGA_086307.1	717.41	1432.80	1433.75	-0.95	2	72	86	R	AASFNIIPSSTGAAK	A	0	-	33.5
		749.44	1496.86	1497.84	-0.98	2	106	119	R	VPTVDVSVVDLTVR	L	0	-	94.8
29	LjT29P04.130.nd	749.44	1496.86	1497.84	-0.98	2	238	251	R	VPTVDVSVVDLTVR	I	0	-	94.8
30	chr3.CM0110.130.nc	484.44	966.87	967.47	-0.60	2	143	150	R	DVDNQIHK	A	0	-	28.5
		519.92	1037.83	1038.51	-0.68	2	143	151	R	DVDNQIHK	-	1	-	29.7
		876.91	1751.80	1752.88	-1.09	2	20	33	K	FYNLFTQLHDVQK	H	0	-	55.5
		552.41	1102.82	1103.54	-0.72	2	56	64	K	HWTYVVDGK	V	0	-	58.3
		704.54	2110.93	2110.93	-0.34	3	123	139	K	LHEDIIPPNGYMEYFNK	L	0	Oxidation (M)	38.1
		429.49	856.97	857.52	-0.55	2	7	14	K	LITEVGVK	T	0	-	54.0
		522.93	1043.84	1044.51	-0.67	2	72	80	R	VEAIDEQNK	T	0	-	58.8
		710.40	1418.78	1419.69	-0.91	2	43	55	K	VHEGDWHGIGSVK	H	0	-	50.3
		484.43	966.85	967.47	-0.62	2	116	122	R	WTIEYEK	L	0	-	22.0
		762.88	1523.75	1524.72	-0.98	2	84	96	K	YTLFGGDIDPHYK	N	0	-	59.1
30	chr3.CM0110.30.nc	710.40	1418.78	1419.69	-0.91	2	43	55	K	VHEGDWHGIGSVK	Q	0	-	50.3
31	LjSGA_014613.2	518.44	1034.86	1035.56	-0.70	2	5	14	K	FAVGTETIAK	K	0	-	73.0
		786.88	1571.75	1572.84	-1.08	2	23	39	K	GVTTIIGGDSVAAVEK	V	0	-	78.6
31	LjSGA_047542.1	786.88	1571.75	1572.84	-1.08	2	50	66	K	GVTTIIGGDSVAAVEK	V	0	-	78.6
32	chr2.LjT43N03.40.nd	481.47	960.92	961.53	-0.62	2	155	162	R	IIGFDNKR	Q	1	-	64.6
		539.96	1077.91	1078.59	-0.68	2	146	154	K	KAYPNAFIR	I	1	-	36.9
		761.91	1521.80	1522.77	-0.97	2	126	139	K	LPMFGTTDASQVLK	E	0	Oxidation (M)	81.6
		457.42	912.82	913.39	-0.58	2	112	119	K	SPGYDGR	Y	0	-	60.4
32	chr1.LjT23D08.110.nc	457.42	912.82	913.39	-0.58	2	116	123	K	SPGYDGR	Y	0	-	60.4
32	chr1.LjT23D08.120.nc	457.42	912.82	913.39	-0.58	2	117	124	K	SPGYDGR	Y	0	-	60.4
32	LjSGA_030971.1	457.42	912.82	913.39	-0.58	2	56	63	K	SPGYDGR	Y	0	-	60.4
32	LjSGA_080821.1	457.42	912.82	913.39	-0.58	2	56	63	K	SPGYDGR	Y	0	-	60.4
33	chr5.CM0260.650.nd	572.50	1142.99	1143.63	-0.64	2	102	111	K	IFGSFVSFLK	S	0	-	66.9
		472.52	943.03	943.56	-0.53	2	26	33	R	VLLTLEEK	K	0	-	46.1
		557.02	1112.02	1112.64	-0.63	2	146	156	R	VTAVDLSLAPK	L	0	-	76.9
		952.45	1902.88	1903.96	-1.08	2	84	101	K	YPEPSLVTPPEFASVGSK	I	0	-	81.3
34	chr1.CM0248.160.nc	600.00	1197.99	1198.66	-0.66	2	84	94	K	ALEQLQDAIAK	S	0	-	57.6
		814.00	1625.98	1626.88	-0.90	2	181	195	K	LVVETTANQDPLVTK	G	0	-	98.3
35	LjSGA_082478.1	812.43	1622.84	1623.86	-1.02	2	80	95	K	IIGATNPAQSEPGTIR	G	0	-	78.8
		876.44	1750.86	1751.95	-1.09	2	79	95	R	KIIGATNPAQSEPGTIR	G	1	-	59.4
		611.94	1221.87	1222.64	-0.77	2	30	40	K	LLTVESFAEK	H	0	-	59.8
36	LjSGA_031559.1	484.93	967.85	968.46	-0.61	2	90	97	K	FADENFVK	K	0	-	46.2
		812.46	1622.90	1623.90	-0.99	2	133	147	K	HVVFQQVVEGLDVVK	N	0	-	78.1
		755.89	1509.77	1510.72	-0.95	2	6	19	K	VFFDMTIGGQPAGR	I	0	Oxidation (M)	62.7
36	chr1.CM0231.140.nd	812.46	1622.90	1623.90	-0.99	2	133	147	K	HVVFQQVVEGLDVVK	E	0	-	78.1
		755.89	1509.77	1510.72	-0.95	2	6	19	K	VFFDMTIGGQPAGR	I	0	Oxidation (M)	62.7

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
36	LjSGA_090105.1	484.93	967.85	968.46	-0.61	2	90	97	K	FADENFVK	K	0	-	46.2
37	chr1.CM0133.420.nc	621.27	1860.80	1861.85	-1.05	3	46	62	K	AMANTHADIIDSPEAYK	F	0	Oxidation (M)	34.9
		502.99	1003.97	1004.54	-0.57	2	63	71	K	FVVDMPGLK	L	0	-	40.6
		510.97	1019.93	1020.53	-0.61	2	63	71	K	FVVDMPGLK	L	0	Oxidation (M)	25.2
		782.94	1563.87	1564.74	-0.87	2	77	90	K	VSMEENTLVVSGER	R	0	Oxidation (M)	88.1
38	LjT42M11.210.nc	886.03	1770.05	1771.00	-0.95	2	225	240	K	ELTLQEATIALSILK	Q	0	-	92.9
39	chr3.CM0282.370.nc	795.47	1588.92	1589.91	-0.99	2	94	109	K	ALEGADIVIIPAGVPR	K	0	-	89.7
		659.44	1316.87	1317.69	-0.82	2	116	127	R	DDLFINAGIVK	G	0	-	34.2
		609.97	1217.93	1218.70	-0.76	2	171	181	R	LFGVTTLDVVR	A	0	-	53.0
		761.40	1520.78	1521.73	-0.95	2	80	93	R	SEVVGYYGEEQLGK	A	0	-	60.0
39	chr3.CM0282.420.nc	609.97	1217.93	1218.70	-0.76	2	9	19	R	LFGVTTLDVVR	A	0	-	53.0
40	chr1.CM0027.160.nc	529.97	1586.88	1587.90	-1.01	3	74	89	K	AAAVLSSHDPPIVLAK	V	0	-	21.1
		536.94	1071.87	1072.55	-0.68	2	206	216	R	GESSVSGPVVR	L	0	-	76.7
		432.44	862.87	863.41	-0.55	2	463	470	K	ISPYDGGRR	T	0	-	46.6
		598.42	1194.82	1195.57	-0.75	2	151	162	K	SADDATAFIGTK	K	0	-	50.6
		702.44	1402.86	1403.77	-0.91	2	380	392	K	VVVGDSLQDVVFK	S	0	-	58.7
41	chr1.CM0051.30.nc	957.96	1913.90	1914.99	-1.09	2	29	47	K	FTITTFSPYVAITSSGK	K	0	-	94.8
		510.49	1018.96	1019.53	-0.57	2	4	13	K	GPGLYTDIGK	K	0	-	40.3
		462.49	922.96	923.47	-0.51	2	158	166	K	SNAGLSFTK	D	0	-	40.4
42	LjSGA_065420.1	531.52	1061.02	1061.62	-0.60	2	75	84	R	ALHIVGPDLK	I	0	-	62.8
		612.98	1223.95	1224.65	-0.70	2	87	97	K	LSFLYPATTGR	N	0	-	42.3
		715.60	2143.78	2143.98	-0.20	3	56	74	K	QLNMVDPDEKDSNGNLPSR	A	1	Oxidation (M)	62.9
		643.97	1285.92	1286.65	-0.73	2	41	51	K	VDYPIIADPER	E	0	-	61.3
		401.51	801.01	801.46	-0.45	2	105	111	R	VVESLQK	A	0	-	21.1
43	chr5.CM0328.690.nd	925.38	1848.74	1849.92	-1.18	2	325	340	R	DAEQQDVLLFVDNIFR	F	0	-	87.5
		687.90	1373.78	1372.69	1.09	2	172	183	R	IMNVIGEPIDEK	G	0	Oxidation (M)	30.9
		431.45	860.89	861.44	-0.56	2	78	85	K	ITDEVTKG	G	0	-	23.0
		728.96	1455.90	1456.83	-0.94	2	241	253	K	TVLIMELINNVAK	A	0	-	57.3
44	LjSGA_071976.1.1	784.47	1566.92	1567.86	-0.93	2	74	88	R	TALSHVDNLITGVTK	G	0	-	67.0
		910.93	1819.84	1820.91	-1.07	2	3	19	K	TILSSETMDIPDGVSIG	V	0	Oxidation (M)	74.0
45	chr3.CM0115.260.nc	664.46	1326.91	1327.69	-0.79	2	349	360	R	EMIAGVNPVIR	L	0	Oxidation (M)	63.5
		644.91	1287.80	1288.60	-0.80	2	762	772	R	HASDEIYLGER	E	0	-	38.9
46	LjSGA_014026.1	859.48	1716.94	1717.90	-0.96	2	53	67	R	ILDVVYNASNELVR	T	0	-	62.3
		834.93	1667.85	1668.77	-0.93	2	35	49	R	LDTGNFSWGSETVTR	K	0	-	80.7
47	LjSGA_038243.1	834.93	1667.85	1668.77	-0.93	2	35	49	R	LDTGNFSWGSETVTR	K	0	-	80.7
		859.48	1716.94	1717.90	-0.96	2	53	67	R	LLDVVYNASNELVR	T	0	-	62.3
47	LjSGA_040678.1	834.93	1667.85	1668.77	-0.93	2	33	47	R	LDTGNFSWGSETVTR	K	0	-	80.7
		859.48	1716.94	1717.90	-0.96	2	51	65	R	LLDVVYNASNELVR	T	0	-	62.3
48	LjT36L22.20.nd	642.49	1282.96	1283.71	-0.75	2	282	292	R	DLINILEDAIR	N	0	-	60.8
48	LjSGA_075236.1	642.49	1282.96	1283.71	-0.75	2	23	33	R	DLINILEDAIR	N	0	-	60.8

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
49	chr1.CM0378.70.nc	563.65	1687.93	1688.88	-0.94	3	1	14	-	MKPIDDKQETVTIR	A	1	Oxidation (M)	64.2
		678.98	1355.94	1356.69	-0.75	2	29	40	K	TELSTHNIDTVK	Y	0	-	59.2
		475.53	949.04	949.57	-0.53	2	62	70	R	VGISRPPPK	S	0	-	51.4
50	chr3.CM0116.300.nc	774.53	1547.04	1547.90	-0.86	2	75	89	K	EVLAVPIAPNVSLAR	Q	0	-	59.9
		569.01	1136.00	1136.63	-0.63	2	198	207	K	LLNLHSVADR	N	0	-	58.8
		667.34	1999.00	2000.11	-1.11	3	160	177	R	VVLHPIVSPLSEFAHVEK	G	0	-	42.0
51	chr3.CM0091.670.nd	797.36	1592.71	1593.71	-1.01	2	48	61	R	GFGFVFTTSEEAMR	S	0	Oxidation (M)	40.6
		557.94	1113.87	1114.57	-0.71	2	76	85	R	NITVNEAQR	G	0	-	47.1
		739.86	1477.70	1477.65	0.06	2	62	75	R	SAIEGMGNELDGR	N	0	Oxidation (M)	77.3
52	chr6.CM0420.60.nd	678.66	2032.95	2034.10	-1.15	3	218	238	K	EKPSIGTVIAVGPGLGEEGK	R	0	-	29.1
		587.51	1173.01	1173.66	-0.65	2	206	217	K	TAGLLLTATK	E	0	-	94.8
		658.45	1314.88	1314.61	0.27	2	156	167	K	YAGTEVEFNGTK	H	0	-	26.6
52	chr4.CM0006.280.nc	587.51	1173.01	1173.66	-0.65	2	179	190	K	TAGLLLTATK	E	0	-	94.8
53	chr1.CM0113.140.nc	587.44	1172.86	1173.57	-0.71	2	56	67	R	ATDQAGGTGQLR	R	0	-	95.7
54	chr4.CM0558.260.nc	761.25	2280.71	2281.13	-0.41	3	164	184	K	AEEFPVFDKVDVNGDSAAPLYK	Y	1	-	58.8
		653.44	1304.87	1305.68	-0.81	2	217	228	R	YAPTTSPLSTIEK	D	0	-	63.7
55	chr3.LjT44N20.60.nd	739.90	1477.79	1478.74	-0.95	2	241	253	R	GYISPPQFVTNPEK	S	0	-	35.7
		777.96	1553.90	1554.90	-1.00	2	145	160	K	LGLLSVTSKANPVSILK	R	0	-	77.2
		486.52	971.02	970.56	0.47	2	58	66	R	RALQAGIDK	L	1	-	44.6
56	CM1729.90.nc	1060.40	2118.79	2119.11	-0.32	2	288	308	K	LVDITNGAGDAFVGGLAQLVR	E	0	-	93.9
57	LjSGA_067203.1	855.47	1708.92	1709.87	-0.95	2	51	66	K	TLLATEYGEISATDVK	G	0	-	93.5
58	LjSGA_008893.1	856.95	1711.88	1712.84	-0.96	2	149	164	K	DGAADPTFLYFAQLK	E	0	-	67.4
		617.48	1232.94	1233.62	-0.68	2	102	111	K	LDEENQVLFK	K	0	-	25.6
		531.99	1061.97	1062.57	-0.60	2	67	75	K	VVDIVDTFR	L	0	-	62.7
58	chr5.CM0299.300.nc	531.99	1061.97	1062.57	-0.60	2	67	75	K	VVDIVDTFR	L	0	-	62.7
59	LjSGA_059392.1	935.94	1869.86	1871.02	-1.15	2	163	181	K	LVFTPTVGGSPGLSVDIGR	R	0	-	90.1
60	chr2.CM0210.60.nc	763.96	1525.91	1526.79	-0.88	2	358	371	K	GIVDSEDLPINISR	E	0	-	67.9
		604.97	1207.92	1208.62	-0.70	2	317	326	K	RAPFDLFDTK	K	1	-	48.5
60	LjSGA_048339.1	763.96	1525.91	1526.79	-0.88	2	174	187	K	GIVDSEDLPINISR	E	0	-	67.9
61	chr6.CM1829.160.nc	813.46	1624.90	1625.94	-1.04	2	432	447	K	DLVSSLVSGLLTIGPR	F	0	-	85.7
62	LjT16G18.150.nd	624.40	1246.79	1247.55	-0.76	2	107	118	K	MEAEGNQSGTPK	S	0	-	82.5
63	LjT04E07.20.nc	867.47	1732.92	1733.88	-0.97	2	155	171	K	SGGLGDLNYPVLVSDVTK	S	0	-	81.6
63	LjT18K22.30.nc	867.47	1732.92	1733.88	-0.97	2	161	177	K	SGGLGDLNYPVLVSDVTK	S	0	-	81.6
64	LjT33L17.40.nc	523.97	1045.92	1046.60	-0.68	2	130	138	R	FALLVEDLK	V	0	-	71.6
		601.98	1201.94	1202.70	-0.76	2	129	138	R	RFALLVEDLK	V	1	-	49.7
65	chr1.CM0442.310.nd	508.01	1014.00	1014.57	-0.57	2	16	26	K	LVIVGDGGTGK	T	0	-	79.6
		614.95	1227.89	1227.61	0.27	2	146	155	K	NLQYYEISAK	S	0	-	21.8

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
65	chr1.CM0442.350.nd	508.01	1014.00	1014.57	-0.57	2	16	26	K	LVIVGDGGTGK	T	0	-	79.6
		614.95	1227.89	1227.61	0.27	2	146	155	K	NLQYYEISAK	S	0	-	21.8
65	LjSGA_031947.1	508.01	1014.00	1014.57	-0.57	2	15	25	K	LVIVGDGGTGK	T	0	-	79.6
		614.95	1227.89	1227.61	0.27	2	145	154	K	NLQYYEISAK	S	0	-	21.8
66	LjSGA_011457.1	542.42	1082.82	1083.47	-0.65	2	33	42	K	ATDEGYDVSK	L	0	-	49.8
		927.85	1853.68	1854.81	-1.13	2	46	62	K	TPQSDTPPEEGPQDTK	G	0	-	60.5
67	LjT32C22.170.nd	645.41	1288.80	1289.60	-0.80	2	97	108	R	AAEEGIEIDSK	F	0	-	68.2
		468.46	934.90	935.47	-0.58	2	83	91	R	KGGLSTMDK	S	1	-	41.0
68	chr3.CM0996.130.nd	892.37	1782.73	1783.82	-1.09	2	11	27	K	ESLTATTYESVEGGANR	T	0	-	78.1
69	chr5.CM0148.90.nd	1044.90	2087.79	2088.94	-1.15	2	107	126	K	SNVPVSETESTGEPSESTPR	D	0	-	77.9
70	LjSGA_037505.1	629.41	1256.80	1257.62	-0.82	2	23	34	R	EDAEGVIGAEIR	N	0	-	77.7
71	chr1.CM0033.430.nc	567.00	1131.99	1132.69	-0.70	2	118	128	K	VSGVSLALFK	E	0	-	58.9
72	chr1.CM0001.670.nc	512.95	1023.88	1024.60	-0.72	2	244	254	K	IGGIGTVPVGR	V	0	-	65.8
		487.96	973.90	974.54	-0.64	2	236	243	R	LPLQDVYK	I	0	-	23.4
72	chr1.CM0192.320.nd	512.95	1023.88	1024.60	-0.72	2	90	100	K	IGGIGTVPVGR	V	0	-	65.8
		487.96	973.90	974.54	-0.64	2	82	89	R	LPLQDVYK	I	0	-	23.4
72	chr2.LjT12G08.20.nc	512.95	1023.88	1024.60	-0.72	2	244	254	K	IGGIGTVPVGR	V	0	-	65.8
		487.96	973.90	974.54	-0.64	2	236	243	R	LPLQDVYK	I	0	-	23.4
72	chr5.CM0909.50.nc	512.95	1023.88	1024.60	-0.72	2	244	254	K	IGGIGTVPVGR	V	0	-	65.8
		487.96	973.90	974.54	-0.64	2	236	243	R	LPLQDVYK	I	0	-	23.4
73	chr5.CM0052.420.nd	530.46	1058.90	1059.55	-0.65	2	79	86	K	IPDWFLNR	K	0	-	50.3
		710.41	1418.81	1419.68	-0.87	2	95	106	K	YHQVVSNALDMK	L	0	Oxidation (M)	58.2
73	LjSGA_085279.1	530.46	1058.90	1059.55	-0.65	2	78	85	K	IPDWFLNR	K	0	-	50.3
		710.41	1418.81	1419.68	-0.87	2	94	105	K	YHQVVSNALDMK	L	0	Oxidation (M)	58.2
74	LjSGA_042082.1	753.49	1504.97	1505.81	-0.84	2	24	36	K	AVQFETVPLDLFK	G	0	-	48.2
		539.50	1076.99	1077.59	-0.60	2	5	14	K	VYGPIFASPK	R	0	-	53.5
75	chr5.CM0260.520.nd	713.49	1424.97	1425.86	-0.89	2	52	64	R	LNIAQVLTVISQK	Q	0	-	74.0
76	chr1.CM0105.500.nc	655.44	1308.87	1309.67	-0.80	2	38	48	K	VESYWAPLFAK	L	0	-	56.2
77	chr3.LjT03D10.60.nd	585.46	1168.91	1169.60	-0.69	2	131	140	K	FLDGIYVSEK	G	0	-	63.2
		649.47	1296.93	1297.69	-0.76	2	130	140	R	KFLDGIYVSEK	G	1	-	44.9
77	LjSGA_071678.1	585.46	1168.91	1169.60	-0.69	2	48	57	K	FLDGIYVSEK	G	0	-	63.2
		649.47	1296.93	1297.69	-0.76	2	47	57	R	KFLDGIYVSEK	G	1	-	44.9
77	chr3.CM0160.930.nd	585.46	1168.91	1169.60	-0.69	2	129	138	K	FLDGIYVSEK	G	0	-	63.2
		649.47	1296.93	1297.69	-0.76	2	128	138	R	KFLDGIYVSEK	G	1	-	44.9
78	chr1.CM0017.210.nc	711.94	1421.87	1422.66	-0.79	2	28	40	R	ELAEDGYSGVEVR	V	0	-	50.8
		423.00	843.99	844.47	-0.48	2	55	62	R	TQAVLGEK	G	0	-	34.7

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
78	LjSGA_009417.2	711.94	1421.87	1422.66	-0.79	2	28	40	R	ELAEDGYSGVEVR	V	0	-	50.8
		423.00	843.99	844.47	-0.48	2	55	62	R	TQAVLGEK	G	0	-	34.7
79	chr1.LjT43O05.80.nd	561.40	1120.79	1121.51	-0.72	2	131	140	R	GVMISDNQSR	F	0	Oxidation (M)	56.8
80	chr4.CM0387.130.nc	685.95	1369.88	1370.73	-0.85	2	157	167	R	TNIFSQFFLVR	H	0	-	56.3
		600.95	1199.89	1200.65	-0.75	2	44	56	K	VALVTGGDSGIGR	A	0	-	44.5
81	LjSGA_123620.1	756.92	1511.83	1511.78	0.05	2	27	41	R	AVENGAVAVSEPELK	E	0	-	70.7
82	LjSGA_068070.1	605.99	1209.97	1210.72	-0.75	2	34	44	K	ILEEVALIPSK	R	0	-	69.9
83	chr3.CM0005.500.nc	859.96	1717.91	1718.87	-0.96	2	126	142	K	EVAGDAPLFTTSDLGVK	K	0	-	56.9
		536.96	1071.91	1072.49	-0.58	2	60	68	R	FAVDEHNNK	Q	0	-	39.0
84	LjSGA_093090.1	717.41	1432.80	1433.70	-0.90	2	11	23	R	LTPDYDALDVANK	I	0	-	66.2
85	LjSGA_036172.1	687.43	1372.84	1373.70	-0.86	2	48	59	R	EGDILTLESER	E	0	-	66.1
86	chr4.CM0007.620.nd	585.45	1168.88	1169.60	-0.72	2	33	43	K	EDNVTLGPAVR	D	0	-	46.2
		714.92	1427.83	1428.71	-0.88	2	150	162	R	IEDVTPIPSDSTR	R	0	-	55.1
86	LjT35M05.50.nd	585.45	1168.88	1169.60	-0.72	2	26	36	K	EDNVTLGPAVR	D	0	-	46.2
		714.92	1427.83	1428.71	-0.88	2	143	155	R	IEDVTPIPSDSTR	R	0	-	55.1
87	LjSGA_046195.1	636.45	1270.89	1271.70	-0.80	2	15	26	K	ASDTTLLEVVPVK	V	0	-	65.5
88	chr5.CM0096.480.nc	807.41	1612.81	1613.79	-0.99	2	71	85	K	STGFGLIYDSLENAK	K	0	-	65.4
88	LjSGA_118363.1	807.41	1612.81	1613.79	-0.99	2	35	49	K	STGFGLIYDSLENAK	K	0	-	65.4
89	chr1.CM0378.40.nc	827.47	1652.94	1653.84	-0.90	2	186	200	K	VLQFAGIDDVFTSSR	G	0	-	65.0
89	chr2.LjT09A11.20.nc	827.47	1652.94	1653.84	-0.90	2	201	215	K	VLQFAGIDDVFTSSR	G	0	-	65.0
89	chr4.CM0042.1380.nc	827.47	1652.94	1653.84	-0.90	2	198	212	K	VLQFAGIDDVFTSSR	G	0	-	65.0
89	LjSGA_025794.2	827.47	1652.94	1653.84	-0.90	2	195	209	K	VLQFAGIDDVFTSSR	G	0	-	65.0
90	chr4.CM0179.510.nd	743.94	1485.87	1486.69	-0.83	2	39	51	R	TTPSYVAFTDTER	L	0	-	46.9
		627.44	1252.87	1253.64	-0.76	2	28	38	R	VEIIPNDQQNR	T	0	-	54.9
90	chr1.CM0133.1430.nc	743.94	1485.87	1486.69	-0.83	2	60	72	R	TTPSYVAFTDTER	L	0	-	46.9
90	chr3.CM0452.230.nd	743.94	1485.87	1486.69	-0.83	2	40	52	R	TTPSYVAFTDTER	L	0	-	46.9
90	chr6.CM0118.650.nc	743.94	1485.87	1486.69	-0.83	2	40	52	R	TTPSYVAFTDTER	L	0	-	46.9
90	chr6.CM0118.670.nc	743.94	1485.87	1486.69	-0.83	2	40	52	R	TTPSYVAFTDTER	L	0	-	46.9
90	LjSGA_038906.1	743.94	1485.87	1486.69	-0.83	2	40	52	R	TTPSYVAFTDTER	L	0	-	46.9
91	LjSGA_085074.2	516.93	1031.84	1032.51	-0.67	2	84	93	K	DQQLSVSEAK	V	0	-	64.7
92	chr1.LjT01D01.60.nd	608.48	1214.95	1215.71	-0.76	2	38	49	K	LSAAIASILETK	L	0	-	63.8
92	LjSGA_079444.1	608.48	1214.95	1215.71	-0.76	2	23	34	K	LSAAIASILETK	L	0	-	63.8

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
93	chr2.CM0021.220.nc	628.99	1255.97	1256.73	-0.76	2	84	95	R	SIVGATLEVIQK	R	0	-	63.5
93	chr4.CM0175.570.nd	628.99	1255.97	1256.73	-0.76	2	80	91	R	SIVGATLEVIQK	K	0	-	63.5
94	chr1.CM0109.50.nd	707.67	2119.99	2121.18	-1.19	3	19	39	K	LVQIEHALTAVGSGQTSLGIK	A	0	-	60.9
95	LjSGA_043401.1	717.41	1432.80	1433.75	-0.95	2	189	203	R	AASFNIIPSSTGAAK	V	0	-	33.5
		1016.48	2030.94	2032.07	-1.13	2	156	174	R	FGIVEGLMTTVHSITATQK	T	0	-	56.1
96	chr1.CM0029.40.nc	468.48	934.94	935.47	-0.53	2	36	43	R	IGDYVDVR	V	0	-	59.7
97	LjSGA_029241.1	637.96	1273.91	1274.61	-0.70	2	21	32	K	ENVSEALEAAR	I	0	-	58.2
97	LjSGA_044797.1	637.96	1273.91	1274.61	-0.70	2	21	32	K	ENVSEALEAAR	I	0	-	58.2
98	chr4.CM0501.190.nd	829.46	1656.91	1657.93	-1.02	2	100	114	R	TYLNLPSSEIVPATLK	K	0	-	58.2
98	LjSGA_048933.1	829.46	1656.91	1657.93	-1.02	2	77	91	R	TYLNLPSSEIVPATLK	K	0	-	58.2
99	chr1.CM0206.150.nd	580.49	1158.97	1159.66	-0.70	2	23	33	K	ILFLGLDNAGK	T	0	-	58.0
99	chr4.CM0429.130.nd	580.49	1158.97	1159.66	-0.70	2	23	33	K	ILFLGLDNAGK	T	0	-	58.0
99	CM0385.100.nd	580.49	1158.97	1159.66	-0.70	2	23	33	K	ILFLGLDNAGK	T	0	-	58.0
100	chr4.CM0429.210.nc	674.52	1347.03	1347.78	-0.75	2	61	72	R	EFVPFVASVLIK	A	0	-	41.5
		474.53	947.05	947.59	-0.54	2	32	39	R	HPLILSIR	D	0	-	40.5
		705.98	1409.94	1410.73	-0.79	2	50	60	K	TWLAQDYLFVR	E	0	-	38.3
101	LjSGA_051623.1	421.50	840.99	841.48	-0.49	2	63	69	K	VDRSLPR	G	1	-	41.4
102	chr2.CM0056.690.nd	638.97	1275.93	1276.63	-0.71	2	109	119	K	VYEGIPPPYDK	M	0	-	57.3
103	LjSGA_013905.2	429.49	856.97	857.51	-0.54	2	68	75	R	INGSLARK	A	1	-	20.8
		557.48	1112.94	1113.64	-0.70	2	56	65	K	LITPSILSDR	L	0	-	56.8
103	chr1.CM0113.320.nd	557.48	1112.94	1113.64	-0.70	2	59	68	K	LITPSILSDR	L	0	-	56.8
103	chr3.CM0216.350.nc	557.48	1112.94	1113.64	-0.70	2	60	69	K	LITPSILSDR	L	0	-	56.8
104	chr4.LjT06I07.80.nd	853.89	1705.77	1706.86	-1.09	2	78	98	R	VGGAAAAGGAAPAEAPAAEK	K	0	-	56.7
105	chr4.CM0044.290.nd	524.46	1046.90	1047.56	-0.66	2	70	78	K	FVEVVEAQK	Q	0	-	55.6
106	chr1.CM0105.70.nd	534.99	1067.97	1068.70	-0.74	2	387	395	K	LITKILVNR	I	1	-	48.0
106	chr1.CM0982.190.nd	534.99	1067.97	1068.70	-0.74	2	90	98	K	LITKILVNR	I	1	-	48.0
106	chr1.CM1255.70.nc	534.99	1067.97	1068.70	-0.74	2	150	158	K	LITKILVNR	I	1	-	48.0
106	chr1.CM1875.100.nc	534.99	1067.97	1068.70	-0.74	2	270	278	K	LITKILVNR	I	1	-	48.0
106	chr2.CM0020.70.nd	534.99	1067.97	1068.70	-0.74	2	573	581	K	LITKILVNR	I	1	-	48.0
106	chr2.CM0695.40.nd	534.99	1067.97	1068.70	-0.74	2	516	524	K	LITKILVNR	I	1	-	48.0
106	chr6.CM0066.560.nc	534.99	1067.97	1068.70	-0.74	2	526	534	K	LITKILVNR	I	1	-	48.0
106	LjT47D03.240.nd	534.99	1067.97	1068.70	-0.74	2	261	269	K	LITKILVNR	I	1	-	48.0

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
106	LjT13L03.70.nd	534.99	1067.97	1068.70	-0.74	2	248	256	K	LITKILVNR	I	1	-	48.0
106	LjSGA_005191.1	534.99	1067.97	1068.70	-0.74	2	194	202	K	LITKILVNR	I	1	-	48.0
106	LjSGA_027221.1	534.99	1067.97	1068.70	-0.74	2	264	272	K	LITKILVNR	I	1	-	48.0
106	LjSGA_043425.1	534.99	1067.97	1068.70	-0.74	2	331	339	K	LITKILVNR	I	1	-	48.0
106	LjSGA_049007.1	534.99	1067.97	1068.70	-0.74	2	326	334	K	LITKILVNR	I	1	-	48.0
106	LjSGA_050485.1	534.99	1067.97	1068.70	-0.74	2	52	60	K	LITKILVNR	I	1	-	48.0
106	LjSGA_057788.2	534.99	1067.97	1068.70	-0.74	2	247	255	K	LITKILVNR	I	1	-	48.0
106	LjSGA_069294.1	534.99	1067.97	1068.70	-0.74	2	132	140	K	LITKILVNR	I	1	-	48.0
106	LjSGA_070239.1	534.99	1067.97	1068.70	-0.74	2	348	356	K	LITKILVNR	I	1	-	48.0
106	LjSGA_071661.1	534.99	1067.97	1068.70	-0.74	2	319	327	K	LITKILVNR	I	1	-	48.0
106	LjSGA_144027.1	534.99	1067.97	1068.70	-0.74	2	64	72	K	LITKILVNR	I	1	-	48.0
106	chr1.CM1956.240.nc	534.99	1067.97	1068.70	-0.74	2	905	913	K	LITKILVNR	I	1	-	48.0
106	chr2.LjT12G08.70.nc	534.99	1067.97	1068.70	-0.74	2	136	144	K	LITKILVNR	I	1	-	48.0
106	chr6.CM0037.630.nd	534.99	1067.97	1068.70	-0.74	2	198	206	K	LITKILVNR	I	1	-	48.0
106	LjSGA_024652.2	534.99	1067.97	1068.70	-0.74	2	239	247	K	LITKILVNR	I	1	-	48.0
106	LjT17C09.90.nc	534.99	1067.97	1068.70	-0.74	2	951	959	K	LITKILVNR	L	1	-	48.0
107	chr5.CM0071.360.nd	534.99	1067.97	1068.70	-0.74	2	420	428	K	LITKIIVNR	I	1	-	48.0
107	chr5.CM0357.500.nc	534.99	1067.97	1068.70	-0.74	2	1036	1044	K	LITKIIVNR	I	1	-	48.0
108	chr4.LjT08E06.90.nc	534.99	1067.97	1068.70	-0.74	2	480	488	K	LITKLLVNR	I	1	-	48.0
109	chr1.CM0033.150.nd	483.97	965.93	966.48	-0.55	2	207	214	K	IDAYTQTR	A	0	-	54.8
		543.52	1085.02	1085.63	-0.61	2	83	92	K	VLGESLDLIK	Y	0	-	40.8
109	chr1.CM0033.160.nd	483.97	965.93	966.48	-0.55	2	183	190	K	IDAYTQTR	A	0	-	54.8
		543.52	1085.02	1085.63	-0.61	2	59	68	K	VLGESLDLIK	Y	0	-	40.8
110	LjT46P06.210.nd	636.91	1271.81	1272.72	-0.91	2	257	266	K	LCLLEKQLSR	C	1	Propionamide (C)	44.4
111	chr1.CM0029.350.nd	710.00	1417.98	1418.79	-0.81	2	102	114	R	VNQAIYLLTTGAR	E	0	-	53.7
111	LjSGA_013603.1	710.00	1417.98	1418.79	-0.81	2	28	40	R	VNQAIYLLTTGAR	E	0	-	53.7
112	chr2.CM0250.40.nc	505.95	1009.89	1009.47	0.43	2	249	257	K	ESSKTTDSR	D	1	-	36.2
		534.99	1067.97	1068.70	-0.74	2	999	1007	K	LITKILVNR	I	1	-	48.0
113	chr4.CM0042.770.nc	450.52	899.02	899.54	-0.52	2	92	99	K	DVILIATR	R	0	-	33.8
		641.94	1281.86	1281.61	0.25	2	181	191	K	DVVFEYPITEA	-	0	-	27.2
		534.99	1067.96	1068.56	-0.60	2	167	175	K	LETFAAVYR	K	0	-	53.1
114	chr4.CM0087.970.nc	629.93	1257.84	1257.66	0.19	2	298	309	R	IQNAGTEVVEAK	A	0	-	28.5

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
		609.97	1217.93	1218.70	-0.76	2	234	244	K	LFGVTTLDVVR	A	0	-	53.0
115	chr2.LjT39I02.70.nc	849.43	1696.84	1697.94	-1.09	2	45	60	K	VSNWGATLVSLVLPDK	H	0	-	51.6
116	chr6.CM0139.590.nd	650.94	1299.86	1300.65	-0.79	2	44	55	K	TLNVEEAPSDVK	V	0	-	51.5
117	LjSGA_088290.1	756.42 756.49	1510.82 1510.96	1511.90 1511.87	-1.08 -0.91	2 2	201 201	214 214	R R	KVDTLAIQIVSIGR QVDTLAIQIVSIGR	Q Q	1 0	- -	40.5 49.0
118	chr2.CM0191.540.nc	440.44	878.86	879.43	-0.57	2	23	30	K	TFGEALDK	T	0	-	50.6
118	LjT16O05.90.nd	440.44	878.86	879.43	-0.57	2	2	9	K	TFGEALDK	T	0	-	50.6
118	LjSGA_086166.1	440.44	878.86	879.43	-0.57	2	23	30	K	TFGEALDK	T	0	-	50.6
119	LjSGA_016382.1	773.46	1544.91	1545.75	-0.85	2	156	170	K	TAAEETKPAAEETKA	-	1	-	54.2
120	LjSGA_020557.1	541.94	1081.87	1082.54	-0.66	2	536	544	R	NSAKHQGWR	S	1	-	48.6
121	chr6.CM0679.70.nc	579.98	1157.94	1158.68	-0.74	2	107	117	R	FLIAPSLVSGR	I	0	-	48.0
122	chr4.CM0087.1060.nc	589.31 524.00 473.00	1764.92 1045.98 943.99	1765.92 1046.58 944.52	-1.01 -0.59 -0.53	3 2 2	157 72 60	173 80 67	K R R	HIDFSLTSLPGGRRPGR IFEGEALLR NLLTLDEK	V R N	0 0 0	- - -	27.2 50.3 29.8
123	chr1.CM0544.80.nc	579.95	1157.88	1158.62	-0.74	2	4	15	K	AVAVLGSSDINVK	G	0	-	47.9
124	LjSGA_063286.1	516.97	1031.93	1032.60	-0.67	2	33	40	R	LINYLLER	G	0	-	47.8
125	chr1.CM0145.90.nc	869.42	1736.82	1737.89	-1.07	2	52	67	K	ETPEAHVFSDLPGLK	K	0	-	47.7
127	LjSGA_027840.1	595.97	1784.87	1785.86	-0.99	3	8	23	K	ESFITEAHNAPVTSQR	K	0	-	47.2
128	LjB14K02.60.nc	838.97	1675.92	1676.86	-0.94	2	532	547	K	FDIDANGILSVTAVDK	G	0	-	47.0
128	LjSGA_129817.1	838.97	1675.92	1676.86	-0.94	2	1	16	-	FDIDANGILSVTAVDK	G	0	-	47.0
129	LjSGA_064891.1	819.51	1637.00	1637.90	-0.90	2	59	73	K	ELDLVPTLPQSSLAR	Q	0	-	46.9
130	LjT41N19.20.nd	734.46 552.52	1466.90 1103.02	1467.80 1103.66	-0.91 -0.64	2 2	597 174	610 183	K K	GGINVIQIDEAALR SFSLLSLPK	E V	0 0	- -	46.2 31.0
131	LjSGA_059569.1	471.99	941.97	942.61	-0.64	2	355	363	R	LLVAVSLTK	L	0	-	45.0
132	LjSGA_020081.2	486.50	970.99	971.53	-0.53	2	1	8	-	RANQQLSR	X	1	-	43.5
133	chr5.CM0953.170.nc	536.42	1070.83	1070.56	0.28	2	20	28	R	NNVNNKVMR	D	1	-	45.9
134	LjT07L17.10.nd	516.97	1031.93	1032.60	-0.67	2	3	10	R	LNLYIIR	Q	0	-	45.8
135	chr5.CM0357.40.nd	664.46	1326.91	1326.73	0.17	2	208	219	R	EMLAGVNPVIIR	R	0	Oxidation (M)	45.8
136	chr1.CM0222.290.nd	763.90	1525.79	1526.74	-0.96	2	25	37	R	LVQSPNSFFMDVK	C	0	Oxidation (M)	45.6
138	LjSGA_106255.1	582.95	1163.89	1163.65	0.24	2	34	43	R	LEGGQLRHVR	D	1	-	39.7
139	LjT11L09.120.nd	689.88	688.88	689.36	-0.48	1	235	240	K	DISDIK	L	0	-	45.2
140	LjSGA_091805.2	447.44	892.86	893.42	-0.56	2	97	103	K	EFSNLER	C	0	-	45.1

Continues...

Supplemental Table S2.16: (mature_LotusAA GeLC-MS/MS Peptides continued)

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
141	chr2.CM0056.380.nc	657.48	1312.94	1313.70	-0.76	2	57	68	R	HITYAEGSPLVK	S	0	-	45.0
142	chr4.CM0429.60.nd	721.42	1440.83	1441.75	-0.91	2	23	35	K	GGLFDFGHPLLNR	I	0	-	43.3
144	LjSGA_033282.0.1	463.58	1387.73	1388.64	-0.91	3	6	16	K	QKVDVEEEER	N	1	-	43.8
		463.59	1387.76	1386.70	1.06	3	6	16	K	QKVIVEEEER	N	1	-	28.5
		463.58	1387.73	1387.66	0.07	3	6	16	K	QKVNVEEEER	N	1	-	37.6
145	LjSGA_053764.1	550.53	1099.04	1099.65	-0.61	2	47	56	K	IGVLTVELEK	T	0	-	42.4
146	LjSGA_079668.1	602.95	1203.89	1204.57	-0.67	2	92	102	K	ETGVQVSDSR	D	0	-	42.8
147	LjT48O01.60.nd	530.47	1058.93	1059.57	-0.65	2	398	406	R	TLIDLVCVQR	G	0	-	42.4
148	LjSGA_009509.2	626.94	1251.86	1252.78	-0.92	2	72	84	K	VSVVPSAAALVIK	A	0	-	42.7
		735.95	2204.84	2205.24	-0.40	3	17	40	R	VTGGEVGAASSLAPKIGPLGLSPK	K	1	-	22.0
150	CM0458.170.nd	486.45	970.88	970.56	0.32	2	1013	1020	K	LNLQQLSR	L	0	-	41.2
151	chr4.CM0128.40.nc	486.45	970.88	971.58	-0.70	2	93	100	K	VEIKQISR	D	1	-	41.2
153	LjSGA_016038.1	539.32	1614.93	1615.89	-0.96	3	105	118	K	APILIVKPQEEDHK	K	0	-	33.4
		585.02	1168.03	1168.62	-0.59	2	52	62	K	AQSVILNGDPR	E	0	-	39.3
154	LjSGA_009196.2	572.94	1143.87	1144.61	-0.74	2	38	48	K	AESIILTG DAR	E	0	-	40.6

Supplemental Table S2.17: The complete list of the 25 peptides identified in the “mature_LotusEST_TIGR” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein's hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.7. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	TC9431	939.28	1876.55	1875.71	0.84	2	116	133	R	ESEEEGSSSSSSSESSR	R	0	-	114.5
		574.91	1147.81	1148.49	-0.69	2	27	36	R	GSEEGEKEER	E	1	-	42.7
2	CN825001	693.91	1385.81	1386.67	-0.87	2	155	168	R	QSQGTGPGQLES AK	R	0	-	75.2
		581.61	1741.80	1742.88	-1.08	3	28	42	R	STTPHQIQVHTTTHR	Y	0	-	58.2
		595.92	1189.82	1190.57	-0.75	2	43	52	R	YETGVNPQQR	Y	0	-	50.6
3	TC8009	485.44	968.86	969.49	-0.63	2	215	224	R	AHASTEGVAK	Y	0	-	40.1
		862.26	2583.76	2584.40	-0.63	3	292	316	K	AQGLAVGSSLVEEDKLN LATS LLEK	A	1	-	63.8
		910.03	1818.05	1819.06	-1.00	2	165	181	K	LVAQIPEGGVILLE NV R	F	0	-	56.3
		732.94	1463.87	1464.82	-0.94	2	225	237	K	YLKPAVAGFLMQK	E	0	-	31.7
4	TC14860	716.98	1431.94	1432.74	-0.80	2	268	281	R	EAGTTLAVVSEQTK	A	0	-	77.9
		553.50	1104.99	1105.61	-0.62	2	246	255	K	VAYALSQN LK	V	0	-	53.0
5	TC8554	679.01	1356.00	1356.76	-0.77	2	98	110	K	IAVVVGTVTDDIR	V	0	-	78.4
6	TC10602	559.41	1116.80	1117.50	-0.70	2	76	86	R	AQGDADSAIDR	L	0	-	70.6
6	TC11545	559.41	1116.80	1117.50	-0.70	2	86	96	R	AQGDADSAIDR	L	0	-	70.6
7	AV410268	859.62	2575.85	2575.43	0.42	3	15	35	-	LLLV L I N K L D C Y L P F C Y H I L	-	1	Propionamide (C)	29.1
8	TC14826	743.02	1484.03	1484.86	-0.83	2	169	182	K	QLPSGLLLVTGPYK	I	0	-	64.0
9	TC14170	882.45	1762.88	1763.95	-1.07	2	148	165	R	VAMIGFAASLLGEALTGK	G	0	Oxidation (M)	63.8
10	TC18990	885.42	1768.83	1769.95	-1.12	2	37	54	K	IASGTDIVSAAPNVSLQK	A	0	-	58.7
11	TC9972	573.46	1144.90	1145.59	-0.70	2	107	117	K	DAVSTDVLQAK	D	0	-	58.5
13	TC16731	742.93	1483.84	1484.78	-0.94	2	65	78	K	GNVQPDTVLQTVSK	T	0	-	49.5
14	TC8165	624.47	1246.93	1247.62	-0.69	2	271	281	K	IASFLDPDGWK	T	0	-	46.8
15	TC10840	456.98	911.95	912.54	-0.59	2	31	39	R	GLVG E I I G R	F	0	-	43.5
16	TC8322	914.98	2741.92	2742.36	-0.44	3	118	142	K	ANLSESQDILAT IETETQDIPDAR	T	0	-	43.3
17	TC14090	577.42	1152.82	1153.56	-0.74	2	373	383	K	ANSEATLGTYK	G	0	-	41.5
18	TC8725	631.43	1260.84	1261.62	-0.78	2	87	98	K	DLIAAMEADV K	N	0	Oxidation (M)	39.6

Supplemental Table S2.18: The complete list of the 4 peptides identified in the “mature_LotusNT” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.8. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	chr3.CM0164.170.nd	773.85	1545.68	1545.65	0.02	2	578	589	R	TRDEEEEEQPR	F	1	-	74.3
2	LjT03L06.120.nd	759.39	1516.76	1517.71	-0.95	2	133	145	K	AIEGYVLNHPEYN	-	0	-	65.0
3	chr6.CM0679.100.nd	843.36	1684.72	1685.79	-1.07	2	6	21	K	SLEDAFSSFGTVAEAR	V	0	-	81.4
4	LjSGA_121732.1	718.48	1434.95	1433.85	1.11	2	86	97	-	VLNSILRQLNHHK	S	1	-	48.1

Supplemental Table S2.19: The complete list of the 11 peptides identified in the “mature_NCBInr” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein's hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.9. The observed mass (D), expected mass (D), calculated mass (D), delta (D), charge, start position (Start), end position (End), amino acid (AA) residue before the peptide (Residue before), the peptide AA sequence (Peptide), the AA residue after the peptide (Residue after), miss cleavage, modification, and MOWSE score (Score) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	gi 7230391	774.89	2321.66	2322.18	-0.51	3	392	411	K	MIPTKPMVVETFSQYPPLGR	F	0	2 Oxidation (M)	65.8
1	gi 48527431	774.89	2321.66	2322.18	-0.51	3	392	411	K	MIPTKPMVVETFSQYPPLGR	F	0	2 Oxidation (M)	65.8
1	gi 89275337	774.89	2321.66	2322.18	-0.51	3	203	222	K	MIPTKPMVVETFSQYPPLGR	F	0	2 Oxidation (M)	65.8
2	Unknown/dead	756.54	2266.60	2267.12	-0.52	3	974	991	R	NLMCLSNETWPLTRISFR	I	1	Oxidation (M); Propionamide (C) Propionamide (C)	38.1
		751.19	2250.56	2251.12	-0.56	3	974	991	R	NLMCLSNETWPLTRISFR	I	1		34.3
3	gi 1297072	705.89	1409.77	1410.68	-0.90	2	434	445	K	QSHFANAQPQQR	E	0	-	51.6
4	gi 4585271	618.94	1235.86	1236.68	-0.82	2	96	106	K	VPYSILMSLAK	D	0	Oxidation (M)	47.8
5	gi 2462734	598.41	1194.80	1195.54	-0.73	2	272	281	R	IGEETYEER	M	0	-	43.6
5	gi 15219744	598.41	1194.80	1195.54	-0.73	2	271	280	R	IGEETYEER	M	0	-	43.6
5	gi 15219746	598.41	1194.80	1195.54	-0.73	2	268	277	R	IGEETYEER	V	0	-	43.6
5	Unknown/dead	598.41	1194.80	1195.54	-0.73	2	272	281	R	IGEETYEER	M	0	-	43.6

Supplemental Table S2.20: The complete list of the 10 peptides identified in the “mature_SPROT” GeLC-MS/MS analysis ordered by the protein to which they are predicted to belong. The protein’s hit number and identifier are shown in the two first columns. Further details of the peaks (proteins) can be found in Supplemental Table S2.10. The observed mass (*D*), expected mass (*D*), calculated mass (*D*), delta (*D*), charge, start position (*Start*), end position (*End*), amino acid (*AA*) residue before the peptide (*Residue before*), the peptide *AA* sequence (*Peptide*), the *AA* residue after the peptide (*Residue after*), miss cleavage, modification, and MOWSE score (*Score*) of the peptides are shown in the next thirteen columns.

Hit no.	Identifier	Observed mass	Expected mass	Calc. mass	Delta	Charge	Start	End	Residue before	Peptide	Residue after	Miss cleavage	Modification	Score
1	EMB1_DAUCA	593.43	1184.85	1185.60	-0.75	2	16	28	R	QGETVVPGGTGGK	S	0	-	72.2
2	SEEP_RAPSA	593.43	1184.85	1185.64	-0.79	2	16	28	K	KGETVVPGGTGGK	S	1	-	72.2
2	EM6_ARATH	593.43	1184.85	1185.64	-0.79	2	16	28	K	KGETVVPGGTGGK	S	1	-	72.2
3	EMP1_ORYSA	593.43	1184.85	1185.60	-0.75	2	19	31	R	EGQTVVPGGTGGK	S	0	-	69.9
3	EM2_WHEAT	593.43	1184.85	1185.60	-0.75	2	18	30	R	EGQTVVPGGTGGK	S	0	-	69.9
4	PSB5A_ARATH	976.92	1951.82	1952.92	-1.10	2	183	201	R	FSVGSGSPYAYGVLD SGYK	Y	0	-	80.6
4	PSB5B_ARATH	976.92	1951.82	1952.92	-1.10	2	183	201	R	FSVGSGSPYAYGVLD SGYK	F	0	-	80.6
5	EM1_ARATH	917.36	1832.70	1833.82	-1.12	2	132	148	K	SGGERAEEEGIEIDSK	F	1	-	56.6
7	TIP31_ARATH	605.95	1209.89	1210.56	-0.67	2	14	24	R	ADEATHPDSIR	A	0	-	46.3
7	TIP32_ARATH	605.95	1209.89	1210.56	-0.67	2	14	24	R	ADEATHPDSIR	A	0	-	46.3

Supplemental Table S3.

Protein identification	Peptides matched	Sequence coverage (%)	MOWSE score	Hit number	Predicted annotation
chr6.CM0014.300.nc	6	19.4	115	196	Glutamine synthetase
chr2.LjT01H08.60.nc	2	5.9	59	379	Glutamine synthetase
LjSGA_030247.1	1	11.1	52	444	Glutamine synthetase
LjSGA_019428.1	3	26.1	66	196	Glutamine synthetase
LjT32D02.120.nc	2	6.7	58	384	Glutamine synthetase
LjSGA_005533.1	1	3.2	102	226	Dihydrodipicolinate synthase
LjSGA_042035.1	5	20.5	404	37	Dihydrodipicolinate synthase
LjSGA_043096.1	4	29.2	125	184	Dihydrodipicolinate synthase
LjT41N19.20.nd	18	28.0	791	13	Methionine synthase
chr5.CM0341.270.nd	1	11.5	49	13	Methionine synthase
LjSGA_094289.1	2	11.2	45	13	Methionine synthase
LjSGA_071971.1	2	12.5	66	342	5-methyltetrahydropteroyl-triglutamate--homocysteine S-methyltransferase
LjSGA_056527.2	1	12.2	49	13	Methionine synthase
LjSGA_027059.1	5	15.7	85	85	Acetohydroxy acid isomeroreductase
LjT06B16.110.nc	2	6.3	114	200	Argininosuccinate synthase
chr2.CM0102.150.nd	1	3.2	63	356	Homoserine kinase
chr1.LjT48M07.70.nc	1	4.4	75	302	Pyridoxal-5-phosphate-dependent enzyme, beta subunit
LjSGA_011044.2	4	11.2	110	211	Phosphoglycerate dehydrogenase
LjSGA_147294.1	1	9.8	105	219	Acetohydroxy acid isomeroreductase precursor
chr2.CM0272.170.nc	1	3.3	55	404	Phosphoserine aminotransferase
chr4.CM0042.1530.nc	1	2.9	62	361	Aspartate-semialdehyde dehydrogenase
LjSGA_019672.2	3	10.4	69	329	2-isopropylmalate synthase
chr5.CM0200.1260.nc	3	5.7	53	429	Phosphoglycerate dehydrogenase-like protein
chr1.LjT14I13.60.nd	2	6.3	112	207	Argininosuccinate synthase
LjSGA_021575.2	2	17.0	89	261	Argininosuccinate synthase

Supplemental Table S3. Pathway analysis of “amino acid biosynthesis” in green seeds. The total number of protein identifications for the pathway “amino acid biosynthesis” with the predicted annotation. In mature seeds the LjT41N19.20.nd is the only identified protein in the amino acid biosynthesis.

Supplemental Table S5

Pathway	No. of enzymes
Glycolysis / Gluconeogenesis	20
Pyruvate metabolism	17
Starch and sucrose metabolism	15
Glycine, serine and threonine metabolism	15
Purine metabolism	14
Carbon fixation	14
Flavonoid biosynthesis	11
Propanoate metabolism	11
Butanoate metabolism	10
Glutathione metabolism	10
Alanine and aspartate metabolism	10
Fructose and mannose metabolism	10
Glyoxylate and dicarboxylate metabolism	9
Tryptophan metabolism	9
Pentose phosphate pathway	8
Fatty acid biosynthesis	8
Biosynthesis of unsaturated fatty acids	8
Aminoacyl-tRNA biosynthesis	8
Citrate cycle (TCA cycle)	8
Tyrosine metabolism	8
Nucleotide sugars metabolism	7
Ascorbate and aldarate metabolism	7
Nitrogen metabolism	7
Valine, leucine and isoleucine degradation	7
Benzoate degradation via CoA ligation	7
Valine, leucine and isoleucine biosynthesis	7
Lysine degradation	6
alpha-Linolenic acid metabolism	6
Limonene and pinene degradation	6
Fatty acid metabolism	6
Glutamate metabolism	6
Arginine and proline metabolism	6
Lysine biosynthesis	6
Reductive carboxylate cycle (CO ₂ fixation)	6
Selenoamino acid metabolism	5
Bile acid biosynthesis	5
Phenylpropanoid biosynthesis	5
Galactose metabolism	5
Phenylalanine metabolism	5
Glycerolipid metabolism	5
Methionine metabolism	5
Pentose and glucuronate interconversions	5

Supplemental Table S5: Comparative pathway analysis in legumes. Pathways with five or more enzymes represented in the total set of protein identifications from *Lotus*, *Medicago*, and soybean.