Wheat mitochondrial proteomes provide new links between antioxidant defence and plant salinity tolerance.

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ABSTRACT

The mitochondrial proteome and differences associated with salt tolerance have been investigated in Australian commercial varieties of wheat. Mitochondria isolated from shoots were used to generate a wheat mitochondrial reference map, 68 unique wheat mitochondrial proteins were identified from 192 gel spots using 2D PAGE and LC-MS/MS. This analysis also provided MS/MS spectra for 199 proteotypic peptides as a foundation for the development of targeted proteomics for study of the respiratory apparatus in wheat. Using this reference map and 2D DIGE we have found quantitative differences in the shoot mitochondrial proteomes of v. Wyalkatchem and v. Janz, two commercially important wheat varieties that are known from a range of experiments to have differing salinity tolerance. These proteins included Mn-superoxide dismutase (Mn-SOD), cysteine synthase, nucleotide diphosphate kinase and the voltage dependent anion channel (VDAC). Antibodies to the mitochondrial alternative oxidase (AOX), previously linked to reduced ROS formation from the electron transport chain and salt tolerance in *Arabidopsis*, also showed a commensurate higher abundance in v. Wyalkatchem in both control and salt-treated conditions. Together, the data presented here suggest that changes in mitochondrial ROS defense pathways in the mitochondrial proteomes of key Australian correlate with whole-plant salinity tolerance.

KEYWORDS

Wheat

Salinity

Mitochondria

Proteome

Alternative Oxidase

Manganese Superoxide Dismutase

Differential In Gel Electrophoresis (DIGE)

Quantitative Proteomics

INTRODUCTION

Wheat is an important crop worldwide, both nutritionally and economically. Due to the size and complexity of the wheat genome, many molecular investigations into wheat have lagged behind other plant species, particularly the model plants, rice and Arabidopsis. However, wheat genetic resources are increasing in size and diversity, and large collections of ESTs are now housed in various databases.¹ Chromosome 3B has recently been physically mapped² and completion of the entire genome sequence is likely to occur in the next few years.³ These advances are increasing the feasibility of applying large scale proteomic approaches to gain mechanistic insight into stress tolerance of this important crop species. Salinity is a severe impediment to agricultural productivity and with the increased use of marginal land required to maintain world food supply, breeders will need to produce crop and fodder plants that exhibit high salinity tolerance. Salinity is an acute problem in the Australian wheat growing regions.⁴ Salinity tolerant species give similar crop yields when exposed to high NaCl concentrations and their tolerance is believed to involve two distinct mechanisms; (1) sodium exclusion, preventing Na⁺ from entering leaves⁵ and (2) tissue tolerance, maintaining cellular function despite accumulating high concentrations of Na⁺ in the plant.⁵ The biochemical mechanisms underpinning tissue tolerance are poorly understood and elucidating them will likely define a new set of targets for molecular crop improvement.⁶ As tolerance is reported as the difference in biomass production under control and salt treatment,⁵⁻⁶ primary metabolic pathways such as the balance of photosynthesis and respiration, that define net CO₂ assimilation, represent key targets for investigation.

The effect of salinity on mitochondrial respiration is yet to be fully characterised, in fact, there are contradictory physiological reports showing that respiration rates increase in response to salt stress,⁷ while others show that it can decrease.⁸ It is likely that these responses probably differ according to species, plant organ, developmental stage, and the severity of salinity treatment. In varietal studies, a salt-sensitive wheat genotype has been reported to have increased respiration rate in response to salt stress, while a salt-tolerant wheat genotype was able to maintain a normal respiration rate,⁹ suggesting that the ability to maintain respiratory homeostasis is linked to salinity

tolerance. A metabolomic comparison of two barley varieties with differing salinity tissue tolerance has also showed that tricarboxylic acid cycle intermediates were higher in abundance in a tolerant variety,¹⁰ which suggests that respiratory metabolism may play a key role in mediating tissue tolerance in this species as well. Other reported links between mitochondrial function and salinity tolerance in plants include enhanced salinity tolerance of *Arabidopsis* by over-expression of mitochondrial proteins.¹¹ There is also clear evidence of overlap between stress defence pathways during abiotic stresses such as temperature, salinity and drought that focus on antioxidant defence in both *Arabidopsis* and rice.¹² Links between such environmental stress tolerances and mitochondrial function in wheat include the link between the alternative pathway of respiration with freezing,¹³ low temperature¹⁴ and drought,¹⁵ as well as the link of mitochondrial proline metabolism with salinity and drought tolerance,¹⁶ and the relatively high degree of ROS-induced damage of mitochondrial proteins compared to those of other organelles in wheat cells.¹⁷

Proteomic techniques have been employed to describe the whole-cell protein responses to various abiotic stresses in many plant species¹⁸ and comparative proteomics has identified varietal specific differences in stress response in a range of crop species, including grape,¹⁹ peanut,²⁰ and wheat.²¹ But these studies rarely enrich protein extracts for the study of lower abundant organelle proteomes. Plant mitochondrial proteomics has been employed to produce inventories of mitochondrial-localised proteins²² as well as identifying which proteins are induced by stress or susceptible to stress-induced damage.²³ However, none of these reports have used mitochondrial proteomics to assess varietal differences in a crop plant.

In this study we report a wheat shoot mitochondrial proteome 2D gel reference map and 199 proteotypic peptides, both are useful resources for wheat mitochondrial targeted proteomics. Using this map and DIGE gels we have quantitatively compared variations in shoot mitochondrial protein abundance between the salt tolerant cultivar Wyalkatchem, and the salt sensitive cultivar Janz. Further we have exposed both varieties to salt stress to determine the mitochondrial protein variations induced under this stress and to identify potential breeding targets for future improvements in wheat salinity tolerance.

EXPERIMENTAL PROCEDURES

Plant growth and salt treatment. For the reference map, seeds of wheat cv. Calingiri were grown in vermiculite in total darkness at constant 24° C for 10 days, at constant 65% humidity. For all other experiments, wheat seeds cv. Wyalkatchem and Janz were grown for 10 days in a recirculating hydroponic solution, with 16/8 photoperiod, 300 $\mu\text{mol m}^{-2} \text{s}^{-1}$ light intensity, day temperature 24° C and night temperature 20° C, at constant 65% humidity. The nutrient solution contained the following 16 mM NO_3^- , 6 mM K^+ , 5 mM Ca^{2+} , 2 mM Mg^{2+} , 2 mM SO_4^{2-} , 500 μM NH_4^+ , 500 μM H_2PO_4^- , 90 μM Fe^{2+} , 10 μM BO_3^{3-} , 2 μM Mn^{2+} , 300 nM Zn^{2+} , 200 nM Cu^{2+} , 100 nM MoO_3 . For plants subjected to salt treatment, NaCl concentration was increased by 50 mM per day between day one and day four, and NaCl concentration remained 200 mM from day four until harvest.

Biomass and respiration measurements. For biomass measurements, shoots were harvested from roots then dried at 65° C for three days and weighed. For respiration measurements, 50 mg of fresh tissue from the first emerging leaf was chopped into ~five mm slices, incubated in one ml respiration buffer (5 mM KH_2PO_4 , 10 mM TES, 10 mM NaCl, 2 mM MgSO_4 , 0.1% (w/v) BSA, pH 7.2) in darkness for 30 min, and respiration was measured in a Clark-type oxygen electrode (Hansatech) for 10 min in darkness. Respiration rates are expressed per one mg of fresh tissue.

Mitochondrial isolation. For all analyses, mitochondria were isolated from whole shoots according to Day *et al.*,²⁴ using differential centrifugation followed by a 0-4.4% PVP-40 gradient. Briefly, ~80 g of leaf tissue was homogenised in 400 mL grinding buffer (300 mM sucrose, 25 mM $\text{Na}_4\text{P}_2\text{O}_7$, 10 mM $\text{K}_4\text{P}_2\text{O}_7$, 2 mM EDTA, 1% (w/v) PVP-40, 1% (w/v) BSA, pH 7.5) using a Polytron homogeniser (Kinematica). Brei was filtered through four layers of Miracloth (Calbiochem) and centrifuged at 1100 g for five min. The supernatant was centrifuged at 18000 g for 20 min, and the resulting pellet was resuspended in 90 ml of wash buffer (300 mM sucrose, 0.1% (w/v) BSA, 10 mM TES, pH 7.5). This was centrifuged at 1100 g for five min, and the supernatant centrifuged at 18000 g for 20 min. The resulting pellet was resuspended in 6-10 ml of wash buffer

and layered onto four continuous 0-4.4% (w/v) PVP-40 Percoll gradients (28% (v/v) percoll, 2.2% (w/v) PVP-40, 300 mM sucrose, 0.1% (w/v) BSA, 10 mM TES, pH 7.5), and centrifuged at 40000 g for 40 min. Mitochondria formed a yellow/brown band between 3.5-4% PVP-40 region of the gradients. The less dense fraction of the gradients (0-3% PVP-40) were aspirated and discarded, the mitochondrial region of the gradients were gently removed and diluted in approximately 320 ml of final wash buffer (300 mM sucrose, 10 mM TES, pH 7.5), and centrifuged at 31000 g for 15 min. The supernatant was discarded, and the pellet was resuspended in approximately 40 ml of final wash buffer, and centrifuged at 31000 g for 15 min. Resulting mitochondrial pellet was resuspended in approximately one ml of final wash buffer. Mitochondria analysed in the reference map were subjected to a second dimension of purification by free-flow electrophoresis by the same method outline in Huang *et al.*^{22a}

Two dimensional polyacrylamide gel electrophoresis (2D PAGE). Procedures for both IEF/SDS-PAGE and Differential In Gel Electrophoresis (DIGE) IEF/SDS-PAGE were identical as outlined below, except CyDye labeling steps were omitted for IEF/SDS-PAGE, and gels were stained with Coomassie brilliant blue G-250. IEF/SDS-PAGE DIGE was conducted according to Eubel *et al.*²⁵ Briefly, 50 µg of acetone-precipitated mitochondrial proteins were resuspended in 10 µL lysis solution (40 mM Tris pH 8.5, 4% (w/v) CHAPS, 8M urea) and labeled for 30 min with 400 pmol of CyDye. Cy2 was always used to label the internal standard, while Cy3 and Cy5 were randomly allocated to the 12 protein samples. Proteins underwent IEF on a 24 cm pH 3-10 non-linear IEF strip, in rehydration solution (8 M urea, 2% (w/v) CHAPS, 0.5% (v/v) IPG buffer, 18 mM DTT, and 0.005% (w/v) bromophenol blue). Following IEF, strips were equilibrated for 15 min in buffer A (1.5 M Tris pH 8.8, 6 M urea, 2% (w/v) SDS, 26% glycerol (v/v), 0.005% bromophenol blue (w/v), 65 mM DTT), then for 15 min in buffer B (identical to buffer A except DTT is replaced by 135 mM IAA), then briefly rinsed in gel buffer, before being loaded onto a 12% (w/v) acrylamide gel. Electrophoresis was conducted at 15 mA per gel for 18 h. Gels were scanned using a Amersham Typhoon Trio laser scanner (GE Healthcare), at 488 nm for Cy2, 532 nm for Cy3, and 633 nm for

Statistical analysis of DIGE images. Statistical analysis of DIGE images was conducted with the DeCyder software package (GE Healthcare). Matched protein spots that displayed t-test $p < 0.05$ when compared between genotypes and/or treatments were deemed statically significant, and therefore selected for identification by mass spectrometry.

Protein identification by LC-MS/MS. Protein identification was conducted according to Meyer *et al.*²⁶ Briefly, gel-bound proteins were excised using a spot picker (Gel Company) and digested with trypsin, then peptides were extracted from gel spots and analysed using an Agilent XCT Ultra Ion Trap mass spectrometer (Agilent Technologies), after LC separation with a home made reverse-phase column (Microsorb C18 silica, bead size 5 μm , pore size 10 nm, Varian) pumped by an Agilent 1100 HPLC (Agilent Technologies) running a 5-60% Acetonitrile, 0.1% formic acid gradient over nine minutes. The first MS step detected ions at scan range of 200-1400 m/z and scan rate 8100 $m/z\ s^{-1}$. Ions with intensity 25000 cps were selected for MS/MS at scan range 70-2200 m/z and scan rate 26000 $m/z\ s^{-1}$. Protein spots analysed for the reference map were excised directly from the gel, whereas proteins identified in the DIGE experiments were identified from matched preparative gels (500 μg protein), where the three biological replicates in the quantitative experiment were pooled and run as for the reference map gel.

Bioinformatics. Raw mass spectrometry data were processed into peak lists (.mgf format) using Data Analysis for MSD Trap Software (version 3.3, Bruker Daltonics). Peak list files were searched using the Mascot search engine (V2.2.03, Matrix Science)²⁷ against three databases: wheat TC (TaGI, release 11, 216,452 sequences),²⁸ wheat EST (TaGI, release 11, 1,034,368 sequences),²⁸ and MSDB (release 20063108, number 3,239,079 sequences). Peptide matches were called positive above a threshold MOWSE score of 51. This cut-off score was chosen because it yielded a false discovery rate of less than 5% for the concatenated set of 192 protein spots of the reference map

searched against the wheat TC database using a target-decoy strategy.

Immunoblots. Anti-Mn-SOD antibodies were obtained from Stressgen (Ann Arbor, USA) and Anti-AOX antibodies were kindly provided by Elthon *et al.*²⁹ 30 µg of mitochondrial proteins were separated via SDS-PAGE using a Criterion mini gel (10-20% Tris-HCl, Bio-Rad) following manufactures instructions and transferred to a nitrocellulose membrane (Hybond C+ Extra, GE Healthcare) by standard procedures. Following overnight blocking with 1% (w/v) blocking solution (Amersham ECL Advance, GE Healthcare), membranes were incubated with primary antibodies (anti-Mn-SOD, 1:5000; anti-AOX, 1:5000) at room temperature for one h, followed by an appropriate secondary antibody (anti-Rabbit IgG POD, 1:20000 or anti-Mouse IgG POD, 1:20000) at room temperature for one h. Chemiluminescence was visualised using an Amersham ImageQuant RT-ECL camera (GE Healthcare) and band intensity quantified using Amersham Image-Quant TL software (GE Healthcare).

RESULTS AND DISCUSSION

Mitochondria have been isolated from wheat and utilised in foundation plant biology studies over four decades, investigating plant respiratory metabolism,³⁰ cytoplasmic male sterility,³¹ the mitochondrial genome,³² organelle RNA processing and editing³³ and the composition of electron transport chain complexes.³⁴ However, a systematic analysis of the wheat mitochondrial proteome has not been reported.

Wheat Mitochondrial Reference Map - Using mitochondria purified by differential centrifugation, Percoll gradient purification and free-flow electrophoresis from shoot tissue of a leading Australian wheat variety, v. Calingiri, a 2D gel reference map was developed (Figure 1). The protein spots were systematically excised and identified and the corresponding mass spectrometry matches to a wheat TC (tentative consensus) database are presented in Supplementary Table 1. Protein descriptions in Table 1 were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue. A table documenting unfiltered peptide matches is presented in Supplementary Table 2. We identified high quality MS/MS spectra for 199 peptides from 68 mitochondrial proteins. These high-quality mass spectra are provided as evidence for proteotypic peptides, and m/z values and peak intensities for precursor and the three most intense MS/MS fragment ions are presented in Supplemental Table 4. This data set provides a transition list to form a foundation for targeted proteomics to study the respiratory apparatus in wheat. A total of 51 high-quality peptides from 23 contaminating proteins, mainly located in the plastid, based on homology to Arabidopsis proteins of known location³⁵ were excluded from further analysis. The number of proteins identified in this study is lower than many proteomic investigations of mitochondria from other species, even those based on 2D gel separations.²² This is mainly due to the limitation of matching proteins to an organism like wheat with an unsequenced genome, as many lower expressed genes are not present in EST libraries, and the redundancy and truncation of sequences in such libraries greatly increases the threshold of peptide ion scores required to maintain acceptable FDR values. In total 27 of the mitochondrial protein identifications presented here (40%)

are only supported by single peptide matches above the ion score threshold of 51, although 15 of these identifications (22%) are further supported by 38 peptides from the same gel spots matching to the same proteins in the 10-51 ion score range. Single peptides above the ion score threshold have often been considered insufficient for a confident match. However, each of these spectra were manually inspected and showed that our relatively high MOWSE score used to call positive matches was in fact sufficient to exclude non-specific matches. This method of calling positive matches is supported by Gupta *et al.*³⁶ which shows that the “two-peptide rule” has little utility in lowering false positive rates in proteomic datasets and that the focus should be on spectra quality in lowering false positive matching.

This reference dataset enables us to investigate inter-species differences in mitochondrial proteomes by comparing the wheat proteome with previously published proteomes from Arabidopsis and rice.²² Supplementary Table 3 shows the closest homologous protein from Arabidopsis and rice for each protein in our wheat mitochondrial set, and details whether these homologues were detected in published mitochondrial proteomes from Arabidopsis and rice. This comparison shows that almost all proteins detected in wheat mitochondria have rice and Arabidopsis homologues previously shown to be localised to mitochondria. There is a good coverage of TCA cycle enzymes and representative subunits for Complex I, II, III, IV and V of the electron transport chain. In addition, representative proteins from the branched chain amino acid degradation pathway and the mitochondria-localised photorespiratory apparatus (GDC/SHMT) are present. Amongst mitochondrial proteins known to vary during environmental stress or involved in stress tolerance, we identified mitochondrial isoforms of heat shock proteins 22, 60, 70 and 90, several antioxidant/redox related proteins including a ferredoxin, Mn-SOD and MDHAR. We also found a nucleotide diphosphate kinase implicated in heat stress response in other plants.³⁷

A number of non-mitochondrial proteins were identified from our reference map (Supplementary Table 1), these included some plastid glycolytic enzymes, highly abundant photosynthetic proteins

and plastid molecular chaperones, which is a common problem in isolating mitochondria from plant tissue. The list of contaminating proteins (Supplementary Table 5) provides a resource for other researchers to exclude these proteins from wheat mitochondrial studies.

Salinity responses in wheat varieties - Field seed yield observations suggest that the cultivar Wyalkatchem exhibits higher salinity tolerance than Janz in the wheat growing regions of Western Australia (Dr B. Biddulph, WA Dept Agriculture, pers.comm). This observation is also reflected in farm practice, with v. Wyalkatchem increasing in use by farmers in salinity prone regions of Western Australia to represent over 30% of the wheat crop in 2009, while Janz use decreased from ~1% of the crop in 2005 to less than 0.3% in 2009.³⁸ Given the hypothesis that mitochondrial respiration can be involved in wheat salinity tolerance, we measured biomass accumulation and mitochondrial respiration rates in shoots from v. Wyalkatchem and v. Janz in hydroponics under control and salt treatments (Figure 2). The 200 mM salt treatment reduced biomass accumulation in both varieties during seedling establishment. Wyalkatchem exhibited higher salinity tolerance than Janz, based on the proportion of biomass retained under salt treatment. Salt treatment induced higher respiration rates in both varieties, an effect corroborated by other studies.^{7, 9} To investigate if the mitochondrial proteomes of Wyalkatchem and Janz differed under control and salt treatments we used 2D DIGE, performed MS/MS on the proteins changing in abundance and compared our result to the reference map (Figure 1.). Four experimental sets were compared: Wyalkatchem control, Janz control, Wyalkatchem salt and Janz salt. Three biological replicate mitochondrial purifications were performed from each variety and treatment and six DIGE gels prepared and analysed. Ten protein spots showed significant differences in abundance ($p < 0.05$ between varieties or treatments) across all biological replicates. These spots were picked from preparative gels from the two varieties, similar to the reference gel (Figure 1), and peptides from in-gel trypsinated samples identified using LC-MS/MS. All 2D DIGE images are presented in supplemental Figure 1, and abundance data and protein match information for the spots of interest are presented in Table 1. Several of the proteins (spots 53, 194, 136) were identified as chloroplastic contaminants based on identifications and

comparison to the reference map (Supplementary Figure 3), and we do not attempt to interpret these difference data any further. However, five mitochondrial proteins were found to change in abundance under salt treatment. The implications for mitochondrial function of each of these changes and possible role in salinity tolerance are discussed below.

Manganese superoxide dismutase (Mn-SOD) - Two Mn-SOD protein spots were identified in the reference gel, distinct by a change in pI (Figure 1, spots 191 and 192). One of these spots, as well as a further Mn-SOD spot not identified on the reference gel, exhibited significantly different abundance values between varieties and treatments in the DIGE experiment (Table 1, spots 191 and 193). Spot 193 displayed higher abundance under salt stress in both varieties, showing that this particular Mn-SOD isoform is induced by salt stress. However, spot 191 exhibited a different response, as it was more abundant in Wyalkatchem than Janz, under both control and salinity treatments. The apparent varietal difference in MnSOD abundance was confirmed by Western blot (Figure 3). MnSOD is encoded at a single locus on the long-arm of Chr 2 in wheat, but due to the hexaploid nature of wheat, this means there are three copies of Mn-SOD derived from each of the parental Chr 2s, namely 2A, 2B and 2D.³⁹ To determine whether the isoforms of Mn-SOD resolved by 2D DIGE actually represented the products of different genes, we studied mass spectra matching to the two expressed Mn-SOD sequences available in the databases that differ in 395 of 652 nucleotides and 6 of 180 amino acids (Supplementary Figure 2). This reveals that the protein encoded by gi19957070 was exclusively identified in Wyalkatchem, and only the products of TC325434 were identified in Janz. Analysis of the sequences from Calingiri identified in the reference gel also only reveal the presence of peptides from the TC325434 sequence. As the genomes of Chr 2A, B and D are not yet determined, we cannot link these transcripts definitively to the parental genome, but it seems very unlikely that the difference between gi19957070 and TC325424 could arise as SNPs of the same gene between wheat varieties.

Mn-SOD is a mitochondrial ROS defence that catalyses the detoxification of superoxide, a highly

reactive ROS species. Several studies have shown that salt stress increases ROS production⁴⁰ and other studies have shown that Mn-SOD activity can increase under salt stress,⁴¹ presumably in response to increased ROS concentrations in the mitochondrion. Furthermore, tolerant varieties of pea, tomato and wheat have been shown to exhibit higher Mn-SOD activity than sensitive varieties⁴¹⁻⁴² and compellingly, transgenic Mn-SOD over-expression enhances salinity tolerance in *Arabidopsis*.^{11b} These results show that Mn-SOD is a key determinant of whole-plant salinity tolerance. Our data, consistent with expression of a specific wheat Mn-SOD isoform in the salt-tolerant Wyalkatchem, may indicate that wheat Mn-SODs possess distinct molecular properties that contribute to salinity tolerance, such as a more robust structure or altered kinetics. These data strengthen the correlation between Mn-SOD abundance and whole-plant salinity tolerance, and identifies two proteotypic peptides (Supplemental Figure 2) from a specific Mn-SOD isoform that is correlated to salinity tolerance in wheat.

Nucleoside diphosphate kinase (NDPK) - A nucleoside diphosphate kinase (NDPK3) was found in one protein spot on the reference gel (spot 129). In the DIGE experiment this spot exhibited higher abundance in Wyalkatchem compared to Janz (Table 1, spot 129), and the abundance of NDPK was significantly lower under salinity treatment in both cultivars. NDPK is known to be located in the intermembrane space of plant mitochondria.⁴³ The function of NDPK is to balance nucleoside triphosphate pools by catalysing the transfer of a phosphate group from ATP to other nucleoside energy carriers in the cell (CTP, GDP, TTP and UTP).⁴³ ATP is produced by catabolism, while other NTPs are consumed during anabolic pathways, so it is widely thought that NDPK links ATP production to protein synthesis and other anabolic pathways.⁴⁴ NDPK has previously been shown as a target of proteolytic breakdown during oxidative stress,^{23a} to associate with ANT during heat stress in pea mitochondria,³⁷ and to be one of three mitochondrial components involved in ATP cycling and transport whose function is impaired in a reversible ROS-dependent fashion during heat induced programmed cell death.⁴⁵ Although our data does not link NDPK to salt stress response, it does show that NDPK abundance is a flexible component of plant mitochondrial metabolism that differs

between these wheat cultivars.

Voltage dependent anion carrier (VDAC)

VDAC was found in two protein spots in the reference gel (spots 99, 100). A decrease in protein abundance during salt treatment was observed for two spots in both wheat varieties (Table 1, spots 97 and 99) which were identified as voltage dependent anion carrier (VDAC), or porin. One of these spots in the DIGE gel matched to the previously unidentified spot 97 from the reference gel (Figure 1). VDAC is a beta barrel protein found on the outer mitochondrial membrane responsible for passage of <1000 Da components into the intermembrane space. Oxidative modification and losses of VDAC function have been observed in mitochondria during fruit senescence,⁴⁶ overexpression of rice VDAC induces mitochondrial-mediated programmed cell death in plants and animal cells⁴⁷ and bacterial pathogen attack leads to rapid gene induction of four of the mitochondrial VDACs in Arabidopsis.⁴⁸ Hence, far from being static components of the outer membrane, dynamic changes in VDAC function and abundance have been found to influence mitochondrial respiration.⁴⁹ The potential for changes in VDAC function in plant mitochondria remains largely unstudied.

Cysteine synthase - Cysteine synthase (CysS) was found in two gel spots in the reference gel (spots 69 and 72). The DIGE experiment showed that v. Wyalkatchem and v. Janz exhibited different abundances of these cysteine synthase (CysS) containing protein spots (Table 1, spots 69 and 72). The differences were reciprocal; the more basic protein spot (pI 6.4) had greater abundance in Wyalkatchem, while the more acidic spot (pI 6.2) was more abundant in Janz. Peptide mass spectrometry indicated that both spots in both varieties were best matched to the same wheat transcript consensus sequence (TC282262). This could suggest that two spots arise from post-translational modification of CysS, and that this differs between the two varieties. Mitochondrial CysS binds to β -cyanoalanine synthase (CAS) to form the cysteine synthase complex, which utilises serine, acetyl-CoA, and cyanide substrates to produce cysteine.⁵⁰ The cysteine produced in this reaction is utilised in a wide variety of general cellular processes, but is needed at high levels for the

synthesis of the glutathione pool.⁵¹ Also, considering its substrates, the cysteine synthase complex regulates the amount of serine exported to the chloroplast during photorespiration, the amount of acetyl-CoA entering the TCA cycle, and helps to prevent cyanide toxicity.⁵² Given this multiplicity of cellular roles, it is plausible that post-translational modification would regulate CysS activity. Recent evidence from phosphoproteomic studies has identified a C terminal phosphorylated serine (S341) in the Arabidopsis homolog of the wheat protein identified in this study (At3g61440).⁵³ Although our data does not link CysS to salt stress or salinity tolerance, it suggests that the abundance of different CysS isoforms, or a post-translational modification, is a flexible component of plant mitochondrial metabolism that differs between these wheat cultivars.

Alternative oxidase – As the literature shows the mitochondrial alternative oxidase (AOX) can prevent over-reduction of the respiratory chain, especially during stress,⁵⁴ is induced by salt stress,^{11a} is more abundant in salt-tolerant crop varieties⁵⁵ and over-expression enhances salinity tolerance in Arabidopsis,^{11a} we decided to directly test if AOX was also increasing in abundance under our salt treatment. The AOX protein is reported to be insoluble in buffers used for isoelectric focusing⁵⁶ and is not detected in our reference gel analysis (Figure 1) or the 2D DIGE experiment, thus the best option for its quantification was via western blotting. Using monoclonal antibodies specific for AOX, we found that v. Wyalkatchem has a higher AOX abundance than v. Janz, both constitutively and under salt treatment (Figure 3). Although Janz did induce AOX under saline conditions, the abundance in isolated mitochondria still did not match the level found in mitochondria isolated from Wyalkatchem.

Conclusion

It is well documented that the antioxidant network in plant mitochondria depends upon the complementary functions of several proteins and pathways.⁵⁷ Plants, such as pea and Arabidopsis, exposed to environmental stresses accumulate ROS, and significant changes in ascorbate/glutathione cycle components, superoxide dismutases, peroxiredoxins, and catalase are observed in organelles

(for review see⁵⁸). Here we identify Mn-SOD and AOX as mitochondrial proteins that correlate (Pearson's correlation coefficient $r = 0.4 - 0.7$) with salinity tolerance of a commercially important wheat variety. Both these proteins are crucial components of the mitochondrial antioxidant network, and both proteins have been previously linked to salinity tolerance in a number of plant species. In plant mitochondria superoxide is detoxified by dismutation into H_2O_2 by MnSOD.⁵⁹ The H_2O_2 detoxification route is either by a thioredoxin-dependent peroxiredoxin⁶⁰ or by the ascorbate/glutathione cycle which begins with the degradation of H_2O_2 to H_2O by ascorbate peroxidase (APX) in the presence of ascorbate.⁵¹ The ascorbate is recycled in a cycle involving the Glu-Cys-Gly tripeptide glutathione (GSH), and the replenishing enzymes monodehydroascorbate reductase (MDHAR), dehydroascorbate reductase (DHAR), and glutathione reductase (GR).^{51, 57b, 61} In addition to increases in Mn-SOD to detoxify superoxide, and changes in CysS that synthesises Cys required for GSH synthesis, we observed increases in AOX that is thought to prevent the over-reduction of the mitochondrial ubiquinone pool, and thus lower the rate of formation of superoxide from the electron transport chain. The link of salinity tolerance to antioxidant defense is further supported by the lack of changes in the mitochondrial proteome of many other components identified in the reference map, for example no changes were observed in over 60 identified components of the TCA cycle, ETC complexes, or of the variety of molecular chaperones and heat shock proteins (Figure 1). Together, the data presented here suggest that mitochondrial ROS defense pathways are the major differences that occur in the mitochondrial proteomes of key Australian wheat varieties, and that these differences correlate (Pearson's correlation coefficient $r = 0.4 - 0.7$) with whole-plant salinity tolerance.

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FIGURE CAPTIONS

Figure 1: 2D reference gel of the wheat mitochondrial proteome. 500 µg protein from FFE-purified wheat mitochondria were separated by IEF/SDS-PAGE. Gel was stained with colloidal Coomassie blue. 192 protein spots were excised and digested with trypsin, tryptic peptides were analysed via LC-MS/MS. Protein identification data is shown in supplementary Tables 1 and 2.

Figure 2: Biomass accumulation (a) and respiration rates (b) in Wyalkatchem and Janz under control (white bars) and salinity (grey bars) treatments. For biomass measurements, shoots were taken from 10 day old shoots plants, then dried at 60° C for three days and weighed. Six biological replicates were performed. For respiration measurements, the first leaf was taken from nine-day old plants, chopped into five mm segments, equilibrated in respiration buffer for 30 min in darkness, and oxygen consumption was assayed in a Clark-type oxygen electrode for 10 minutes in darkness. Four biological replicates were performed. Error bars represent SEM.

Figure 3: Representative immunoblot images of wheat mitochondrial samples with antibodies raised against AOX (a) and Mn-SOD (b). Three biological replicates were assessed. Abundance was quantified from Western blot images using Amersham ImageQuant TL (GE Healthcare). W represents Wyalkatchem, J represents Janz. White bars represent control treatment, grey bars represent salt treatment, error bars represent SEM.

TABLES.

Table 1: Changes in abundance and protein identification information for protein spots that displayed significant differences ($p < 0.05$) in abundance in the DIGE experiment. Spot numbers refer to supplementary Figure 1. Abundance data was calculated with Amersham DeCyder software, after measured spot intensity was normalised to the internal standard (pooled mixture of all 12 samples). W represents Wyalkatchem, J represents Janz, white bars represent control treatment, grey bars represent salinity treatment, error bars represent SEM. Accession refers to the highest scoring match in the wheat TC database (TaGI release 11). MOWSE score is the probability-based score of match quality calculated by the Mascot search engine. Number of peptides refers to the number of matched peptides with ions score greater than 51 ($p < 0.05$).

SUPPORTING INFORMATION AVAILABLE

Supplementary Figure 1: DIGE images detailing protein spots that exhibited significant differences in abundance between varieties or treatments. The experiment compared protein abundance in mitochondria isolated from four experimental groupings: Wyalkatchem control, Janz control, Wyalkatchem salt, and Janz salt. Three biological replicates were performed. DIGE gels contained 50 µg mitochondrial proteins labeled with Cy3 (green) and 50 µg mitochondrial proteins labeled with Cy5 (red). Cy3 and Cy5 images were overlayed, such that protein spots equally abundant in the two samples are yellow, protein spots more abundant in Cy3 sample are green, and protein spots more abundant in Cy5 sample are red. Numbered protein spots showed significant difference in abundance between varieties or treatments ($p < 0.05$). For these spots, abundance data and protein identification details are shown in Table 1. Spot numbers follow the reference gel in Figure 1.

Supplementary Figure 2: MS/MS spectra of Mn-SOD peptides detected only in Wyalkatchem spot 191 are shown in (a) and (c). MS/MS spectra of Mn-SOD peptides detected in Wyalkatchem spot 193 as well as Janz spots 191 and 193, are shown in (b) and (d). Detected ions matched to the theoretical fragment y-series and b-series ions masses by Mascot are annotated on the spectra. ClustalW sequence alignment of the two amino acid sequences (gi19957070 and TC325434) is shown in (e).

Supplementary Figure 3: Changes in abundance and protein identification information for contaminating protein spots that displayed significant differences ($p < 0.05$) in abundance according to salt treatment in the DIGE experiment. All three spots are from proteins localised to the plastid. Spot numbers refer to supplementary Figure 1. Abundance data was calculated with Amersham DeCyder software, after measured spot intensity was normalised to the internal standard (pooled mixture of all 12 samples). W represents Wyalkatchem, J represents Janz, white bars represent control treatment, grey bars represent salinity treatment. Accession refers to the highest scoring match in the wheat TC database (TaGI release 11). MOWSE score is the probability-based score of match quality calculated by the Mascot search engine. Number of peptides refers to the number of matched peptides with ions score greater than 51 ($p < 0.05$).

Supplementary Table 1: Wheat mitochondrial proteins confidently identified in this study. Identified proteins are listed by functional class. Spot number refers to Figure 1. Accession refers to the highest-scoring match in the wheat TC database (TaGI release 11). Protein descriptions in Table 1 were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue from either species. Matched peptides is the number of peptides with ions score >51 matched to that accession. For single peptide matches, numbers in brackets denotes low scoring peptides (ions score between 10-50) from the same gel spot that also matched that accession. Gel MW and gel pI were determined from Figure 1, calc MW and calc pI were calculated using Mascot.

Supplementary Table 2: Unfiltered peptide-level information for 192 protein spots analysed in Figure 1 and results from search against three databases (Wheat TC, Wheat EST, MSDB). Spot number refers to Figure 1. Prot_hit_num is the ranking of each protein hit. Prot_score is calculated by Mascot based on combined MOWSE scores of matched peptides. Protein hits presented here were filtered according to prot_score ($p < 0.05$). Prot_acc and prot_desc are accession code and description line of the protein match, copied directly from the database. Prot_mass is the theoretical MW of the protein, calculated by Mascot. Prot_match is the number of peptides matched to that accession (ions score cut-off of 0). Prot-cover is the percentage of the sequence covered by matched peptides. Pep_exp_mz is the observed m/z of the peptide. Pep_exp_mr is experimental m/z transformed to a relative molecular mass. Pep_calc is the relative molecular mass calculated from the matched peptide sequence. Pep_delta is the difference (error) between the experimental and calculated masses. Pep_miss is the number of missed cleavages. Pep_score is the ions score of each peptide. Pep_res_before, pep_seq, and pep_res_after are sequence of the peptide in 1-letter code, along with the residues that bracket the peptide sequence in the protein (if the peptide forms the protein terminus, then a dash is shown instead). Pep_var_mod details any modifications to the peptide.

Supplementary Table 3: Cross-species comparison of mitochondrial proteins detected in this study. Accession refers to the wheat TC database (TaGI release 11). Arabidopsis homologue is the highest scoring hit returned when the accession was BLAST-searched against TAIR 7. Mitochondrial localisation details publications that report the Arabidopsis homologue gene as being mitochondrial-localised. Rice homologue is the highest scoring hit returned when the accession was BLAST-searched against Osa 5. Mitochondrial localisation – Huang 2009 details whether that homologue gene was detected in a 2D gel study of FFE-purified rice mitochondrial proteins (Huang 2009).

Supplementary Table 4: Detailed mass spectral information for the 199 peptides derived from 68 mitochondrial proteins confidently identified in this study (ions score >51). Spot number refers to Figure 1. Accession refers to the highest-scoring match in the wheat TC database (TaGI release 11). Protein descriptions were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue. Matched peptides is the number of peptides with ions score >51 matched to that accession. Ions score and predicted masses were determined by the Mascot search engine. Observed masses and intensities were extracted from raw peak list files. Table contains m/z values and peak intensities for precursor and the three most intense MS/MS fragment ions.

Supplementary Table 5: Detailed mass spectral information for the 51 peptides derived from 23 contaminating proteins confidently identified in this study (ions score >51). Spot number refers to Figure 1. Accession refers to the highest-scoring match in the wheat TC database (TaGI release 11). Protein descriptions were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue. Matched peptides is the number of peptides with ions score >51 matched to that accession. Ions score and predicted masses were determined by the Mascot search engine. Observed masses and intensities were extracted from raw peak list files. Table contains m/z values and peak intensities for precursor

and the three most intense MS/MS fragment ions.

Figure 1

Figure 2

Figure 3

a) AOX

b) Mn-SOD

Table 1

Spot	Abundance data	Description	Accession	MOWSE score	# Peptides
193		Manganese superoxide dismutase	TC326013	130	2
191		Manganese superoxide dismutase	gi19957070* (W), TC325434 (J)	145 (W), 132 (J)	2 (W), 2(J)
129		Nucleoside diphosphate kinase	TC280395	132	2
72		Cysteine synthase	TC330390	150	2
69		Cysteine synthase	TC330390	124	2
97		Outer mitochondrial membrane porin	TC277580	116	2
99		Outer mitochondrial membrane porin	TC307500	146	2

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TABLE OF CONTENTS SYNOPSIS AND GRAPHIC

TOC graphic

TOC synopsis

Here we investigate the mitochondrial proteome and differences associated with salinity tolerance in Australian varieties of wheat. We present a 2D reference map of the mitochondrial proteome from v. Calingiri, and use 2D DIGE and western blot to identify quantitative differences between mitochondrial proteomes of v. Wyalkatchem and v. Janz, under both control and salt-treated conditions. Proteins shown to differ in abundance include: Mn-SOD, cysteine synthase, NDPK, VDAC and AOX.

Supplementary table 1

Wheat mitochondrial proteins confidently identified in this study. Identified proteins are listed by functional class. Spot number refers to Figure 1. Accession refers to the highest-scoring match in the wheat TC database (TaGI release 11). Protein descriptions in Table 1 were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue from either species. Matched peptides is the number of peptides with ions score >51 matched to that accession. For single peptide matches, numbers in brackets denotes low scoring peptides (ions score between 10-50) from the same gel spot that also matched that accession. Gel MW and gel pl were determined from Figure 1, calc MW and calc pl were calculated using Mascot.

Funtional class	Spot number	Accession	Protein	# Matched peptides	MOWSE score	% Cov.	Gel MW	Gel pl	Calc MW	Calc pl
Electron Transport Chain	10	TC294283	Succinate dehydrogenase subunit 1	1 (4)	52	2.2	63	5.8	84	6.9
	17	TC287805	Mitochondrial processing peptidase beta subunit	1 (5)	69	1.7	58	5.5	58	5.5
	22, 23	TC312825	ATP synthase beta chain	10	917	20.2	51, 51	5, 5.1	75	6.6
	22, 23	CF554354	ATP synthase beta chain	1 (0)	66	22	51, 51	5, 5.1	6	4.2
	27, 28, 29, 30	TC277166	ATP synthase alpha subunit	8	444	13.6	51, 51, 51, 51	5.7, 5.7, 5.8, 5.8	78	9.2
	34	TC278636	Mitochondrial processing peptidase alpha subunit	2	112	8	51	6.3	41	8.7
	35	TC282024	Mitochondrial processing peptidase alpha subunit	3	175	14.7	51	6.5	33	9.6
	94	TC282611	Gamma carbonic anhydrase	1 (1)	84	5.3	30	7	46	8.8
	78	CA698948	Cytochrome oxidase VIB	3	161	17.4	31	3.5	24	5.1
	91	CK197437	NADH-cytochrome b5 reductase	1 (0)	53	6	28	6.6	21	9.4
	106	TC286019	ATP synthase 24 kDa subunit	4	176	15	27	5.4	38	8.4
	106, 107	TC287957	ATP synthase 24 kDa subunit	4	217	11	27, 27	5.4, 5.7	43	9.1
	113, 114	CK194120	ATP synthase delta chain	1	123	4.1	24, 24	4.1, 4.4	25	9.2
	116	CK217579	ATP synthase D chain	1 (4)	70	3.6	24	4.6	33	8.8
	119	CK213510	Complex 1 subunit B13	1 (0)	74	9.3	20	4	38	8.3
	138	TC303680	Complex 1 subunit B22	1 (1)	67	4.2	17	6.5	26	7.5
	139	CK194459	Complex 1 subunit PDSW	1 (0)	62	6.7	16	6.7	19	9.5
	183	TC280819	Complex 1 carbonic anhydrase	1 (3)	58	2.2	32	6.3	38	6.9
	185	TC301455	NADH-ubiquinone oxidoreductase 24 kDa subunit	2	83	6.4	27	6.1	49	8.1
TCA cycle	19	TC290685	Lipoamide dehydrogenase	4	194	14.2	53	6.5	45	5.8
	20, 156	TC279818	Lipoamide dehydrogenase	7	364	19.7	53, 53	6.9, 6.8	55	8
	39	TC281405	2-oxoglutarate dehydrogenase E2 subunit	2	157	5.5	47	5.6	63	8
	40	TC279660	Fumarase	2	153	8.1	47	6.8	41	9.4
	40	TC284402	Fumarase	2	157	6.2	47	6.8	38	8.8
	53	TC278426	Succinyl-CoA ligase beta chain	1 (2)	58	2.8	43	5.4	43	9.4
	62	TC312589	Pyruvate dehydrogenase E1 beta subunit	2	96	5.4	40	4.7	43	8.9
	63	TC279495	Pyruvate dehydrogenase E1 beta subunit	2	97	4.7	40	5	56	8.8
	65, 66	CK154109	Succinyl-CoA ligase alpha chain	2	151	13.9	38, 38	6.3, 6.8	17	9.9
	70, 178	TC278653	Malate dehydrogenase	3	230	9.9	35, 35	6.1, 5.7	37	9.2
C,N,P metabolism	71, 73	TC278151	Malate dehydrogenase	3	257	10	35, 35	6.2, 6.5	42	8.2
	25, 26, 157	TC296475	Methylmalonate semi-aldehyde dehydrogenase	8	398	11.5	51, 51, 51	5.4, 5.5, 5.9	77	8.6
	26	TC307553	Methylmalonate semi-aldehyde dehydrogenase	1 (3)	58	4	51, 5.5		42	9.2
	28, 29, 30	TC284017	Aldehyde dehydrogenase	8	561	16.8	51, 51, 51	5.7, 5.8, 5.8	68	5.6
	30	TC295031	Aldehyde dehydrogenase	1 (0)	56	3.1	51	5.8	38	10
	46	TC287863	Formate dehydrogenase	3	136	7.9	43	6.6	51	8.6
	57	TC289939	Isovaleryl-CoA dehydrogenase	3	171	8.4	43	6	60	9.5
	69, 72	TC282262	Cysteine synthase	2	146	6.2	34, 34	6.1, 6.3	38	9.2
	89	TC297356	Adenylate kinase	2	161	7.8	30	6.5	41	8.3
	96	TC283468	Adenylate kinase	1 (0)	166	7.2	30	7.1	42	9.8

	169	TC334873	Aspartate aminotransferase	1 (5)	53	2.2	43	5.2	60	9.1
Photorespiration	2, 3, 4, 147	TC283187	Glycine decarboxylase P subunit	9	651	12.4	97, 97, 97, 85	6.2, 6.2, 6.3, 6.3	90	6
	38, 77	TC356717	Serine hydroxymethyltransferase	7	341	15.4	51, 33	6.9, 6.7	64	9
	50	TC298963	Aminomethyltransferase	2	101	6	43	7.5	43	8.6
	131	CK215900	Glycine decarboxylase H subunit	1 (0)	133	5.2	16	3.8	35	6.8
Molecular Chaperones	149, 151	TC308079	Heat shock protein 70	3	90	6.5	64, 64	5.1, 5.3	55	8.9
	149	TC324780	Heat shock protein 70	1 (0)	54	5.2	64	5.1	25	10
	150, 151	TC292635	Heat shock protein 70	2	77	6.2	64	5.2	41	5.6
	11	TC302569	Heat shock protein 60	14	561	32.3	58	4.5	66	4.9
	11	TC279929	Heat shock protein 60	8	341	15.4	58	4.5	32	8.9
	13, 14, 15, 16, 148, 159	TC338148	Heat shock protein 60	10	1007	18.2	58, 58, 58, 58, 72, 47	4.9, 5.1, 5.1, 5.2, 5.0, 5.4	74	7.9
	15	TC282575	Heat shock protein 60	4	407	11	58	5.1	45	8.6
	155	TC317092	Heat shock protein 60	6	335	17.6	55	4.6	66	6.7
	81	TC297661	GrpE co-chaperone	3	165	9	30	3.8	45	6.2
	93	TC283205	Prohibitin	1 (1)	54	4.1	28	6.8	40	8.5
	102	TC295614	Chaperonin 20	1 (4)	68	4.7	27	4.5	35	9.1
	105	TC278575	Chaperonin 20	2	106	6.9	26	5.2	36	9.1
	121	TC308127	Heat shock protein 22	1 (0)	53	3.1	20	5	31	9
	141	TC277946	Chaperonin 10	1 (3)	78	1	14	7.5	32	9
	143	TC295456	Heat shock protein 90	1 (2)	65	2.7	93	4.1	58	5
Antioxidant defense	192	TC362013	Mn superoxide dismutase	1 (6)	103	2	25	6.5	59	9.5
	39	TC314827	Monodehydroascorbate reductase	1 (0)	77	3.4	47	5.6	44	7.7
Metabolite Transport	99, 100	TC277379	Outer mitochondrial membrane porin	2	104	5.7	26, 26	8.0, 8.3	42	9
Unknown	123	CK164007	Uncharacterised CBS domain-containing protein	2	83	5.8	17	7.1	36	9
	128	TC362955	Ferredoxin	3	135	8.4	17	4.6	38	8.8
	161	TC282084	Uncharacterised DJ-1 domain-containing protein	2	95	6.2	46	5.5	45	5.8
	185	TC307909	Uncharacterised fumarylacetoacetate hydrolase family prote	1 (0)	55	4.1	28	6.3	36	8.7
Contaminants	6	TC309836	Transketolase	4	157	9.4	70	5.4	66	7
	6	TC283917	Transketolase	2	74	9.5	70	5.4	28	8.8
	31, 33, 76, 86, 87, 134, 182	TC356437	RuBisCo large subunit	4	327	5.7	51, 51, 34, 30, 16, 32	6.2, 6.3, 6.6, 6.3, 5.2, 6.1	77	8.8
	51, 53	TC317220	RuBisCo activase	3	152	8.7	43	5.3	60	9
	68	TC283350	Fructose-bisphosphate aldolase	1 (3)	81	2.6	40	5.3	38	9.1
	82	TC287942	Inorganic pyrophosphatase	2	103	6.9	31	4.3	35	5.2
	103, 104	TC298182	Triosephosphate isomerase	1 (2)	169	6.3	27, 27	5.0, 5.2	49	6.9
	111, 112	TC278554	Peroxiredoxin	2	104	6.5	25, 25	4.3, 4.5	37	8.6
	126	CK216997	Cu/Zn superoxide dismutase	1 (1)	51	4.3	17	5.1	37	10.6
	136	TC349826	RuBisCo small subunit	1 (5)	74	10	16	6	37	9.2
	160	TC310800	6-phosphogluconate dehydrogenase	1 (3)	54	2.7	47	5.7	69	6.3
	163	TC316257	3-oxoacyl synthase	2	89	5.1	45	6.4	50	5.7
	163	TC291224	3-oxoacyl synthase	2	102	10.2	45	6.4	28	6.5
	167	TC334565	Pyruvate dehydrogenase E1 alpha subunit	1 (1)	52	3.4	40	5.6	41	10
	175	TC281478	Fructose-bisphosphate aldolase	1 (6)	73	2.9	40	5.6	48	7.1
	176	TC342749	Fructose-bisphosphate aldolase	2	121	7.4	40	5.8	39	9.7
	13, 14	TC282663	Heat shock protein 60	5	288	18.6	58, 58	4.9, 5.1	40	9.4
	14	TC323689	Heat shock protein 60	5	214	8.3	58	5.1	79	8.6
	5	TC318499	Heat shock protein 70	2	110	4.3	67	4.3	69	5.1
	145	TC322003	Heat shock protein 90	1 (1)	85	2.3	95	5.5	71	8.2
	5	TC299996	Heat shock protein 70	6	223	9.1	67	4.3	87	5.2
	146	TC287865	Heat shock protein 90	1 (2)	72	1.5	85	5.4	81	5.6

|

146 TC331352 Heat shock protein 90

1 (0)

63

4.5

85

5.4

34

9.9

Supplementary table 2

Unfiltered peptide-level information for 192 protein spots analysed in Figure 1 and results from search against three databases (Wheat TC, Wheat EST, MSDB). Spot number refers to Figure 1. Prot_hit_num is the ranking of each protein hit. Prot_score is calculated by Mascot based on combined MOWSE scores of matched peptides. Protein hits presented here were filtered according to prot_score (p<0.05). Prot_acc and prot_desc are accession code and description line of the protein match, copied directly from the database. Prot_mass is the theoretical MW of the protein, calculated by Mascot. Prot_match is the number of peptides matched to that accession (ions score cut-off of 0). Prot-cover is the percentage of the sequence covered by matched peptides. Pep_exp_mz is the observed m/z of the peptide. Pep_exp_mr is experimental m/z transformed to a relative molecular mass. Pep_calc is the relative molecular mass calculated from the matched peptide sequence. Pep_delta is the difference (error) between the experimental and calculated masses. Pep_miss is the number of missed cleavages. Pep_score is the ions score of each peptide. Pep_res_before, pep_seq, and pep_res_after are sequence of the peptide in 1-letter code,along with the residues that bracket the peptide sequence in the protein (if the peptide forms the protein terminus, then a dash is shown instead). Pep_var_mod details any modifications to the peptide.

1 2	Mascot output																	
	nohit																	
	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod	
	1	TC283187	UniRef100_Q22575 Cluster: Glycine decarboxylase P subunit; n=1; x Tritordeum sp. Rep: Glycine decarboxylase P subunit - x Tritordeum sp, partial (62%)	425	89535	9	13.7	469.32	936.6254	936.4301	0.1953	0	54.09	R	VDNVYGD	N		
	1							491.6	981.1854	980.5039	0.6815	0	29.31	K	ADAHNNVLK	G		
	1							611.45	1220.885	1220.659	0.2268	0	60.06	K	IAILNANYMAK	R		
	1							647.99	1293.965	1293.651	0.3149	0	32.88	R	EYAAFPAAWLR	G		
	1							752.96	1503.905	1503.699	0.2067	0	107.49	K	ITCADANIAEEAR	K	Carbamidomethyl (C)	
	1							789.52	1577.025	1576.748	0.2778	0	57.33	K	LNATVEMMPVTDPK	F	2 Oxidation (M)	
	1							821.04	1640.065	1639.868	0.1972	0	10.01	R	GVNGTVAHFIDLR	G		
	1							905.55	1809.085	1808.956	0.1294	0	62.83	K	LGTVTVQELPYFDTVK	I		
	1							617.7	1850.078	1850.84	-0.7617	0	10.83	K	DLSLCHSMPLGSC	TMK	Oxidation (M)	
	2	TC290766	UniRef100_Q22575 Cluster: Glycine decarboxylase P subunit; n=1; x Tritordeum sp. Rep: Glycine decarboxylase P subunit - x Tritordeum sp, partial (33%)	274	37153	5	22.3	750.02	1498.025	1497.852	0.174	0	37.96	R	IIGVSDSSGKPALR	M		
	2							752.96	1503.905	1503.699	0.2067	0	107.49	K	ITCADANIAEEAR	K	Carbamidomethyl (C)	
	2							789.52	1577.025	1576.748	0.2778	0	57.33	K	LNATVEMMPVTDPK	F	2 Oxidation (M)	
	2							905.55	1809.085	1808.956	0.1294	0	62.83	K	LGTVTVQELPYFDTVK	I		
	2							617.7	1850.078	1850.84	-0.7617	0	10.83	K	DLSLCHSMPLGSC	TMK	Oxidation (M)	
	3	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
		1	TC283187	UniRef100_Q22575 Cluster: Glycine decarboxylase P subunit; n=1; x Tritordeum sp. Rep: Glycine decarboxylase P subunit - x Tritordeum sp, partial (62%)	707	89535	16	17.9	437.38	872.7454	872.4967	0.2487	0	49.31	K	IVAVGTDAK	G	
		1							469.38	936.7454	936.4301	0.3153	0	56.47	R	VDNVYGD	N	
1								491.31	980.6054	980.5039	0.1015	0	35.7	K	ADAHNNVLK	G		
1								529.02	1056.025	1056.556	-0.5309	0	61.83	K	GNINIEELR	K		
1								1057.75	1056.743	1056.556	0.1864	0	14.14	K	GNINIEELR	K		
1								600.96	1199.905	1199.603	0.3021	0	59.32	K	ATAGIEPEDVAK	R		
1								611.49	1220.965	1220.659	0.3068	0	63.41	K	IAILNANYMAK	R		
1								647.91	1293.805	1293.651	0.1549	0	52.51	R	EYAAFPAAWLR	G		
1								752.97	1503.925	1503.699	0.2267	0	97.51	K	ITCADANIAEEAR	K	Carbamidomethyl (C)	
1								781.5	1560.985	1560.753	0.2327	0	70.94	K	LNATVEMMPVTDPK	F	Oxidation (M)	
1								789.52	1577.025	1576.748	0.2778	0	39.93	K	LNATVEMMPVTDPK	F	2 Oxidation (M)	
1								821.11	1640.205	1639.868	0.3372	0	7.06	R	GVNGTVAHFIDLR	G		
1								547.86	1640.558	1639.868	0.69	0	32.5	R	GVNGTVAHFIDLR	G		
1								905.55	1809.085	1808.956	0.1294	0	87.99	K	LGTVTVQELPYFDTVK	I		
1								905.61	1809.205	1808.956	0.2494	0	22.35	K	LGTVTVQELPYFDTVK	I		
1								784.45	2350.328	2350.284	0.0444	0	39.92	K	HLAPFLPSHPVIPTGGFPLPET			
2		TC346658	homologue to UniRef100_Q22575 Cluster: Glycine decarboxylase P subunit; n=1; x Tritordeum sp. Rep: Glycine decarboxylase P subunit - x Tritordeum sp, partial (20%)	160	31464	5	20	600.96	1199.905	1199.603	0.3021	0	59.32	K	ATAGIEPEDVAK	R		
2								611.49	1220.965	1220.659	0.3068	0	63.41	K	IAILNANYMAK	R		
2								821.11	1640.205	1639.868	0.3372	0	7.06	R	GVNGTVAHFIDLR	G		
2							547.86	1640.558	1639.868	0.69	0	32.5	R	GVNGTVAHFIDLR	G			
2							712.02	2133.038	2132.086	0.952	0	4.63	-	NQGLSTQPSVHVSSIHDLT	-			
4	prot_hit_nu	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod		
	1	TC283187	UniRef100_Q22575 Cluster: Glycine decarboxylase P subunit; n=1; x Tritordeum sp. Rep: Glycine decarboxylase P subunit - x Tritordeum sp, partial (62%)	445	89535	9	10.6	437.38	872.7454	872.4967	0.2087	0	38.16	K	IVAVGTDAK	G		
	1							491.34	980.6654	980.5039	0.1615	0	47.72	K	ADAHNNVLK	G		
	1							529.41	1056.805	1056.556	0.2491	0	56.01	K	GNINIEELR	K		
	1							547.92	1093.825	1093.559	0.2664	0	69.76	R	FCDALISIR	E	Carbamidomethyl (C)	
	1							600.97	1199.925	1199.603	0.3221	0	50.67	K	ATAGIEPEDVAK	R		
	1							647.54	1293.065	1293.651	-0.5851	0	47.6	R	EYAAFPAAWLR	G		
	1							781.5	1560.985	1560.753	0.2327	0	83.45	K	LNATVEMMPVTDPK	F	Oxidation (M)	
	1							789.49	1576.965	1576.748	0.2178	0	61.61	K	LNATVEMMPVTDPK	F	2 Oxidation (M)	
	1							905.63	1809.245	1808.956	0.2894	0	51.14	K	LGTVTVQELPYFDTVK	I		
	5	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
		1	TC299996	homologue to UniRef100_A4ZYQ0 Cluster: Chloroplast heat shock protein 70; n=1; Pennisetum glaucum Rep: Chloroplast heat shock protein 70 - Pennisetum americanum (Pearl mil	473	86607	9	12.9	437.37	872.7254	872.4426	0.2829	0	44.63	K	LDCPAIGK	Q	Carbamidomethyl (C)
1								451.43	900.8454	900.4665	0.379	0	60.03	R	TPVDNSLR	D		
1								485.93	969.8454	969.5243	0.3211	0	19.42	K	HIETTLTR	G		
1								491.96	981.9054	981.5859	0.3196	0	77.35	R	IPAVQDLVK	K		
1								694.47	1386.925	1386.736	0.19	0	59.67	K	EIDEVILVGGSTR	I		
1								705.53	1409.045	1408.683	0.3621	0	68.79	K	NQAESVIYQTEK	Q		
1								791.04	1580.065	1579.8	0.266	0	14.11	K	AVITVPAYFNDSQR	T		
1								799.93	1597.845	1597.638	0.2074	0	60.33	K	TGDGGDVIDADFTDSN	-		
1								862.54	1723.065	1722.883	0.1826	0	68.41	R	INEPTAASLAYGFKE	K		
2		TC318499	similar to UniRef100_A7PGX4 Cluster: Chromosome chr17 scaffold_16, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr17 scaffold_16, whole genome sh	162	68852	3	5.7	506.98	1011.945	1011.571	0.3742	0	25.55	R	IPAVQETVR	K		
2								691.46	1380.905	1380.652	0.2533	0	68.31	K	NQADSIVIYQTEK	Q		
2							862.54	1723.065	1722.883	0.1826	0	68.41	R	INEPTAASLAYGFKE	K			
3	TC345059	similar to UniRef100_Q1SKX2 Cluster: Chaperone DnaK; n=1; Medicago truncatula Rep: Chaperone DnaK - Medicago truncatula (Barrel medic), partial (73%)	144	75687	4	7.2	437.37	872.7254	872.4426	0.2829	0	44.63	K	LDCPAIGK	Q	Carbamidomethyl (C)		
3							506.98	1011.945	1011.571	0.3742	0	25.55	R	IPAVQETVR	K			
3							862.54	1723.065	1722.883	0.1826	0	68.41	R	INEPTAASLAYGFKE	K			
3							968.13	1934.245	1935.029	-0.7834	0	5.52	K	VFSGLTTACLLAWPTSR	S			
6	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod	
	1	TC309836	similar to UniRef100_Q7SIC9 Cluster: Transketolase, chloroplast; n=1; Zea mays Rep: Transketolase, chloroplast - Zea mays (Maize), partial (64%)	340	65834	6	12.5	422.91	843.8054	844.4443	-0.6388	0	49.24	K	FGASAPAPK	I		
	1							568.11	1134.205	1134.596	-0.39	0	21.52	K	SVTDKPTMIK	V	Oxidation (M)	
	1							586.44	1170.865	1170.624	0.241	0	59.5	K	ESVLPEAVTAR	I		
	1							680.43	1358.845	1358.698	0.1478	0	67.99	R	NLSQQCLNALAK	V	Carbamidomethyl (C)	
	1							725.52	1449.025	1448.751	0.2744	0	68.85	K	EYGITAENVIAAAK	S		
	1							1030.21	2058.405	2058.103	0.3024	0	73.22	K	VVPLIGGSADLASSNMTLLIM	S	Oxidation (M)	
	2	TC283917	similar to UniRef100_Q7SIC9 Cluster: Transketolase, chloroplast; n=1; Zea mays Rep: Transketolase, chloroplast - Zea mays (Maize), partial (13%)	160	27753	3	12.9	422.91	843.8054	844.4443	-0.6388	0	49.24	K	FGASAPAPK	I		
	2							586.44	1170.865	1170.624	0.241	0	59.5	K	ESVLPEAVTAR	I		
	2							711.9	1421.785	1421.74	0.0453	0	51.66	K	EYGITAESVIAAAK	S		
	3	CV522195	similar to UniRef100_Q7SIC9 Cluster: Transketolase, chloroplast; n=1; Zea mays Rep: Transketolase, chloroplast - Zea mays (Maize), partial (8%)	118	6993	3	52.3	422.91	843.8054	844.4443	-0.6388	0	49.24	K	FGASAPAPK	I		
	3							586.44	1170.865	1170.624	0.241	0	59.5	K	ESVLPEAVTAR	I		
3							540.24	1617.698	1616.762	0.9365	0	9.1	-	LDVYMYTSSGRPGR	Y	Oxidation (M)		

7	nohit																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
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[illegible]

3	TC295031	homologue to UniRef100_Q93X16 Cluster: Mitochondrial aldehyde dehydrogenase ALDH2; n=1; Hordeum vulgare Rep: Mitochondrial aldehyde dehydrogenase ALDH2 - Hordeum vulg	88	37984	2	5.3	397.9	793.7854	793.397	0.3884	0	31.74 K	FVDAASGK	T			
3							596.37	1190.725	1190.505	0.2203	0	56.44 R	VSEGDAEDVDR	A			
31	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC356437	UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - Triticum aestiv	286	77238	7	9.7	511.43	1020.845	1020.524	0.3214	0	74.79 K	DTDLAAFR	V		
1	1							558.9	1115.785	1115.576	0.2097	0	51.15 R	VALEACVQAR	N	Carbamidomethyl (C)	
1	1							655.48	1308.945	1308.675	0.2707	0	58.13 R	EMTLGFVDLLR	D	Oxidation (M)	
1	1							655.53	1309.045	1308.675	0.3707	0	47.46 R	EMTLGFVDLLR	D	Oxidation (M)	
1	1							670.44	1388.865	1338.634	0.2311	0	30.43 K	FEFEPVDITDK	-		
1	1							704.49	1406.965	1406.661	0.3049	0	27.98 K	LTYYTPEYETK	D		
1	1							604.17	1809.488	1809.803	-0.3144	0	43.77 K	GHYLNATAGTCEEMIK	R	Carbamidomethyl (C); Oxidation (M)	
32	nohit																
33	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC356437	UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - Triticum aestiv	177	77238	5	6.1	559.32	1116.625	1115.576	1.0497	0	68.96 R	VALEACVQAR	N	Carbamidomethyl (C)	
1	1							655.3	1308.585	1308.675	-0.0893	0	48.28 R	EMTLGFVDLLR	D	Oxidation (M)	
1	1							655.49	1308.965	1308.675	0.2907	0	50.12 R	EMTLGFVDLLR	D	Oxidation (M)	
1	1							670.37	1338.725	1338.634	0.0911	0	15.83 K	FEFEPVDITDK	-		
1	1							704.45	1406.885	1406.661	0.2249	0	42.34 K	LTYYTPEYETK	D		
2	2	TC343520	homologue to UniRef100_P27807 Cluster: Histone H2B.1; n=1; Triticum aestivum Rep: Histone H2B.1 - Triticum aestivum (Wheat), partial (79%)	94	50855	3	6.6	559.32	1116.625	1115.576	1.0497	0	68.96 R	VALEACVQAR	N	Carbamidomethyl (C)	
2	2							565.47	1428.925	1128.553	0.3729	0	9.45 K	YCVDFSII	-	Carbamidomethyl (C)	
2	2							670.37	1338.725	1338.634	0.0911	0	15.83 K	FEFEPVDITDK	-		
34	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC278636	similar to UniRef100_Q9FNU9 Cluster: Mitochondrial processing peptidase alpha-chain; n=1; Dactylis glomerata Rep: Mitochondrial processing peptidase alpha-chain - Dactylis glom	142	37603	3	10.3	477.94	953.8654	953.5909	0.2745	0	15.94 R	KPVEQLLK	A		
1	1							715.54	1428.065	1428.761	0.3042	0	68.45 R	LNPLVNEFDQIK	S		
1	1							802.03	1602.045	1601.851	0.1942	0	58.08 K	AVDAITLADVSTVAEK	I		
35	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC282024	similar to UniRef100_Q9FNU9 Cluster: Mitochondrial processing peptidase alpha-chain; n=1; Dactylis glomerata Rep: Mitochondrial processing peptidase alpha-chain - Dactylis glom	215	33391	3	14.7	715.5	1428.985	1428.761	0.2242	0	68.37 R	LNPLVNEFDQIK	S		
1	1							788.37	1574.725	1573.82	0.9055	0	94.6 K	AVDGITLADVSSVAEK	I		
1	1							986.65	1971.285	1970.991	0.2945	0	51.86 R	ELTSLATPGQVDQTQLDR	A		
36	nohit																
37	nohit																
38	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC356717	UniRef100_A6XMY5 Cluster: Serine hydroxymethyltransferase; n=1; Triticum monococcum Rep: Serine hydroxymethyltransferase - Triticum monococcum (Einkorn wheat) (Small spe	570	64252	10	18.1	441.81	881.6054	881.4494	0.156	0	37.94 R	FAESLTSK	G		
1	1							459.48	916.9454	916.5494	0.396	0	29.4 K	SAVLFRPK	L		
1	1							500.37	998.7254	998.4457	0.2797	0	60.25 K	YSEGYPGAR	Y		
1	1							521.38	1040.745	1040.482	0.264	0	55.65 R	GFVEEDFAK	V		
1	1							546.46	1090.905	1090.614	0.292	0	85.1 K	LIVAGASAYAR	L		
1	1							623.86	1245.705	1245.624	0.0814	0	74.05 R	ALEAFNLDPEK	W		
1	1							870.05	1738.085	1737.831	0.2546	0	77.54 R	LDESTGLIDYDQLEK	S		
1	1							580.41	1738.208	1737.831	0.3773	0	59.95 R	LDESTGLIDYDQLEK	S		
1	1							1007.57	2013.125	2013.053	0.0723	0	75.66 K	GYDIVSGGTDNHLVLVNLK	K		
2	2	TC297018	UniRef100_A6XMY5 Cluster: Serine hydroxymethyltransferase; n=1; Triticum monococcum Rep: Serine hydroxymethyltransferase - Triticum monococcum (Einkorn wheat) (Small spe	504	51668	10	21.8	1036.09	2070.165	2069.871	0.2944	0	76.82 R	YCGNEYDMMAEITLQK	R	Carbamidomethyl (C); Oxidation (M)	
2	2							441.81	881.6054	881.4494	0.156	0	37.94 R	FAESLTSK	G		
2	2							459.48	916.9454	916.5494	0.396	0	29.4 K	SAVLFRPK	L		
2	2							495.85	989.6854	989.4454	0.24	0	49.65 R	HDVEEYAK	Q		
2	2							521.38	1040.745	1040.482	0.264	0	55.65 R	GFVEEDFAK	V		
2	2							533.96	1065.905	1065.55	0.3559	0	44.65 K	QFPTIGFEK	E		
2	2							546.46	1090.905	1090.614	0.292	0	85.1 K	LIVAGASAYAR	L		
2	2							793.54	1585.065	1584.793	0.2724	0	48.7 K	NTVPGDVSAMVPGGIR	M	Oxidation (M)	
2	2							870.05	1738.085	1737.831	0.2546	0	77.54 R	LDESTGLIDYDQLEK	S		
2	2							580.41	1738.208	1737.831	0.3773	0	59.95 R	LDESTGLIDYDQLEK	S		
2	2							1007.57	2013.125	2013.053	0.0723	0	75.66 K	GYDIVSGGTDNHLVLVNLK	K		
39	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC281405	similar to UniRef100_Q0E0X4 Cluster: Os02g0514700 protein; n=1; Oryza sativa Japonica Group Rep: Os02g0514700 protein - Oryza sativa subsp. japonica (Rice), partial (69%)	242	63021	6	10.1	535.98	1069.945	1069.53	0.4154	0	41.27 K	LGLMSCFVK	A	Carbamidomethyl (C); Oxidation (M)	
1	1							693.41	1384.805	1384.582	0.2238	0	86.04 R	DADTMNFDIEK	G	Oxidation (M)	
1	1							910.55	1819.085	1818.875	0.2107	0	27.6 K	SAAPAETHVAPSEEAPOK	E		
1	1							1003.19	2004.365	2004.078	0.2875	0	86.74 K	FIASEGDTVTPGTIVAIVSK	S		
1	1							669.16	2004.458	2004.078	0.3802	0	59.79 K	FIASEGDTVTPGTIVAIVSK	S		
1	1							669.25	2004.728	2004.078	0.6502	0	45.51 K	FIASEGDTVTPGTIVAIVSK	S		
2	2	TC300398	weakly similar to UniRef100_A7R3T7 Cluster: Chromosome undetermined scaffold_567, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome undetermined scaff	99	42033	4	8.3	748.57	1495.125	1494.678	0.4473	0	12.16 K	HGQQLGLMSCFVK	A	Carbamidomethyl (C); Oxidation (M)	
2	2							1003.19	2004.365	2004.078	0.2875	0	86.74 K	FIASEGDTVTPGTIVAIVSK	S		
2	2							669.16	2004.458	2004.078	0.3802	0	59.79 K	FIASEGDTVTPGTIVAIVSK	S		
2	2							669.25	2004.728	2004.078	0.6502	0	45.51 K	FIASEGDTVTPGTIVAIVSK	S		
3	3	TC291354	similar to UniRef100_Q0E0X4 Cluster: Os02g0514700 protein; n=1; Oryza sativa Japonica Group Rep: Os02g0514700 protein - Oryza sativa subsp. japonica (Rice), partial (75%)	96	61930	2	3.7	535.98	1069.945	1069.53	0.4154	0	41.27 K	LGLMSCFVK	A	Carbamidomethyl (C); Oxidation (M)	
3	3							693.41	1384.805	1384.582	0.2238	0	54.79 R	DTEGMNFDIEK	G	Oxidation (M)	
4	4	TC314827	similar to UniRef100_Q9SPM2 Cluster: Monodehydroascorbate reductase; n=1; Zantedeschia aethiopica Rep: Monodehydroascorbate reductase - Zantedeschia aethiopica (White cal	77	43513	1	3.4	689.04	1376.065	1375.683	0.3824	0	76.51 R	DVADADSLVSSLGK	G		
40	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
1	1	TC279660	similar to UniRef100_A7Q0H2 Cluster: Chromosome chr7 scaffold_42, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr7 scaffold_42, whole genome shot	224	41566	5	14.1	606.43	1210.845	1210.671	0.1745	0	16.17 R	FIPSLLELHK	S		
1	1							681.97	1361.925	1361.65	0.2758	0	66.57 K	AIMQAAEEVAEGK	L	Oxidation (M)	
1	1							682.03	1362.045	1361.65	0.3958	0	90.78 K	AIMQAAEEVAEGK	L	Oxidation (M)	
1	1							727.03	1452.045	1451.697	0.3488	0	42.84 K	VNMEYGLDPTIGK	A	Oxidation (M)	
1	1							913.56	1825.105	1824.904	0.2014	0	74.18 R	MYQLAQGGTAVGTGLNTK	K	Oxidation (M)	
2	2	TC284402	similar to UniRef100_A7Q0H2 Cluster: Chromosome chr7 scaffold_42, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr7 scaffold_42, whole genome shot	154	37829	3	6.2	546.88	1091.745	1091.561	0.1844	0	76.34 K	IGYDNAAAVAK	K		
2	2							546.93	1091.845	1091.561	0.2844	0	76.99 K	IGYDNAAAVAK	K		
2	2							583.42	1164.825	1164.603	0.2228	0	77.46 R	LLGDASVSFEK	N		
41	nohit																

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66	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK154109	similar to UniRef100_P68209 Cluster: Succinyl-CoA ligase [GDP-forming] subunit alpha-1, mitochondrial precursor; n=1; Arabidopsis thaliana Rep: Succinyl-CoA ligase [GDP-forming]	148	16676	2	13.9	586.96	1171.905	1171.609	0.297	0	89.52	R	DAGVTVVESPAK	I	
	1							594.96	1187.905	1187.59	0.3158	0	60.56	K	IGSTMFELFK	Q	Oxidation (M)
67	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC337054	homologue to UniRef100_P15290 Cluster: Oxalate oxidase GF-2.8 precursor; n=1; Triticum aestivum Rep: Oxalate oxidase GF-2.8 precursor - Triticum aestivum (Wheat), partial (96%)	51	57096	2	2.8	316.33	630.6454	630.3701	0.2754	0	36.31	R	ISNIGK	G	
	1							337.23	1008.668	1008.498	0.1698	0	15.15	R	ATEIGIMMK	G	Oxidation (M)
68	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC283350	homologue to UniRef100_A5BDH7 Cluster: Fructose-bisphosphate aldolase; n=1; Vitis vinifera Rep: Fructose-bisphosphate aldolase - Vitis vinifera (Grape), partial (61%)	168	37856	4	12.8	474.34	946.6654	946.4906	0.1749	0	35.68	R	ALQNTCLK	T	Carbamidomethyl (C)
	1							492.9	983.7854	983.5763	0.2091	0	81.18	K	AAQEAILLR	A	
	1							668.42	1334.825	1334.672	0.1537	0	36.47	R	ATPEQVADYTLK	L	
	1							756.04	1510.065	1509.84	0.2252	0	14.63	R	TVVSIPIGNSSELAVK	E	
	2	TC281478	homologue to UniRef100_Q9LLD7 Cluster: Fructose-bisphosphate aldolase; n=1; Avena sativa Rep: Fructose-bisphosphate aldolase - Avena sativa (Oat), partial (86%)	90	48175	4	8	474.34	946.6654	946.4906	0.1749	0	35.68	R	ALQNTCLK	T	Carbamidomethyl (C)
	2							694.14	1386.265	1386.71	-0.4448	0	39.76	R	LASIGLENTEANR	Q	
	2							694.49	1386.965	1386.71	0.2552	0	18.31	R	LASIGLENTEANR	Q	
	2							756.04	1510.065	1509.84	0.2252	0	14.63	R	TVVSIPIGNSSELAVK	E	
	3	TC277472	homologue to UniRef100_Q9LLD7 Cluster: Fructose-bisphosphate aldolase; n=1; Avena sativa Rep: Fructose-bisphosphate aldolase - Avena sativa (Oat), partial (82%)	75	40883	5	10.4	668.42	1334.825	1335.667	-0.8416	0	19.54	R	ATPEEVASYTLR	L	
	3							668.96	1335.905	1335.667	0.2384	0	21.04	R	ATPEEVASYTLR	L	
	3							694.14	1386.265	1386.71	-0.4448	0	39.76	R	LASIGLENTEANR	Q	
	3							694.49	1386.965	1386.71	0.2552	0	18.31	R	LASIGLENTEANR	Q	
	3							756.04	1510.065	1509.84	0.2252	0	14.63	R	TVVSIPIGNSSELAVK	E	
	4	TC323054	similar to UniRef100_A8F703 Cluster: Cytidylyltransferase-related domain; n=1; Thermotoga lettingae TMO Rep: Cytidylyltransferase-related domain - Thermotoga lettingae (strain ATCC	59	47664	1	2.1	492.9	983.7854	984.5604	-0.7749	0	58.77	K	SPSEAILLR	S	
69	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC282262	similar to UniRef100_A5YT86 Cluster: Cysteine synthase; n=1; Glycine max Rep: Cysteine synthase - Glycine max (Soybean), partial (62%)	186	37787	3	9.1	474.42	946.8254	946.5488	0.2767	0	48.1	R	TPLVYLNK	V	
	1							648.44	1294.865	1293.697	1.1686	0	45.21	K	LEFLQPSFSVK	D	
	2	TC330390	similar to UniRef100_Q43153 Cluster: Cysteine synthase precursor; n=1; Spinacia oleracea Rep: Cysteine synthase precursor - Spinacia oleracea (Spinach), partial (69%)	123	34478	2	7.7	665.97	1329.925	1329.729	0.1962	0	92.67	K	AFGAQLVLTDPAK	G	
	2							639.95	1277.885	1277.709	0.1763	0	30.65	K	LIVTVHPSAGER	Y	
	2							665.97	1329.925	1329.729	0.1962	0	92.67	K	AFGAQLVLTDPAK	G	
70	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278653	similar to UniRef100_Q9ZP06 Cluster: Malate dehydrogenase 1, mitochondrial precursor; n=1; Arabidopsis thaliana Rep: Malate dehydrogenase 1, mitochondrial precursor - Arabidop	229	37313	4	9.9	610.43	1218.845	1218.697	0.1482	0	62.14	R	LFQVTTLDVVR	A	
	1							610.45	1218.885	1218.697	0.1882	0	70.19	R	LFQVTTLDVVR	A	
	1							624.44	1246.865	1246.604	0.2613	0	80.55	R	TQEGGTEVVEAK	A	
	1							659.99	1317.965	1317.693	0.2726	0	78.2	R	DDLFNINAGIVK	N	
	2	TC284236	homologue to UniRef100_A7QDN2 Cluster: Malate dehydrogenase; n=1; Vitis vinifera Rep: Malate dehydrogenase - Vitis vinifera (Grape), partial (66%)	78	39306	3	9.3	610.43	1218.845	1218.697	0.1482	0	62.14	K	LFQVTTLDVVR	A	
	2							610.45	1218.885	1218.697	0.1882	0	70.19	K	LFQVTTLDVVR	A	
	2							721.85	2162.528	2162.018	0.5107	0	8.12	R	STCAAAATTPTPTAAAGAEGR		
71	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278151	similar to UniRef100_Q8L5A6 Cluster: Malate dehydrogenase; n=1; Solanum tuberosum Rep: Malate dehydrogenase - Solanum tuberosum (Potato), partial (75%)	147	42040	2	5.7	610.65	1219.285	1218.697	0.5882	0	66.62	K	LFQVTTLDVVR	A	
	1							617.47	1232.925	1232.589	0.337	0	79.91	R	TQDGGTEVVEAK	A	
	2	TC278653	similar to UniRef100_Q9ZP06 Cluster: Malate dehydrogenase 1, mitochondrial precursor; n=1; Arabidopsis thaliana Rep: Malate dehydrogenase 1, mitochondrial precursor - Arabidop	90	37313	2	6.5	610.65	1219.285	1218.697	0.5882	0	66.62	R	LFQVTTLDVVR	A	
	2							624.43	1246.845	1246.604	0.2413	0	23.65	R	TQEGGTEVVEAK	A	
72	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC282262	similar to UniRef100_A5YT86 Cluster: Cysteine synthase; n=1; Glycine max Rep: Cysteine synthase - Glycine max (Soybean), partial (62%)	138	37787	2	6.2	477.23	952.4454	952.509	-0.0636	0	51.85	R	DTAAHLIGR	T	
	1							665.79	1329.565	1329.729	-0.1638	0	86.27	K	AFGAQLVLTDPAK	G	
	2	TC330390	similar to UniRef100_Q43153 Cluster: Cysteine synthase precursor; n=1; Spinacia oleracea Rep: Cysteine synthase precursor - Spinacia oleracea (Spinach), partial (69%)	105	34478	2	7.7	639.43	1276.845	1277.709	-0.8637	0	19.19	K	LIVTVHPSAGER	Y	
	2							665.79	1329.565	1329.729	-0.1638	0	86.27	K	AFGAQLVLTDPAK	G	
73	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278151	similar to UniRef100_Q8L5A6 Cluster: Malate dehydrogenase; n=1; Solanum tuberosum Rep: Malate dehydrogenase - Solanum tuberosum (Potato), partial (75%)	287	42040	5	13.4	637.31	636.3027	636.3119	-0.0092	0	24.17	R	DDLFK	I	
	1							488.18	974.3454	974.5284	-0.1829	0	40.74	K	GELLSSIEK	G	
	1							610.43	1218.845	1218.697	0.1482	0	51.6	K	LFQVTTLDVVR	A	
	1							617.33	1232.645	1232.589	0.057	0	79.74	R	TQDGGTEVVEAK	A	
	1							882.45	1762.885	1762.866	0.0196	0	90.72	K	SGVEEVMGLGELSALEK	E	Oxidation (M)
	2	DR740593	similar to UniRef100_A7QDN2 Cluster: Malate dehydrogenase; n=1; Vitis vinifera Rep: Malate dehydrogenase - Vitis vinifera (Grape), partial (51%)	53	39750	2	6.4	610.43	1218.845	1218.697	0.1482	0	51.6	R	LFQVTTLDVVR	A	
	2							755.55	1509.085	1508.676	0.4098	0	1.03	K	SGPHQEAQEGWQR	N	
74	nohit																
75	nohit																
76	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC314308	UniRef100_A4K4Z3 Cluster: Alpha tubulin-1D; n=1; Triticum aestivum Rep: Alpha tubulin-1D - Triticum aestivum (Wheat), complete	100	87587	3	4.6	511.34	1020.665	1020.524	0.1414	0	73.58	K	DTDILAAFR	V	
	1							704.33	1406.645	1406.661	-0.0151	0	22.87	K	LTYYTPQYETK	D	
	1							934.93	1867.845	1867.892	-0.0466	0	3.88	R	AVCMISNNATAVEVFSR	I	Carbamidomethyl (C)
	2	TC352164	homologue to UniRef100_Q75VC2 Cluster: Ribulose bisphosphate carboxylase large chain; n=9; Quercus Rep: Ribulose bisphosphate carboxylase large chain - Quercus suber (Cork	89	13536	2	16	511.34	1020.665	1020.524	0.1414	0	73.58	K	DTDILAAFR	V	
	2							704.33	1406.645	1405.677	0.9689	0	15.51	K	LTYYTPQYETK	D	
77	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC356717	UniRef100_A6XMY5 Cluster: Serine hydroxymethyltransferase; n=1; Triticum monococcum Rep: Serine hydroxymethyltransferase - Triticum monococcum (Einkorn wheat) (Small spe	134	64252	3	5.3	568.33	567.3227	567.2323	0.0905	0	9.02	-	SCSSK	Y	Carbamidomethyl (C)
	1							623.9	1245.785	1245.624	0.1614	0	78.51	R	ALEAFNLDPEK	W	
	1							869.89	1737.765	1737.831	-0.0654	0	46.17	R	LDESTGLIDYDQLEK	S	
78	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CA698948		285	35105	5	15.1	482.77	963.5254	963.4774	0.048	0	40.66	R	FPTTNQTR	H	
	1							482.83	963.6454	963.4774	0.168	0	50.93	R	FPTTNQTR	H	
	1							658.91	1315.805	1315.698	0.1071	0	47.98	K	SATSTVAEVVPQK	D	
	1							721.82	1441.625	1442.766	-1.1402	0	92.66	K	VPTLAEEYSLPPK	E	
	1							896.22	1790.425	1790.806	-0.3803	0	93.63	K	DTETSPADETAVAVEEK	S	

79	nohit																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
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[illegible]

112	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278554	UniRef100_O81480 Cluster: Thioredoxin peroxidase; n=1; Secale cereale Rep: Thioredoxin peroxidase - Secale cereale (Rye), partial (94%)	165	36943	4	10.6	511.22	1020.425	1020.549	-0.1237	0	66.35	K	YPLVSDVTK	S	
	1							511.78	1021.545	1020.549	0.9963	0	52.69	K	YPLVSDVTK	S	
	1							680.85	1359.685	1359.703	-0.018	0	50.88	R	AAAEYDLPLVGNK	A	
	1							743.44	1484.865	1484.835	0.0303	0	48.01	K	SFGLVIPDQGIALR	G	
113	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK217082	homologue to UniRef100_O81480 Cluster: Thioredoxin peroxidase; n=1; Secale cereale Rep: Thioredoxin peroxidase - Secale cereale (Rye), partial (80%)	66	37565	1	3.7	680.76	1359.505	1359.703	-0.198	0	65.54	R	AAAEYDLPLVGNK	A	
114	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK194120	similar to UniRef100_Q40089 Cluster: ATP synthase subunit delta-, mitochondrial precursor; n=1; Ipomoea batatas Rep: ATP synthase subunit delta-, mitochondrial precursor - Ipomoea batatas	77	25214	1	4.1	597.53	1193.045	1192.686	0.3599	0	76.99	K	LTVNFVLPYK	S	
115	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK161398	homologue to UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - Triticeae	183	42211	5	10.4	805.47	804.4627	804.4381	0.0246	0	15.46	R	IPPTYSK	T	
	1							403.24	804.4654	804.4381	0.0273	0	23.81	R	IPPTYSK	T	
	1							511.31	1020.605	1020.524	0.0814	0	74.68	K	DTDILAAFR	V	
	1							704.37	1406.725	1406.661	0.0649	0	35.8	K	LTYYTPEYETK	D	
	1							733.45	1464.885	1464.747	0.1381	0	48.4	K	TFQGPPHQIQUVER	D	
	2	TC322697	homologue to UniRef100_Q5K3F4 Cluster: Ribulose biphosphate carboxylase large chain; n=1; Anthraxon sp. Hodgkinson 111 Rep: Ribulose biphosphate carboxylase large chain - Anthraxon sp. Hodgkinson 111	77	46993	4	5.7	489.27	488.2627	488.2707	-0.008	0	4.39	R	GLGSR	R	
	2							805.47	804.4627	804.4381	0.0246	0	15.46	R	IPPTYSK	T	
	2							403.24	804.4654	804.4381	0.0273	0	23.81	R	IPPTYSK	T	
	2							733.45	1464.885	1464.747	0.1381	0	48.4	K	TFQGPPHQIQUVER	D	
116	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK217579		245	33297	6	17.5	468.75	935.4854	935.4382	0.0472	0	49.54	K	MLVSDEAR	K	Oxidation (M)
	1							548.33	1094.645	1094.568	0.0773	0	45.19	K	FDALLIEMK	E	Oxidation (M)
	1							688.39	1374.765	1375.633	-0.8675	0	15.08	K	ISTMTADEYFAK	H	
	1							696.79	1391.565	1391.628	-0.0624	0	69.62	K	ISTMTADEYFAK	H	Oxidation (M)
	1							720.41	1438.805	1438.734	0.0711	0	49.12	K	YVDVTPEYKPK	F	
	1							730.36	1458.705	1458.71	-0.0049	0	31.9	R	TFEDVNHQLQTK	F	
	2	CA487123	similar to UniRef100_Q9FT52 Cluster: ATP synthase subunit d, mitochondrial; n=1; Arabidopsis thaliana Rep: ATP synthase subunit d, mitochondrial - Arabidopsis thaliana (Mouse-ear cress)	113	20798	4	19.9	688.39	1374.765	1375.633	-0.8675	0	15.08	K	ISTMTADEYFAK	H	
	2							696.79	1391.565	1391.628	-0.0624	0	69.62	K	ISTMTADEYFAK	H	Oxidation (M)
	2							720.41	1438.805	1437.75	1.0551	0	11.46	K	YVDVTPEYKPK	F	
	2							730.36	1458.705	1458.71	-0.0049	0	31.9	R	TFEDVNHQLQTK	F	
117	nohit																
118	nohit																
119	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	pep_query	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_exec	pep_seq	pep_res_after	pep_var_m
	1	CK213510	similar to UniRef100_A7QGA4 Cluster: Chromosome undetermined scaffold_91, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome undetermined scaffold_91, v	74	38049	1	78	1554.865	2	0.0401	0	73.91	7.20E-05	ETTGVGLDVVPEAR	N		pep_var_mod_pos
120	nohit																
121	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC308127	homologue to UniRef100_Q9ZP25 Cluster: Small heat shock protein Hsp23.5 precursor; n=1; Triticum aestivum Rep: Small heat shock protein Hsp23.5 precursor - Triticum aestivum	53	31299	1	3.1	518.33	1034.645	1034.54	0.1058	0	53.3	R	LELAGDVYR	M	
122	nohit																
123	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK164007	similar to UniRef100_A7NX2 Cluster: Chromosome chr6 scaffold_3, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr6 scaffold_3, whole genome shotgun	197	35560	5	13	342.9	683.7854	684.4283	-0.6428	0	19.71	K	IIVQGR	S	
	1							473.23	944.4454	944.5291	-0.0836	0	55.58	K	SIAGIVTER	D	
	1							998.54	997.5327	997.4869	0.0458	0	16.07	R	LNAYIQGGY	-	
	1							528.83	1055.645	1055.634	0.0116	0	40.9	K	LITVKPETR	V	
	1							576.07	1150.125	1150.518	-0.3921	0	64.81	K	VGDIMTEENK	L	Oxidation (M)
	2	TC329834	homologue to UniRef100_Q2PCD4 Cluster: Type 1 non specific lipid transfer protein precursor; n=1; Triticum aestivum Rep: Type 1 non specific lipid transfer protein precursor - Triticum aestivum	55	42002	1	2.7	577.32	1152.625	1152.535	0.0909	0	54.96	R	CRPYDVSTGR	V	
124	nohit																
125	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK212489	homologue to UniRef100_Q06036 Cluster: 50S ribosomal protein L12-2, chloroplast precursor; n=1; Secale cereale Rep: 50S ribosomal protein L12-2, chloroplast precursor - Secale cereale	83	38636	2	10.4	562.33	1122.645	1122.578	0.0673	0	46.95	R	NLVDHLQER	L	
	1							870.06	2607.158	2607.354	-0.1962	0	35.85	R	LGVSAASFAPAAAAVAAPAAA,T		
126	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK216997	homologue to UniRef100_Q24400 Cluster: Superoxide dismutase [Cu-Zn]; n=1; Triticum aestivum Rep: Superoxide dismutase [Cu-Zn] - Triticum aestivum (Wheat), complete	69	36667	2	8	706.43	1410.845	1411.68	-0.835	0	50.74	K	GGHELSTGNAGGR	L	
	1							736.36	1470.705	1470.736	-0.03	0	18.7	R	AFVVHELEDDLK	G	
127	nohit																
128	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC362955	weakly similar to UniRef100_A7R2V3 Cluster: Chromosome undetermined scaffold_457, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome undetermined scaffold_457, whole genome shotgun	222	37604	3	8.4	487.35	972.6854	972.5426	0.1428	0	64.17	R	LGCQVVLGK	E	Carbamidomethyl (C)
	1							535.31	1068.605	1068.455	0.1509	0	75.91	K	MPAASYEER	Y	Oxidation (M)
	1							628.37	1254.725	1254.73	-0.0041	0	83.82	R	EVVGLAGQTLRL	A	
	2	TC349279	similar to UniRef100_A7R2V3 Cluster: Chromosome undetermined scaffold_457, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome undetermined scaffold_457, whole genome shotgun	132	29675	2	9.2	628.37	1254.725	1254.73	-0.0041	0	83.82	R	EVVGLAGQTLRL	A	
	2							711.4	1420.785	1420.779	0.0068	0	48.47	R	ALVNAGLIEAASHR	L	
129	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK195103	similar to UniRef100_Q5TKF4 Cluster: Nucleoside diphosphate kinase; n=1; Oryza sativa Japonica Group Rep: Nucleoside diphosphate kinase - Oryza sativa subsp. japonica (Rice),	74	15324	1	7.9	649.85	1297.685	1297.604	0.0817	0	73.86	K	ELVSYTSNEEK	W	
130	nohit																
131	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK215900	similar to UniRef100_A2Z9B8 Cluster: Glycine cleavage system H protein, mitochondrial precursor; n=2; Oryza sativa Rep: Glycine cleavage system H protein, mitochondrial precursor	133	35314	1	5.2	871.01	1740.005	1739.931	0.075	0	133.08	K	VKPSSPAELEGLLDSAK	Y	

132	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC282120	homologue to UniRef100_A2Z9B8 Cluster: Glycine cleavage system H protein, mitochondrial precursor; n=2; Oryza sativa Rep: Glycine cleavage system H protein, mitochondrial prec	79	40345	2	6.7	513.76	1025.505	1025.351	0.1546	0	32.42	K	HCEEEDAH	-	Carbamidomethyl (C)
	1							870.98	1739.945	1739.931	0.015	0	46.71	K	VKPSSPAELEGLLDSAK	Y	
133	nohit																
134	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	CK163788	homologue to UniRef100_P05698 Cluster: Ribulose bisphosphate carboxylase large chain precursor; n=3; Hordeum vulgare Rep: Ribulose bisphosphate carboxylase large chain prec	105	35428	2	6.9	655.41	1308.805	1308.675	0.1307	0	58.75	R	EMTLGFVDLLR	D	Oxidation (M)
	1							670.34	1338.665	1338.634	0.0311	0	46.38	K	FEFEPVDTIDK	-	
	2	TC315644	homologue to UniRef100_O20097 Cluster: Ribulose bisphosphate carboxylase large chain; n=1; Collospermum hastatum Rep: Ribulose bisphosphate carboxylase large chain - Collo	73	37922	2	7.9	655.41	1308.805	1308.675	0.1307	0	58.75	R	EMTLGFVDLLR	X	Oxidation (M)
	2							887.41	1772.805	1771.773	1.0329	0	14.45	-	PSMKPMSTTCTAQMAR	M	2 Oxidation (M)
135	nohit																
136	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_r	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC349826	homologue to UniRef100_Q9ZRS5 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Secale cereale Rep: Ribulose bisphosphate carboxylase small chain - Secale cereal	240	37014	6	21.4	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	1							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	1							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	1							691.32	1380.625	1380.569	0.056	0	73.75	R	EHNSSPGYYDGR	Y	
	1							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPLSTEALLK	Q	
	1							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	2	TC321479	UniRef100_Q9FEE4 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxylase small chain - Triticum aestivum (Whea	215	32019	6	25.4	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	2							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	V	
	2							541.89	1081.765	1081.472	0.2936	0	6.22	R	TIGCGACICK	F	2 Carbamidomethyl (C)
	2							691.32	1380.625	1380.569	0.056	0	73.75	R	EHNSSPGYYDGR	Y	
	2							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPLSTEALLK	Q	
	2							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	3	TC334764	homologue to UniRef100_Q9FRZ4 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxylase small chain - Triticum ae	182	33660	6	22.8	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	3							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	3							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	3							644.19	1286.365	1286.669	-0.3038	0	13.22	R	AMQVWPIEGIK	K	Oxidation (M)
	3							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPLSTEALLK	Q	
	3							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	4	TC296554	UniRef100_Q9ZRS5 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Secale cereale Rep: Ribulose bisphosphate carboxylase small chain - Secale cereale (Rye), comp	176	57478	6	11.3	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	4							473.88	945.7454	945.5032	0.2422	0	11.59	R	HYSTLLGR	R	
	4							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	4							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	4							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPLSTEALLK	Q	
	4							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	5	CK216102	homologue to UniRef100_Q9FRZ4 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxylase small chain - Triticum ae	175	37833	6	22.7	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	5							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	5							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	5							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPLSTEALLK	Q	
	5							733.53	2197.568	2197.886	-0.3181	0	5.83	R	ESMLVCECYPCLCIGTFT	-	3 Carbamidomethyl (C); Oxidation (M)
	5							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	6	CK216855	homologue to UniRef100_Q9FRZ4 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxylase small chain - Triticum ae	169	38591	5	17	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	6							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	6							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	6							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPISTEALLK	Q	
	6							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	7	CK213136	homologue to UniRef100_Q9FRZ4 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxylase small chain - Triticum ae	163	36994	5	17.8	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	7							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	7							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	7							968.49	1934.965	1934.04	0.9254	0	13.45	K	FENLSYLPPLSTEALLK	Q	
	7							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	8	CK213773	homologue to UniRef100_Q9ZRS5 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Secale cereale Rep: Ribulose bisphosphate carboxylase small chain - Secale cereal	163	40201	5	16.6	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	8							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	8							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	8							968.49	1934.965	1934.007	0.9584	0	13.45	K	CETLSYLPPLSTEALLK	Q	Carbamidomethyl (C)
	8							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	9	CA677296	homologue to UniRef100_P26667 Cluster: Ribulose bisphosphate carboxylase small chain PW9, chloroplast precursor; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxyla	161	12455	3	23.5	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	9							497.76	993.5054	993.4236	0.0819	0	52.55	K	XYPDAYVR	V	
	9							691.32	1380.625	1380.569	0.056	0	73.75	R	EHNSSPGYYDGR	Y	
	10	CK213771	homologue to UniRef100_Q9ZRS5 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Secale cereale Rep: Ribulose bisphosphate carboxylase small chain - Secale cereal	161	39772	5	16.7	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	10							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	10							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	10							968.49	1934.965	1934.007	0.9584	0	13.45	K	CETLSYLPPISTEALLK	Q	Carbamidomethyl (C)
	10							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	11	TC330962	homologue to UniRef100_P26667 Cluster: Ribulose bisphosphate carboxylase small chain PW9, chloroplast precursor; n=1; Triticum aestivum Rep: Ribulose bisphosphate carboxyla	156	33823	4	14.5	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	11							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	V	
	11							691.32	1380.625	1380.569	0.056	0	73.75	R	EHNSSPGYYDGR	Y	
	11							968.49	1934.965	1934.04	0.9254	0	13.45	K	FENLSYLPPLSTEALLK	Q	
	12	TC333737		153	45732	5	11	590.9	589.8927	589.3336	0.5591	0	4.22	K	ILHHA	-	
	12							453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	12							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	12							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	12							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	13	TC320733	UniRef100_Q9ZRS5 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Secale cereale Rep: Ribulose bisphosphate carboxylase small chain - Secale cereale (Rye), partia	129	22114	4	25.2	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	13							491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	13							961.57	1921.125	1921.045	0.0806	0	19.51	K	FETLSYLPPLSTEALLK	Q	
	13							766.16	2295.458	2295.051	0.4007	0	43.37	K	LPMFGCTDATQVINEVEEAR	R	Carbamidomethyl (C); Oxidation (M)
	14	TC320542	UniRef100_P07398 Cluster: Ribulose bisphosphate carboxylase small chain clone 512; n=2; Triticum aestivum Rep: Ribulose bisphosphate carboxylase small chain clone 512 - Tritic	129	24587	4	20.4	491.3	980.5854	980.4749	0.1105	0	31.39	R	IIGFDNMR	Q	Oxidation (M)
	14							493.14	984.2654	984.4301	-0.1647	0	18.47	R	ASPGYYDGR	Y	
	14							506.77	1011.525	1011.466	0.0593	0	33.33	K	EYPDAYVR	I	
	14							766.16	2295.458	2295.076	0.3819	0	49.32	K	LPMFGCTDATQVINEVEEVK	K	Carbamidomethyl (C); Oxidation (M)
	15	TC321498	UniRef100_Q9ZRS5 Cluster: Ribulose bisphosphate carboxylase small chain; n=1; Secale cereale Rep: Ribulose bisphosphate carboxylase small chain - Secale cereale (Rye), partia	123	23534	4	25.1	453.74	905.4654	905.4971	-0.0316	0	35.15	K	QVDYLIR	S	
	15							491.3	980.5854	980.5113	0.0741	0	18.77	R	IGFTTCAR	C	
	15							961.57	1921.125	1921.045	0.0806	0	19				

[illegible]

	2	TC295402	homologue to UniRef100_P29185 Cluster: Chaperonin CPN60-1, mitochondrial precursor; n=1; Zea mays Rep: Chaperonin CPN60-1, mitochondrial precursor - Zea mays (Maize), pa	146	25805	4	14.1	739.36	1476.705	1476.749	-0.044	0	36.91 R	GISMAVDDVVTNLK	G	Oxidation (M)					
	1							467.17	932.3254	931.4975	0.828	0	64.2 R	VTDALNATK	T						
	2							598.9	1195.785	1195.729	0.0566	0	34.96 K	IGVQIQNALK	T						
	2							598.93	1195.845	1195.729	0.1166	0	8.49 K	IGVQIQNALK	T						
	2							833.39	1664.765	1664.789	-0.0239	0	46.58 K	LLEQNSDLGYDAAK	G						
	3	TC326314	similar to UniRef100_P29185 Cluster: Chaperonin CPN60-1, mitochondrial precursor; n=1; Zea mays Rep: Chaperonin CPN60-1, mitochondrial precursor - Zea mays (Maize), partial	124	40822	4	9.1	467.17	932.3254	931.4975	0.828	0	64.2 R	VTDALNATK	T						
	2							598.9	1195.785	1195.729	0.0566	0	34.96 K	IGVQIQNALK	T						
	3							598.93	1195.845	1195.729	0.1166	0	8.49 K	IGVQIQNALK	T						
	3							833.39	1664.765	1664.789	-0.0239	0	25.24 K	LLEQDNTDLGYDAAK	G						
	149	prot_hit_nu	prot_acc	prot_desc					prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al
	1	TC308079						248	54747	6	16.6	517.31	1032.605	1032.509	0.0967	0	51.93 K	NTENIDLSK	D		
	1							624.83	1247.645	1247.676	-0.0307	0	46.42 K	VQEVSEIFGK	A						
	1							709.93	1417.845	1418.708	-0.8621	0	68.31 K	DVDEVLVGGMTR	V				Oxidation (M)		
	1							782.93	1563.845	1563.805	0.0409	0	24.88 K	AVITVPAYFNDAQR	Q						
	1							888.96	1775.905	1775.905	0.0001	0	44.44 R	INEPTAAALSYGTNNK	E						
	2	TC306448	similar to UniRef100_A2Q199 Cluster: Chaperone DnaK; n=1; Medicago truncatula Rep: Chaperone DnaK - Medicago truncatula (Barrel medic), partial (93%)	66	87117	4	7.1	977.95	1953.885	1953.994	-0.1088	0	11.54 K	GYNPDEAVAMGAIIQGILR	G				Oxidation (M)		
	2							597.78	1193.545	1193.541	0.0043	0	21.92 K	SSGGLSDSDIEK	M						
	2							667.77	1333.525	1332.689	0.8361	0	7.35 -	GLSMSPLLQLCR	M				Oxidation (M)		
	2							782.93	1563.845	1563.805	0.0409	0	24.88 K	AVITVPAYFNDAQR	Q						
	2							977.95	1953.885	1953.994	-0.1088	0	11.54 K	GYNPDEAVAMGAIIQGILR	G				Oxidation (M)		
	3	TC324780		54	25065	1	5.2	603.29	1204.565	1204.594	-0.0281	0	53.99 R	SSGGLSEAEIQK	M						
150	prot_hit_nu	prot_acc	prot_desc					prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC292635	similar to UniRef100_A7QS95 Cluster: Chromosome chr3 scaffold_157, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr3 scaffold_157, whole genome sh	120	40820	3	8.5	562.3	1122.585	1123.47	-0.8848	0	13.25 R	AEMASDDIEK	I				Oxidation (M)		
	1							611.82	1221.625	1221.572	0.053	0	65.2 R	SSGGLSESEIEK	M						
	1							617.79	1233.565	1233.661	-0.0951	0	41.57 K	VQEVVSEIFGK	A						
	2	TC323693		60	24725	2	2.6	330.12	658.2254	658.3762	-0.1508	0	51.74 R	SGLQVR	S						
	2							330.14	658.2654	658.3762	-0.1108	0	60.15 R	SGLQVR	S						
	3	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	52	65917	2	1.1	330.12	658.2254	658.3762	-0.1508	0	49.16 R	SGLGAVR	W						
	3							330.14	658.2654	658.3762	-0.1108	0	52.48 R	SGLGAVR	W						
151	prot_hit_nu	prot_acc	prot_desc					prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC294781		195	55740	5	9.5	446.37	890.7254	890.4345	0.2909	0	46.02 R	SDNIDLSK	D						
	1							484.26	966.5054	966.5611	-0.0556	0	28.84 K	HLNITLTR	S						
	1							577.37	1152.725	1153.481	-0.7554	0	20.68 R	TEMASDDIEK	I				Oxidation (M)		
	1							611.77	1221.525	1221.572	-0.047	0	45.45 R	SSGGLSESEIEK	M						
	1							678.35	1354.685	1354.662	0.0238	0	54.13 R	NTADTTVYSIEK	S						
	2	TC279703	similar to UniRef100_A7QS95 Cluster: Chromosome chr3 scaffold_157, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr3 scaffold_157, whole genome sh	131	31469	3	11.4	562.76	1123.505	1123.47	0.0352	0	31.66 R	AEMASDDIEK	I				Oxidation (M)		
	2							611.77	1221.525	1221.572	-0.047	0	45.45 R	SSGGLSESEIEK	M						
	2							678.35	1354.685	1354.662	0.0238	0	54.13 R	NTADTTVYSIEK	S						
	3	TC277435		124	41745	4	12.2	446.37	890.7254	890.4345	0.2909	0	46.02 R	SDNIDLSK	D						
	3							484.26	966.5054	966.5611	-0.0556	0	28.84 K	HLNITLTR	S						
	3							770.32	1538.625	1537.814	0.8114	0	20.68 K	QYSPSQIGAFVLTK	M						
	4							889.29	1776.585	1775.905	0.6601	0	28.47 R	INEPTAAALSYGTNNK	E						
	4	TC308079						484.26	966.5054	966.5611	-0.0556	0	28.84 K	HLNITLTR	S						
	4							625.34	1248.665	1247.676	0.9893	0	53.69 K	VQEVSEIFGK	A						
	4							889.29	1776.585	1775.905	0.6601	0	28.47 R	INEPTAAALSYGTNNK	E						
152	nohit																				
153	nohit																				
154	prot_hit_nu	prot_acc	prot_desc					prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC282998		50	41010	2	3	604.31	1206.605	1206.592	0.014	0	50.3 K	VDMIVVTDGSR	I				Oxidation (M)		
								604.32	1206.625	1206.592	0.034	0	50.22 K	VDMIVVTDGSR	I				Oxidation (M)		
155	prot_hit_nu	prot_acc	prot_desc					prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC317092	similar to UniRef100_A7PQU6 Cluster: Chromosome chr6 scaffold_25, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr6 scaffold_25, whole genome shot	566	66825	9	17.1	422.37	842.7254	842.5226	0.2029	0	29.38 K	LSGGVAVIK	V						
	1							429.28	856.5454	856.5018	0.0436	0	69.81 R	LGADIIQK	A						
	1							522.3	1042.585	1042.577	0.0083	0	78.69 K	VVNDGVTIAR	A						
	1							525.79	1049.585	1049.514	0.0513	0	46.13 K	SVVEFENAR	V						
	1							637.83	1273.645	1273.677	-0.0311	0	58.83 K	TVQSLVEELEK	K						
	1							751.83	1501.645	1501.642	0.0034	0	41.29 R	ELSQTSDTYDSEK	L						
	1							777.39	1552.765	1552.882	-0.117	0	53.76 K	EILPLLEQTTQLR	A						
	1							818.86	1635.705	1635.77	-0.0646	0	95.75 K	TNDSAGDGTTTASVLAR	E						
	1							885.86	1769.705	1769.898	-0.1927	0	91.88 R	AIELADPMENAGAALIR	E				Oxidation (M)		
	2	TC325813	similar to UniRef100_A7PQU6 Cluster: Chromosome chr6 scaffold_25, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr6 scaffold_25, whole genome shot	432	43260	7	23.5	422.37	842.7254	842.5226	0.2029	0	29.38 K	LSGGVAVIK	V						
	2							429.28	856.5454	856.5018	0.0436	0	69.81 R	LGADIIQK	A						
	2							522.3	1042.585	1042.577	0.0083	0	78.69 K	VVNDGVTIAR	A						
	2							751.83	1501.645	1501.642	0.0034	0	41.29 R	ELSQTSDTYDSEK	L						
	2							818.86	1635.705	1635.77	-0.0646	0	95.75 K	TNDSAGDGTTTASVLAR	E						
	2							885.86	1769.705	1769.898	-0.1927	0	91.88 R	AIELADPMENAGAALIR	E				Oxidation (M)		
	3							763.24	2286.698	2286.258	0.4399	0	25.54 K	ALVAPASLIAHNAGVEGEVIV	I						
	3	TC302569	UniRef100_P08823 Cluster: RuBisCO large subunit-binding protein subunit alpha, chloroplast precursor; n=1; Triticum aestivum Rep: RuBisCO large subunit-binding protein subunit α	285	65769	5	9.1	422.37	842.7254	842.5226	0.2029	0	29.38 K	LSGGVAVIK	V						
	3							429.28	856.5454	856.5018	0.0436	0	69.81 R	LGADIIQK	A						
	3							522.3	1042.585	1042.577	0.0083	0	78.69 K	VVNDGVTIAR	A						
	3							777.39	1552.765	1552.882	-0.117	0	53.76 K	EIPLLEQTTQLR	C						
	4							885.86	1769.705	1768.914	0.7913	0	55.7 R	AIELANPMENAGAALIR	E				Oxidation (M)		
	4	TC297334		266	57525	6	13.9	422.37	842.7254	842.5226	0.2029	0	29.38 K	LSGGVAVIK	V						
	4							429.28	856.5454	856.5018	0.0436	0	69.81 R	LGADIIQK	A						
	4							525.79	1049.585	1049.514	0.0513	0	46.13 K	SVVEFENAR	V						
	4							751.83	1501.645	1501.642	0.0034	0	41.29 R	ELSQTSDTYDSEK	L						
	4							777.39	1552.765	1552.882	-0.117	0	53.76 K	EILPLLEQTTQLR	A						
	4							763.24	2286.698	2286.258	0.4399	0	25.54 K	ALVAPASLIAHNAGVEGEVIV	I						
	5	TC349980		52	48932	1	1.6	429.28	856.5454	856.5018	0.0436	0	51.93 K	LQDLLQK	R						
156	prot_hit_nu	prot_acc	prot_desc					prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC279818	similar to UniRef100_A9PL03 Cluster: Mitochondrial lipamide dehydrogenase; n=1; Populus tremuloides Rep: Mitochondrial lipamide dehydrogenase - Populus tremuloides (Quakir	299	55413	7	19.7	532.83	1063.645	1063.486	0.1599	0	32.17 K	AIDDQAGVMVK	V				Oxidation (M)		

[illegible]

[illegible]

173	1									536.28	1070.545	1070.459	0.0864	0	30.23	K	AMTFDLDDK	I	Oxidation (M)
	prot_hit_nu	prot_acc	prot_desc		prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before		pep_seq	pep_res_al	pep_var_mod
	1	TC293615	similar to UniRef100_Q7X998 Cluster: MRNA-binding protein; n=1; Nicotiana tabacum Rep: MRNA-binding protein - Nicotiana tabacum (Common tobacco), partial (79%)		78	40501	2	4.9	494.18	986.3454	986.4457	-0.1003	0	27.13	R		FAEYASSGR	G	
	1	1							505.77	1009.525	1009.508	0.0174	0	52.54	R		FSELTSAQAK	T	
	2	TC332693			60	24725	1	2.6	330.2	658.3854	658.3762	0.0092	0	59.54	R		SGLQVR	S	
	3	TC297816	homologue to UniRef100_Q93YH4 Cluster: ATP citrate lyase a-subunit; n=1; Lupinus albus Rep: ATP citrate lyase a-subunit - Lupinus albus (White lupin), partial (70%)		59	61232	2	3.5	801.19	800.1827	801.3327	-1.15	0	16.09	R		DNCPSIP	-	Carbamidomethyl (C)
	3	3							577.3	1152.585	1152.519	0.0661	0	42.66	R		SSGMGGVTSGTR	G	
	4	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)		57	65917	1	1.1	330.2	658.3854	658.3762	0.0092	0	56.93	R		SGLGAVR	W	
	5	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog		50	19908	1	4.3	330.2	658.3854	658.365	0.0204	0	49.76	R		SGIGAVVG	-	
174	1	TC356437	UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - Triticum aestiv		207	77238	8	10	323.28	644.5454	644.3493	0.1961	0	27.86	R		pep_seq	pep_res_al	pep_var_mod
	1	1							369.21	736.4054	736.3756	0.0299	0	35.33	R		LEDLR	I	
	1	1							464.6	927.1854	927.4596	-0.2742	0	20.1	R		GGLDFTK	D	
	1	1							481.72	961.4254	961.4716	-0.0462	0	45.73	K		AMHAVDR	Q	Oxidation (M)
	1	1							486.23	970.4454	970.4001	0.0454	0	14.11	R		SQAETGEIK	G	
	1	1							624.32	1246.625	1246.606	0.0198	0	19.7	R		ACYECLR	G	2 Carbamidomethyl (C)
	1	1							704.35	1406.685	1406.661	0.0249	0	22.34	K		FVFCAEAIYK	S	Carbamidomethyl (C)
	1	1							489.27	1464.788	1464.747	0.0408	0	21.8	K		LTYYTPEYETK	D	
	1	1							489.27	1464.788	1464.747	0.0408	0	21.8	K		TFQGPPIQIQUVER	D	
	2	TC297297	homologue to UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - T		153	41717	6	15	323.28	644.5454	644.3493	0.1961	0	27.86	R		LEDLR	I	
	2	2							481.72	961.4254	961.4716	-0.0462	0	45.73	K		SQAETGEIK	G	
	2	2							538.23	1074.445	1074.582	-0.1367	0	17.95	-		IPVSNHALQ	-	
	2	2							624.32	1246.625	1246.606	0.0198	0	19.7	R		FVFCAEAIYK	S	Carbamidomethyl (C)
	2	2							704.35	1406.685	1406.661	0.0249	0	22.34	K		LTYYTPEYETK	D	
	2	2							489.27	1464.788	1464.747	0.0408	0	21.8	K		TFQGPPIQIQUVER	D	
	3	CD904094	weakly similar to UniRef100_Q336L9 Cluster: Expressed protein; n=2; Oryza sativa Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (32%)		61	21747	3	6.9	323.28	644.5454	644.3493	0.1961	0	27.86	K		LEDLR	N	
	3	3							402.68	803.3454	804.409	-1.0635	0	26.96	R		SAASGGISR	T	
	3	3							403.18	804.3454	804.409	-0.0635	0	33.42	R		SAASGGISR	T	
	4	TC332693			55	24725	1	2.6	330.27	658.5254	658.3762	0.1492	0	54.83	R		SGLQVR	S	
	5	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)		52	65917	1	1.1	330.27	658.5254	658.3762	0.1492	0	52.24	R		SGLGAVR	W	
	6	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog		50	19908	1	4.3	330.27	658.5254	658.365	0.1604	0	50.24	R		SGIGAVVG	-	
175	1	TC281478	homologue to UniRef100_Q9LLD7 Cluster: Fructose-bisphosphate aldolase; n=1; Avena sativa Rep: Fructose-bisphosphate aldolase - Avena sativa (Oat), partial (86%)		204	48175	8	16	416.19	415.1827	416.2132	-1.0305	0	12.6	R		pep_seq	pep_res_al	pep_var_mod
	1	1							411.71	821.4054	821.4283	-0.0229	0	27.62	R		GAGGR	R	
	1	1							451.24	900.4654	900.5029	-0.0374	0	38.36	K		TFEVAQK	V	
	1	1							451.24	900.4654	900.5029	-0.0374	0	42.45	K		ANSLAQLGK	Y	
	1	1							451.24	900.4654	900.5029	-0.0374	0	42.45	K		ANSLAQLGK	Y	
	1	1							474.26	946.5054	946.4906	0.0149	0	19.96	R		ALQNTCLK	T	Carbamidomethyl (C)
	1	1							694.4	1386.785	1386.71	0.0752	0	73.15	R		LASIGLENTEANR	Q	
	1	1							755.89	1509.765	1509.84	-0.0748	0	12.16	R		TVVSIPNGPSELAVK	E	
	1	1							796.91	1591.805	1591.955	-0.1494	0	18.4	K		IVDILVEQGIVPGIK	V	
	2	TC277472	homologue to UniRef100_Q9LLD7 Cluster: Fructose-bisphosphate aldolase; n=1; Avena sativa Rep: Fructose-bisphosphate aldolase - Avena sativa (Oat), partial (82%)		194	40883	6	18.4	351.14	700.2654	700.3868	-0.1213	0	27.55	K		TIASPGR	G	
	2	2							411.71	821.4054	821.4283	-0.0229	0	27.62	R		TFEVAQK	V	
	2	2							694.4	1386.785	1386.71	0.0752	0	73.15	R		LASIGLENTEANR	Q	
	2	2							741.8	1481.585	1481.649	-0.0636	0	35.55	R		GILAMDESATCGK	R	Carbamidomethyl (C); Oxidation (M)
	2	2							755.89	1509.765	1509.84	-0.0748	0	12.16	R		TVVSIPNGPSELAVK	E	
	2	2							796.91	1591.805	1591.955	-0.1494	0	18.4	K		IVDILVEQGIVPGIK	V	
	3	TC308802	homologue to UniRef100_Q53P96 Cluster: Fructose-bisphosphate aldolase; n=1; Oryza sativa Japonica Group Rep: Fructose-bisphosphate aldolase - Oryza sativa subsp. japonica (f		144	40296	6	14.4	351.14	700.2654	700.3868	-0.1213	0	27.55	K		TIASPGR	G	
	3	3							451.24	900.4654	900.5029	-0.0374	0	38.36	K		ANSLAQLGK	Y	
	3	3							451.24	900.4654	900.5029	-0.0374	0	42.45	K		ANSLAQLGK	Y	
	3	3							474.26	946.5054	946.4906	0.0149	0	19.96	R		ALQNTCLK	T	Carbamidomethyl (C)
	3	3							741.8	1481.585	1481.649	-0.0636	0	35.55	R		GILAMDESATCGK	R	Carbamidomethyl (C); Oxidation (M)
	3	3							755.89	1509.765	1509.84	-0.0748	0	12.16	R		TVVSIPNGPSELAVK	E	
	3	3							796.91	1591.805	1591.955	-0.1494	0	18.4	K		IVDILVEQGIVPGIK	V	
	4	CK217330	similar to UniRef100_Q9LLD7 Cluster: Fructose-bisphosphate aldolase; n=1; Avena sativa Rep: Fructose-bisphosphate aldolase - Avena sativa (Oat), partial (66%)		139	39045	4	11	576.28	575.2727	574.2785	0.9943	0	4.5	R		APMAAV	-	Oxidation (M)
	4	4							351.14	700.2654	700.3868	-0.1213	0	27.55	K		TIASPGR	G	
	4	4							694.4	1386.785	1386.71	0.0752	0	73.15	R		LASIGLENTEANR	Q	
	4	4							741.8	1481.585	1481.649	-0.0636	0	35.55	R		GILAMDESATCGK	R	Carbamidomethyl (C); Oxidation (M)
	5	TC332693			60	24725	1	2.6	330.17	658.3254	658.3762	-0.0508	0	60.17	R		SGLQVR	S	
	6	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)		58	65917	1	1.1	330.17	658.3254	658.3762	-0.0508	0	57.56	R		SGLGAVR	W	
	7	TC306738			51	37704	2	3.1	416.19	415.1827	416.2132	-1.0305	0	11.09	R		GGAGR	W	
	7	7							330.17	658.3254	658.3762	-0.0508	0	40.37	R		SGLLNR	E	
	8	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog		50	19908	1	4.3	330.17	658.3254	658.365	-0.0396	0	50.09	R		SGIGAVVG	-	
	9	CV781192	similar to UniRef100_Q9SKL4 Cluster: Expressed protein; n=1; Arabidopsis thaliana Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (35%)		49	29581	2	6	330.17	658.3254	658.3762	-0.0508	0	40.75	K		GSIQVR	H	
	9	9							583.39	1164.765	1165.591	-0.8254	0	8.41	-		MLVMCLTDLK	C	
176	1	TC342749	homologue to UniRef100_A7P3F7 Cluster: Fructose-bisphosphate aldolase; n=1; Vitis vinifera Rep: Fructose-bisphosphate aldolase - Vitis vinifera (Grape), partial (67%)		277	39456	7	16.9	508.28	507.2727	508.2315	-0.9588	0	3.39	R		pep_seq	pep_res_al	pep_var_mod
	1	1							395.21	788.4054	788.428	-0.0225	0	23.18	R		MSAGK	E	Oxidation (M)
	1	1							411.25	820.4854	820.4695	0.016	0	31.31	K		TLEVAEK	V	
	1	1							432.73	863.4454	863.4535	-0.008	0	19.91	K		TFVDVLK	D	
	1	1							516.24	1030.465	1030.512	-0.0463	0	44.67	K		NTLTMLR	R	Oxidation (M)
	1	1							701.33	1400.645	1400.726	-0.0805	0	70.74	R		DQNIMPGIK	V	Oxidation (M)
	1	1							711.33	1420.645	1420.687	-0.0413	0	83.45	R		LASIGLDNTEVNR	Q	
	2	TC348453	homologue to UniRef100_A7P3F7 Cluster: Fructose-bisphosphate aldolase; n=1; Vitis vinifera Rep: Fructose-bisphosphate aldolase - Vitis vinifera (Grape), partial (78%)		227	34353	6	16.1	395.21	788.4054	788.428	-0.0225	0	23.18	R		GILAIDESSATCGK	R	Carbamidomethyl (C)
	2	2							411.25	820.4854	820.4695	0.016	0	31.31	K		TLEVAEK	V	
	2	2							411.25	820.4854	820.4695	0.016	0	31.31	K		TFVDVLK	D	
	2	2							432.73	863.4454	863.4535	-0.008	0	19.91	K		NTLTMLR	R	Oxidation (M)
	2	2							436.74	871.4654	871.5127	-0.0472	0	39.12	R		ALQNSVLK	T	
	2	2							516.24	1030.465	1030.512	-0.0463	0	44.67	K		DQNIMPGIK	V	Oxidation (M)
	2	2							701.33	1400.645	1400.726	-0.0805	0	70.74	R		LASIGLDNTEVNR	Q	
177																			

179	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278653	similar to UniRef100_Q9ZP06 Cluster: Malate dehydrogenase 1, mitochondrial precursor; n=1; Arabidopsis thaliana Rep: Malate dehydrogenase 1, mitochondrial precursor - Arabidop	141	37313	3	8.5	373.18	744.3454	744.4017	-0.0563	0	33.91 K	DGLEALK			
	1							610.33	1218.645	1218.697	-0.0518	0	43.29 R	LFVGTTLDVVR	A		
	1							659.89	1317.765	1317.693	0.0726	0	63.44 R	DDLFNNINAGVK	N		
	2	TC284236	homologue to UniRef100_A7QDN2 Cluster: Malate dehydrogenase; n=1; Vitis vinifera Rep: Malate dehydrogenase - Vitis vinifera (Grape), partial (66%)	54	39306	2	9.3	610.33	1218.645	1218.697	-0.0518	0	43.29 K	LFVGTTLDVVR	A		
2								721.71	2162.108	2162.018	0.0907	0	10.39 R	STCAAAATTPPTPAAAGAEGR			
180	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278151	similar to UniRef100_Q8L5A6 Cluster: Malate dehydrogenase; n=1; Solanum tuberosum Rep: Malate dehydrogenase - Solanum tuberosum (Potato), partial (75%)	143	42040	5	13.9	357.76	713.5054	713.4436	0.0619	0	19.67 K	INAGIVK	G		
	1							488.3	974.5854	974.5284	0.0571	0	34.95 K	GELLSSEIK	G		
	1							610.32	1218.625	1218.697	-0.0718	0	24.26 K	LFVGTTLDVVR	A		
	1							617.27	1232.525	1232.589	-0.063	0	38.6 R	TQDGGTEVVEAK	A		
1								882.5	1762.985	1762.866	0.1196	0	25.93 K	SGVEEVMEVLGELSALEK	E	Oxidation (M)	
181	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC341917	similar to UniRef100_A7Q9Z4 Cluster: Chromosome chr8 scaffold_68, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr8 scaffold_68, whole genome shot	134	32026	4	12.8	421.15	840.2854	840.4341	-0.1487	0	34.48 K	VSACGPGEK	S		
	1							472.29	942.5654	942.5684	-0.003	0	14.21 R	LLRFAMVK	V	Oxidation (M)	
	1							535.72	1069.425	1069.483	-0.0574	0	44.18 R	IGADFQNYR	K		
	1							666.31	1330.605	1331.693	-1.0878	0	43.21 K	ITALDAELTTER	D		
182	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC279271	weakly similar to UniRef100_A7PDA4 Cluster: Chromosome chr17 scaffold_12, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr17 scaffold_12, whole gen	57	45733	2	2.6	325.11	648.2054	648.3265	-0.121	0	28.17 K	VIMDR	E	Oxidation (M)	
	1							424.22	846.4254	846.3984	0.027	0	28.65 R	VSYAHRD	G		
	2	TC332693		51	24725	1	2.6	330.17	658.3254	658.3762	-0.0508	0	50.7 R	SGLQVR	S		
	3	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	48	65917	1	1.1	330.17	658.3254	658.3762	-0.0508	0	48.12 R	SGLGAVR	W		
183	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC280619	similar to UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - T	86	42211	2	4.7	481.68	961.3454	961.4716	-0.1262	0	27.43 K	SOAETGEIK	G		
	1							511.24	1020.465	1020.524	-0.0586	0	58.89 K	DTDILAAFR	V		
	2	TC314308	UniRef100_A4K4Z3 Cluster: Alpha tubulin-1D; n=1; Triticum aestivum Rep: Alpha tubulin-1D - Triticum aestivum (Wheat), complete	67	87587	2	3.3	511.24	1020.465	1020.524	-0.0586	0	58.89 K	DTDILAAFR	V		
	2							605.98	1814.918	1813.903	1.0149	0	8.4 K	CGINYQPPSVVPGGDLAK	V		
184	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC280619	similar to UniRef100_Q9LN36 Cluster: F18O14.34; n=1; Arabidopsis thaliana Rep: F18O14.34 - Arabidopsis thaliana (Mouse-ear cress), partial (76%)	151	38440	5	9.7	420.2	838.3854	838.4297	-0.0442	0	21.73 K	AHAVENAK	S		
	1							445.19	888.3654	888.4301	-0.0647	0	24.45 R	ETGQALDR	L		
	1							445.75	889.4854	888.4301	1.0553	0	17.11 R	ETGQALDR	L		
	1							499.3	996.5854	996.495	0.0904	0	57.59 R	TLMNIFDK	A	Oxidation (M)	
2	TC297858		549.29	1096.565	1096.581	-0.0157	0	46.75 K	HGMVAAGALVR	Q	Oxidation (M)						
2			445.19	888.3654	888.4301	-0.0647	0	24.45 R	ETGQALDR	L							
2			445.75	889.4854	888.4301	1.0553	0	17.11 R	ETGQALDR	L							
2			499.3	996.5854	996.495	0.0904	0	57.59 R	TLMNIFDK	A	Oxidation (M)						
3	TC332195	similar to UniRef100_A7NTA5 Cluster: Chromosome chr18 scaffold_1, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr18 scaffold_1, whole genome shot	86	23812	3	7.4	360.16	1077.458	1077.356	0.1025	0	9.93 R	SEHEDTDMD	-			
3			445.19	888.3654	888.409	-0.0435	0	28.74 R	DGGWALDR	-							
3			445.75	889.4854	888.409	1.0765	0	26.74 R	DGGWALDR	-							
4	DR735939		499.3	996.5854	996.495	0.0904	0	57.59 R	TIMNIFDK	T	Oxidation (M)						
5	TC332693		327.64	653.2654	654.4064	-1.141	0	17.5 K	GGPIAK	V							
6	TC282153	weakly similar to UniRef100_A5Y731 Cluster: Src homology-3 domain protein 3; n=1; Cucumis melo Rep: Src homology-3 domain protein 3 - Cucumis melo (Muskmelon), partial (64%)	49	24725	1	2.6	330.19	658.3654	658.3762	-0.0108	0	32.73 R	SGLINR	Q			
6			48	35988	1	2.6	499.3	996.5854	996.5393	0.0462	0	48.33 K	SGLQVR	S			
6														TLFGGIFSR	L		
185	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC301455	similar to UniRef100_A7PUK9 Cluster: Chromosome chr7 scaffold_31, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr7 scaffold_31, whole genome shot	207	49149	5	14.5	412.74	823.4654	823.528	-0.0625	0	38.01 K	IVGVAPIR	V		
	1							458.72	915.4254	915.4913	-0.0658	0	37.81 R	DIEDALLK	H		
	1							522.23	1563.668	1562.773	0.8953	0	69.16 K	VNEILSHYPSNYK	Q		
	1							943.47	1884.925	1884.805	0.1201	0	50.61 K	GSDGYTYNNYEDLTPK	R		
2	TC300056	homologue to UniRef100_P05698 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=3; Hordeum vulgare Rep: Ribulose biphosphate carboxylase large chain prec	86	34242	5	10.5	742.87	2225.588	2225.039	0.549	0	11.22 K	NCGPAGGMTLLLGEPKPPD		2 Carbamidomethyl (C); Oxidation (M)		
2			335	667.9854	667.3402	0.6453	0	15 -	GNGPAPR	V							
2			383.73	765.4454	765.3545	0.091	0	16.63 R	DDFIEK	D							
2			481.71	961.4054	961.4716	-0.0662	0	25.26 K	SOAETGEIK	G							
2			481.77	961.5254	961.4716	0.0538	0	28.77 K	SOAETGEIK	G							
2			655.32	1308.625	1308.675	-0.0493	0	25.75 R	EMTLGFDVLLR	D	Oxidation (M)						
3	TC330136	similar to UniRef100_A7PUK9 Cluster: Chromosome chr7 scaffold_31, whole genome shotgun sequence; n=1; Vitis vinifera Rep: Chromosome chr7 scaffold_31, whole genome shot	83	41395	3	5.7	347.25	692.4854	692.3527	0.1328	0	7.16 -	NMTALK	E	Oxidation (M)		
3			412.74	823.4654	823.528	-0.0625	0	38.01 K	IVGVAPIR	V							
3			458.72	915.4254	915.4913	-0.0658	0	37.81 R	DIEDALLK	H							
4	TC356437	UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - Triticum aestiv	80	77238	5	5.7	383.73	765.4454	765.3545	0.091	0	16.63 R	DDFIEK	D			
4			481.71	961.4054	961.4716	-0.0662	0	25.26 K	SOAETGEIK	G							
4			481.77	961.5254	961.4716	0.0538	0	28.77 K	SOAETGEIK	G							
4			655.32	1308.625	1308.675	-0.0493	0	25.75 R	EMTLGFDVLLR	D	Oxidation (M)						
5	TC307909		801.06	1600.105	1600.832	-0.7262	0	8.7 R	QPMDLLCSLSIRPI	-	Oxidation (M)						
5			727.99	1453.965	1453.877	0.0885	0	7.48 -	LRPTPTTIFVLAR	S							
6	TC332693		737.89	1473.765	1472.788	0.9779	0	55.44 K	AQDTFTPISAVVPK	S							
6			55	24725	1	2.6	330.17	658.3254	658.3762	-0.0508	0	54.87 R	SGLQVR	S			
7	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	52	65917	1	1.1	330.17	658.3254	658.3762	-0.0508	0	52.28 R	SGLGAVR	W			
8	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog	50	19908	1	4.3	330.17	658.3254	658.365	-0.0396	0	50.28 R	SGGAVVG	-			
9	TC302791	homologue to UniRef100_P05698 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=3; Hordeum vulgare Rep: Ribulose biphosphate carboxylase large chain prec	49	47214	3	5.1	435.24	434.2327	433.2173	1.0155	0	6.17 K	GLSSA	-			
9			383.73	765.4454	765.3545	0.091	0	16.63 R	DDFIEK	D							
9			655.32	1308.625	1308.675	-0.0493	0	25.75 R	EMTLGFDVLLR	D	Oxidation (M)						
186	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC356437	UniRef100_P11383 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=2; Triticeae Rep: Ribulose biphosphate carboxylase large chain precursor - Triticum aestiv	221	77238	6	7.5	383.73	765.4454	765.3545	0.091	0	25.7 R	DDFIEK	D		
	1							464.72	927.4254	927.4596	-0.0342	0	35.05 R	AMHAVIDR	Q	Oxidation (M)	
	1							481.85	961.6854	961.4716	0.2138	0	40.52 K	SOAETGEIK	G		
	1							511.18	1020.345	1020.524	-0.1786	0	25.88 K	DTDILAAFR	V		
1			558.75	1115.485	1115.576	-0.0903	0	50.81 R	VALEACVQAR	N	Carbamidomethyl (C)						

187	2	TC323347	homologue to UniRef100_Q9MSY8 Cluster: Ribulose biphosphate carboxylase large chain; n=1; Ungernia flava Rep: Ribulose biphosphate carboxylase large chain - Ungernia flava	166	23182	5	19	655.33	1308.645	1308.675	-0.0293	0	42.68 R	EMTLGFVDLLR	D	Oxidation (M)	
	1	1						347.7	693.3854	693.3697	0.0157	0	22.15 K	AAIAVK	D		
	2	2						383.73	765.4454	765.3545	0.091	0	25.7 R	DDFIK	D		
	2	2						464.72	927.4254	927.4596	-0.0342	0	35.05 R	AMHAVIDR	Q	Oxidation (M)	
	2	2						481.85	961.6854	961.4716	0.2138	0	40.52 K	SOAETGEIK	G		
								655.33	1308.645	1308.675	-0.0293	0	42.68 R	EMTLGFVDLLR	D	Oxidation (M)	
188	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	70	67517	2	2.1	330.16	658.3054	658.3762	-0.0708	0	56.73 R	SGLGAVR	W		
	1	1						354.99	707.9654	708.4031	-0.4376	0	13.49 R	RPPSPR	A		
	2	TC293668	similar to UniRef100_Q6Z2I7 Cluster: SET domain-containing protein-like; n=1; Oryza sativa Japonica Group Rep: SET domain-containing protein-like - Oryza sativa subsp. japonica	60	56612	2	3.8	330.16	658.3054	658.3762	-0.0708	0	38.71 K	SLGOVR	D		
	2	2						708.85	1415.685	1415.744	-0.0588	0	21.31 K	LGLETPAAMLAASR	R	Oxidation (M)	
189	3	TC323693		59	24725	1	2.6	330.16	658.3054	658.3762	-0.0708	0	59.34 R	SGLQVR	S		
	4	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog	55	19908	1	4.3	330.16	658.3054	658.365	-0.0596	0	54.71 R	SGIGAVVG	-		
	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC300777	homologue to UniRef100_P46225 Cluster: Triosephosphate isomerase, chloroplast precursor; n=1; Secale cereale Rep: Triosephosphate isomerase, chloroplast precursor - Secale c	207	48928	6	15.4	458.77	915.5254	915.4161	0.1094	0	12.94 K	TFDVCFK	Q	Carbamidomethyl (C)	
	1	1						538.76	1077.505	1077.582	-0.0764	0	46.26 K	AAAYLSQNLK	V		
190	1	1						590.73	1179.445	1179.556	-0.1106	0	13.04 K	AFADINTDWK	N		
	1	1						610.35	1218.685	1218.62	0.065	0	33.89 K	TNVSADVASTVR	I		
	1	1						748.79	1495.565	1495.698	-0.1323	0	32.95 K	GPDFATICNSVTSK	K	Carbamidomethyl (C)	
	1	1						583.93	1748.768	1749.872	-1.1038	0	67.43 R	IYGGSVNAANCAELAK	K	Carbamidomethyl (C)	
	1	1															
191	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC282871	similar to UniRef100_A2YMU2 Cluster: Ribosome recycling factor, chloroplast precursor; n=2; Oryza sativa Rep: Ribosome recycling factor, chloroplast precursor - Oryza sativa subsp.	147	34449	6	21	331.66	661.3054	661.3282	-0.0228	0	20.95 K	LSEEGK	V		
	1	1						445.24	888.4654	888.4552	0.0102	0	25.99 K	DLSDLQK	I		
	1	1						482.24	962.4654	962.4743	-0.0088	0	26.92 K	MIVEEQAK	E	Oxidation (M)	
	1	1						542.7	1083.385	1083.592	-0.207	0	35.49 R	VTVPPLTSDR	R		
192	1	1						739.77	1477.525	1477.753	-0.2271	0	17.19 K	AIEYQSNFNTVR	T		
	2	TC323693		55	24725	1	2.6	330.19	658.3054	658.3762	-0.0108	0	54.96 R	TIAQINTPDATSLLIQPYDK	S		
	3	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	52	65917	1	1.1	330.19	658.3654	658.3762	-0.0108	0	54.96 R	SGLQVR	W		
	4	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog	50	19908	1	4.3	330.19	658.3654	658.365	0.0004	0	50.37 R	SGIGAVVG	-		
	1	1															
193	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC292572	similar to UniRef100_Q9FQC9 Cluster: Glutathione S-transferase GST 10; n=1; Zea mays Rep: Glutathione S-transferase GST 10 - Zea mays (Maize), partial (84%)	202	34834	7	19.6	380.22	758.4254	758.4286	-0.0032	0	36.43 K	AGLITER	K		
	1	1						429.75	857.4854	857.4719	0.0135	0	28.86 R	GNQTLTGR	K		
	1	1						447.22	892.4254	892.4654	-0.04	0	25.26 K	VLDVYER	R		
	1	1						452.26	902.5054	902.4895	0.0159	0	22.41 R	VAACLLEK	D	Carbamidomethyl (C)	
194	1	1						610.23	1218.445	1218.498	-0.0521	0	46.62 R	YICDQYSDR	G	Carbamidomethyl (C)	
	1	1						616.34	1230.665	1230.676	-0.0107	0	13.49 K	LQPPGQVPFAK	D		
	2	TC323693		55	24725	1	2.6	330.26	658.5054	658.3762	-0.0818	0	29.37 K	DVPFQLEAVDMSK	G	Oxidation (M)	
	3	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	52	65917	1	1.1	330.26	658.5054	658.3762	0.1292	0	54.99 R	SGLQVR	S		
	4	TC317706	homologue to UniRef100_Q9XGU8 Cluster: NADP-specific isocitrate dehydrogenase; n=3; Oryza sativa Rep: NADP-specific isocitrate dehydrogenase - Oryza sativa (Rice), partial (54%)	52	48440	2	3.4	374.88	747.7454	747.3697	0.3757	0	52.4 R	SGLGAVR	W		
195	5	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog	50	19908	1	4.3	330.26	658.5054	658.365	0.1404	0	28.83 R	NLMAGSR	T		
								577.26	1152.505	1151.47	1.0355	0	28.83 R	EVCSQSCPSR	I	Carbamidomethyl (C)	
								330.26	658.5054	658.365	0.1404	0	50.4 R	SGIGAVVG	-		
	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC325434	UniRef100_P93606 Cluster: Manganese superoxide dismutase; n=1; Triticum aestivum Rep: Manganese superoxide dismutase - Triticum aestivum (Wheat), complete	214	37703	5	15.4	331.66	661.3054	661.366	-0.0605	0	34.48 R	LHHQK	H		
196	1	1						494.76	987.5054	987.4185	0.0869	0	48.74 K	YAGEEYEK	V		
	1	1						573.29	1144.565	1143.614	0.9519	0	45.06 K	ALEQLDAAVSK	G		
	1	1						698.37	1394.725	1394.752	-0.0263	0	46.27 K	GDASAVVHLQSAIK	F		
	1	1						821.41	1640.805	1640.862	-0.0567	0	39.8 K	LSVETTPNQDPLVTIK	G		
	2	TC323693		60	24725	1	2.6	330.2	658.3854	658.3762	0.0092	0	60.22 R	SGLQVR	S		
197	3	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	58	65917	1	1.1	330.2	658.3854	658.3762	0.0092	0	57.62 R	SGLGAVR	W		
	4	CA747194	similar to UniRef100_Q4KGY9 Cluster: Oxidoreductase, short chain dehydrogenase/reductase family; n=1; Pseudomonas fluorescens Pf-5 Rep: Oxidoreductase, short chain dehydrog	55	19908	1	4.3	330.2	658.3854	658.365	0.0204	0	54.62 R	SGIGAVVG	-		
	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_cover	pep_exp_n	pep_exp_n	pep_calc_r	pep_delta	pep_miss	pep_score	pep_res_before	pep_seq	pep_res_al	pep_var_mod
	1	TC362013	UniRef100_Q96185 Cluster: Manganese superoxide dismutase; n=1; Triticum aestivum Rep: Manganese superoxide dismutase - Triticum aestivum (Wheat), complete	306	58717	8	14.7	331.7	661.3854	661.366	0.0195	0	27.05 R	LHHQK	H		
	1	1						494.72	987.4254	987.4185	0.0069	0	48.54 K	YAGEEYEK	V		
198	1	1						572.82	1143.625	1143.614	0.0119	0	83.38 K	ALEQLDAAVSK	G		
	1	1						572.83	1143.645	1143.614	0.0319	0	62.27 K	ALEQLDAAVSK	G		
	1	1						659.32	1316.625	1316.626	-0.0007	0	44.65 K	HHATYYVANYNK	A		
	1	1						698.32	1394.625	1394.752	-0.1263	0	35.34 K	GDASAVVHLQSAIK	F		
	1	1						795.91	1589.805	1589.816	-0.0107	0	20.99 K	NLKPISGGGGEAPHGK	L		
199	2	CK163788	homologue to UniRef100_P05698 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=3; Hordeum vulgare Rep: Ribulose biphosphate carboxylase large chain prec	108	35428	3	9.1	821.41	1640.805	1640.862	-0.0567	0	45.86 R	LSHVETTPNQDPLVTIK	G		
	2	2						464.71	927.4054	927.4596	-0.0542	0	24.54 R	AMHAVIDR	Q	Oxidation (M)	
	2	2						558.79	1115.565	1115.576	-0.0103	0	37.73 R	VALEACVQAR	N	Carbamidomethyl (C)	
	3	TC323693		51	24725	1	2.6	330.21	658.4054	658.3762	0.0292	0	50.64 R	EMTLGFVDLLR	D	Oxidation (M)	
	4	TC361139	UniRef100_A1EA16 Cluster: Ribulose biphosphate carboxylase large chain precursor; n=1; Agrostis stolonifera Rep: Ribulose biphosphate carboxylase large chain precursor - Agrc	50	34219	2	4.9	535.53	534.5227	534.2584	0.2643	0	5.1 R	LGSCR	-		
200	5	TC278848	similar to UniRef100_Q0DKA7 Cluster: Os05g0179000 protein; n=3; Oryza sativa Rep: Os05g0179000 protein - Oryza sativa subsp. japonica (Rice), partial (63%)	48	65917	1	1.1	655.35	1308.685	1308.675	0.0107	0	45.33 R	SGLQVR	S		
								330.21	658.4054	658.3762	0.0292	0	45.33 R	SGLGAVR	W		
	1	1															
	2	2															
	2	2															

Supplementary table 3

Cross-species comparison of mitochondrial proteins detected in this study. Accession refers to the wheat TC database (TaGI release 11). Arabidopsis homologue is the highest scoring hit returned when the accession was BLAST-searched against TAIR 7. Mitochondrial localisation details publications that report the Arabidopsis homologue gene as being mitochondrial-localised. Rice homologue is the highest scoring hit returned when the accession was BLAST-searched against Osa 5. Mitochondrial localisation – Huang 2009 details whether that homologue gene was detected in a 2-D gel study of FFE-purified rice mitochondrial proteins (Huang 2009).

Accession	Description	Functional classification	Arabidopsis homo	Description	BLAST score (Mitochondrial)	Rice homologue	Description	BLAST score	Mitochondrial localisation?
TC281405	2-oxoglutarate dehydrogenase E2 subunit	TCA	At5g55070.1	KDC E2-5 2-ox	1396	Heazlewood (2004)	Os04g32330.1	12004.m0833	1775 Yes
TC283468	Adenylate kinase	ATP	At5g63400.1	ADK1 ADK1 (A	896	Heazlewood (2004)	Os12g13380.1	12012.m0531	1012 Yes
TC297356	Adenylate kinase	ATP	At5g63400.1	ADK1 ADK1 (A	1050	Heazlewood (2004)	Os12g13380.1	12012.m0531	1164 Yes
TC284017	Aldehyde dehydrogenase	C met	At1g23800.1	ALDH2B, ALDH	2062	No	Os06g15990.1	12006.m0631	2259 Yes
TC298963	Aminomethyltransferase	GDC/SHMT	At1g11860.2	aminomethyltra	1444	Lee (2008)	Os04g53230.1	12004.m1021	1666 Yes
TC334873	Aspartate aminotransferase	N met	At2g30970.1	ASP1 ASP1 (A	1795	Heazlewood (2004)	Os02g14110.1	12002.m0665	2037 Yes
TC286019	ATP synthase 24 kDa subunit	ETC	At2g21870.1	ATP Fad Identi	700	Heazlewood (2004)	Os02g03860.1	12002.m0573	941 Yes
TC287957	ATP synthase 24 kDa subunit	ETC	At2g21870.1	ATP Fad Identi	698	Heazlewood (2004)	Os02g03860.1	12002.m0573	931 Yes
TC277166	ATP synthase alpha subunit	ETC	AtMg01190.2	ATP1 RNA edit	2338	Heazlewood (2004)	Osm1g00580.1	11706.m0005	2456 Yes
CF554354	ATP synthase beta chain	ETC	At5g08690.1	ATP2c ATP syr	131	Heazlewood (2004)	Os01g49190.1	12001.m1110	135 Yes
TC312825	ATP synthase beta chain	ETC	At5g08690.1	ATP2c ATP syr	2135	Heazlewood (2004)	Os01g49190.1	12001.m1110	2300 Yes
CK217579	ATP synthase D chain	ETC	At3g52300.1	ATPQ ATP7 A1	704	Heazlewood (2004)	Os08g37320.1	12008.m0771	780 Yes
CK194120	ATP synthase delta chain	ETC	At5g47030.1	ATP16 ATP syr	514	Heazlewood (2004)	Os07g31300.1	12007.m0739	588 Yes
TC277946	Chaperonin 10	HSP	At1g14980.1	CPN10 HSP10	367	Heazlewood (2004)	Os07g44740.1	12007.m0869	423 No
TC278575	Chaperonin 20	HSP	At5g20720.2	CPN10, CHCPI	818	Lee (2008)	Os06g09679.2	12006.m3224	908 No
TC295614	Chaperonin 20	HSP	At5g20720.2	CPN10, CHCPI	799	Lee (2008)	Os09g26730.1	12009.m0582	890 Yes
CK213510	Complex 1 subunit B13	ETC	At5g52840.1	NDUFA5 NADH	554	Heazlewood (2004)	Os03g19890.1	12003.m0740	687 Yes
TC303680	Complex 1 subunit B22	ETC	At4g34700.1	NDUFB9 comp	439	Sunderhaus (2004)	Os06g50000.1	12006.m0952	529 No
CK194459	Complex 1 subunit PDSW	ETC	At3g18410.1	NDUFB10-2 N	253	Heazlewood (2004)	Os10g42540.1	12010.m0700	288 Yes
TC282262	Cysteine synthase	AntiOx	At3g61440.1	ARATH;BSAS3	922	Heazlewood (2004)	Os04g08350.3	12004.m3524	1119 Yes
CA698948	Cytochrome oxidase VIB	ETC	At1g22450.1	ATCOX6B2, C	298	Tan (2010)	Os07g42910.1	12007.m0852	374 No
TC362955	Ferredoxin	AntiOx	At3g07480.1	electron carrier	363	Heazlewood (2004)	Os09g33950.1	12009.m0644	444 Yes
TC287863	Formate dehydrogenase	C met	At5g14780.1	FDH FDH (FO	1574	Heazlewood (2004)	Os06g29180.1	12006.m0746	1839 Yes
TC279660	Fumarase	TCA	At2g47510.2	FUM1 FUM1 (F	1288	Heazlewood (2004)	Os03g21950.1	12003.m0759	1393 Yes
TC284402	Fumarase	TCA	At2g47510.2	FUM1 FUM1 (F	1040	Heazlewood (2004)	Os03g21950.1	12003.m0759	1120 Yes
TC280819	Gamma carbonic anhydrase	ETC	At1g19580.1	GAMMACA1 G	1006	Klodmann (2010)	Os01g18070.1	12001.m0834	1089 Yes
TC282611	Gamma carbonic anhydrase	ETC	At1g47260.1	GAMMACA2, A	1136	Heazlewood (2004)	Os12g07220.1	12012.m0471	1289 Yes
CK215900	Glycine decarboxylase H subunit	GDC/SHMT	At1g32470.1	GDH3 glycine c	445	Heazlewood (2004)	Os10g37180.1	12010.m0651	548 Yes
TC283187	Glycine decarboxylase P subunit	GDC/SHMT	At4g33010.1	GDP1 glycine c	1337	Heazlewood (2004)	Os01g51410.1	12001.m1132	3011 Yes
TC297661	GrpE co-chaperone	HSP	At4g26780.1	AR192 AR192;	734	Tan (2010)	Os09g11250.1	12009.m0438	1019 No
TC308127	Heat shock protein 22	HSP	At4g25200.1	ATHSP23.6-MI	235	Van Aken (2009)	Os02g52150.2	12002.m1024	528 No
TC279929	Heat shock protein 60	HSP	At2g28000.1	CH-CPN60A, S	753	Heazlewood (2004)	Os12g17910.1	12012.m0574	919 Yes
TC282575	Heat shock protein 60	HSP	At3g23990.1	HSP60 HSP60	1556	Heazlewood (2004)	Os03g04970.1	12003.m0602	1656 Yes
TC302569	Heat shock protein 60	HSP	At2g28000.1	CH-CPN60A, S	2151	Heazlewood (2004)	Os12g17910.1	12012.m0574	2333 Yes
TC317092	Heat shock protein 60	HSP	At2g28000.1	CH-CPN60A, S	1122	Heazlewood (2004)	Os03g64210.3	12003.m1011	1268 No
TC338148	Heat shock protein 60	HSP	At3g23990.1	HSP60 HSP60	2404	Heazlewood (2004)	Os10g32550.1	12010.m0609	2592 Yes
TC292635	Heat shock protein 70	HSP	At5g09590.1	HSC70-5, mtH	1167	Heazlewood (2004)	Os03g02260.1	12003.m0576	1225 Yes
TC294781	Heat shock protein 70	HSP	At5g09590.1	HSC70-5, mtH	1815	Heazlewood (2004)	Os03g02260.1	12003.m0576	1918 Yes
TC308079	Heat shock protein 70	HSP	At5g09590.1	HSC70-5, mtH	1943	Heazlewood (2004)	Os03g02260.1	12003.m0576	2124 Yes
TC324780	Heat shock protein 70	HSP	At5g09590.1	HSC70-5, mtH	330	Heazlewood (2004)	Os02g53420.1	12002.m1037	375 Yes
TC295456	Heat shock protein 90	HSP	At2g04030.1	EMB1956, CRE	1795	Heazlewood (2004)	Os09g29840.1	12009.m2212	1974 No
TC289939	Isoaryl-CoA dehydrogenase	branched chain AA deg	At3g45300.1	ATIVD, IVD IVD	965	Heazlewood (2004)	Os05g03480.5	12005.m0836	1040 Yes
TC279818	Lipoamide dehydrogenase	GDC/SHMT	At1g48030.2	dihydrolipoamic	1773	Heazlewood (2004)	Os01g22520.1	12001.m0873	1957 Yes
TC290685	Lipoamide dehydrogenase	TCA	At3g17240.3	LPD2 LPD2 (LI	1452	Heazlewood (2004)	Os05g06750.1	12005.m0520	1612 Yes
TC278151	Malate dehydrogenase	TCA	At1g53240.1	MDH-2 malate	944	Heazlewood (2004)	Os05g49880.1	12005.m0905	1029 Yes
TC278653	Malate dehydrogenase	TCA	At1g53240.1	MDH-2 malate	1090	Heazlewood (2004)	Os01g46070.1	12001.m1080	1156 Yes
TC296475	Methylmalonate semi-aldehyde dehydrogenase	branched chain AA deg	At2g14170.1	ALDH6B2 MME	1897	Heazlewood (2004)	Os07g09060.1	12007.m0536	2300 Yes
TC307553	Methylmalonate semi-aldehyde dehydrogenase	branched chain AA deg	At2g14170.3	ALDH6B2 ALDI	952	Heazlewood (2004)	Os07g09060.2	12007.m2908	1213 Yes

TC278636	Mitochondrial processing peptidase alpha subunit	ETC	At1g51980.1	MPP alpha-1 m	558	Heazlewood (20	Os01g09560.1	12001.m0758	955	Yes
TC282024	Mitochondrial processing peptidase alpha subunit	ETC	At1g51980.1	MPP alpha-1 m	432	Heazlewood (20	Os01g09560.1	12001.m0758	710	Yes
TC287805	Mitochondrial processing peptidase beta subunit	ETC	At3g02090.1	MPPBETA MPF	1745	Heazlewood (20	Os03g11410.1	12003.m0659	2030	Yes
TC362013	Mn superoxide dismutase	AntiOx	At3g10920.1	MEE33, MSD1	879	Heazlewood (20	Os05g25850.1	12005.m0687	983	Yes
TC314827	Monodehydroascorbate reductase	AntiOx	At1g63940.4	monodehydroa	1082	Heazlewood (20	Os08g05570.4	12008.m2657	1290	No
CK197437	NADH-cytochrome b5 reductase	ETC	At5g20080.1	CBR1-2 NADH	346	Heazlewood (20	Os01g07910.1	12001.m0741	408	Yes
TC301455	NADH-ubiquinone oxidoreductase 24 kDa subunit	ETC	At4g02580.1	NDUFV2 NADH	1018	Heazlewood (20	Os05g43360.1	12005.m0846	1165	Yes
CK195103	Nucleoside diphosphate kinase	P met	At4g23900.1	NDPK3-2 nucle	137	Heazlewood (20	Os05g51700.3	12005.m0838	142	No
TC277379	Outer mitochondrial membrane porin	Membrane	At3g01280.1	VDAC1 porin, p	879	Heazlewood (20	Os09g19734.3	12009.m2207	1177	Yes
TC283205	Prohibitin	HSP	At5g40770.1	ATPHB3 PRHE	946	Heazlewood (20	Os02g37000.1	12002.m0878	1140	No
TC279495	Pyruvate dehydrogenase E1 beta subunit	TCA	At5g50850.1	PDC E1 beta-3	1553	Heazlewood (20	Os08g42410.1	12008.m0821	1727	Yes
TC312589	Pyruvate dehydrogenase E1 beta subunit	TCA	At5g50850.1	PDC E1 beta-3	1404	Heazlewood (20	Os09g33500.1	12009.m0639	1578	Yes
TC297018	Serine hydroxymethyltransferase	GDC/SHMT	At4g37930.1	STM, SHMT1, S	1690	Heazlewood (20	Os03g52840.3	12003.m1011	1778	Yes
TC356717	Serine hydroxymethyltransferase	GDC/SHMT	At4g37930.1	STM, SHMT1, S	1870	Heazlewood (20	Os03g52840.1	12003.m1025	1999	Yes
TC294283	Succinate dehydrogenase subunit 1	TCA	At5g66760.1	SDH1-1 SDH1-	2797	Heazlewood (20	Os07g04240.1	12007.m0489	2870	Yes
CK154109	Succinyl-CoA ligase alpha chain	TCA	At5g23250.1	succinyl-CoA li	296	Heazlewood (20	Os07g38970.1	12007.m0814	319	Yes
TC278426	Succinyl-CoA ligase beta chain	TCA	At2g20420.1	succinyl-CoA li	1165	Heazlewood (20	Os02g40830.2	12002.m1002	1284	Yes
CK164007	Uncharacterised CBS domain-containing protein	Unknown	At5g10860.1	CBS domain-cc	792	Heazlewood (20	Os03g52690.1	12003.m1024	921	Yes
TC282084	Uncharacterised DJ-1 domain-containing protein	Unknown	At1g53280.1	DJ-1 family pro	993	No	Os01g11880.1	12001.m0780	345	No
TC307909	Uncharacterised fumarylacetoacetate hydrolase family protein	Unknown	At4g15940.1	fumarylacetoac	766	Heazlewood (20	Os03g61330.2	12003.m3494	935	No

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Supplementary table 4

Detailed mass spectral information for the 199 peptides derived from 68 mitochondrial proteins confidently identified in this study (ions score >51). Spot number refers to Figure 1. Accession refers to the highest-scoring match in the wheat TC database (TaGI release 11). Protein descriptions were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue. Matched peptides is the number of peptides with ions score >51 matched to that accession. Ions score and predicted masses were determined by the Mascot search engine. Observed masses and intensities were extracted from raw peak list files. Table contains m/z values and peak intensities for precursor and the three most intense MS/MS fragment ions.

Functional class	Spot number	Accession	Protein	# Matched pep	Peptide sequence	Mods	Ions score	Mr	m/z	Precursor intensity	Fragment ion 1	Fragment 1 mass predicted	Fragment 1 mass observed	Intensity	Fragment ion 2	Fragment 2 predicted	Fragment 2 observed	Intensity	Fragment ion 3	Fragment 3 predicted	Fragment 3 observed	Intensity		
Electron Transport Chain	10	TC294283	Succinate dehydrogenase	1	TQETLTGCELISEAQK		52	1935.9095	969.48	1119590	y10	1134.5460	1134.74	119850	y5	562.2831	562.45	94715	y12	1364.6362	1364.80	82953		
	17	TC287805	Mitochondrial processing	1	HDDIVQQAQK		69	1052.5251	526.73	392169	y7	801.4465	801.57	49696	y8	916.4734	916.62	48121	y6	686.4196	686.51	21735		
	22, 23	TC312825	ATP synthase beta chain	10	IGLFGGAGVYK		56	974.5549	488.36	843975	y7, y6	545.3042, 545.3082	545.39	348250	y8	692.3726	692.48	344898	y9++	403.2320	403.41	93228		
					TIAMDGTGELVR	Ox-M	83	1277.6286	639.95	1670357	y10	1064.5041	1064.67	107926	y8	846.4316	846.56	105843	y7	731.4046	731.53	62114		
					EGVQSFGQVLDGK		88	1362.6780	682.23	1441492	y9	950.4942	950.64	169572	y6	588.3252	588.48	134837	y8	863.4621	863.60	88990		
					VGLTGLTVAEHR		100	1398.7620	700.53	580958	y7	859.4421	859.57	103732	y5	659.3260	659.45	102380	y6	758.3944	758.52	51529		
					VLNTGSPITVPVGR		56	1408.8038	705.51	2575311	y4, b4	428.2616, 428.2504	428.40	755506	y8	838.5145	838.67	428139	yO10, bO10	964.5574, 964.5462	964.66	414473		
					TVLIMELINNVAK	Ox-M	96	1472.8272	737.56	412646	y6	545.3042	545.44	60024	y6	658.3883	658.48	44128	y9	1047.5503	1047.70	43989		
					FTQANSEVSALLGR		93	1491.7681	747.04	829011	y11	616.3777	616.47	53925	y11	1116.6008	1116.73	38011	y9	931.5207	931.66	30898		
					CALVYGMNEPPGAR		52	1677.7603	840.00	2821763	y5	497.2831	497.39	876664	b10	1182.4918	1182.66	387068	y11	1235.5474	1235.72	285394		
22, 23	CF554354	ATP synthase beta chain			MLSPHVLGVVDHYNTAR	Ox-M	61	1824.8941	913.53	867892	y6	761.3689	761.51	138853	y9	1032.4857	1032.64	80280	y10	1145.5698	1145.74	77635		
					IPSAVGYYQPTLATDLGGLQER		129	2185.1379	1093.71	2559294	y13	1370.7274	1370.91	1949412	y7	772.4312	772.59	938820	y16	1718.8708	1719.09	445635		
	27, 28, 29, 30	TC277166	ATP synthase alpha subu	1	EGVESFQGVLDGK		52	1363.6620	682.49	5174170	y9	950.4942	950.63	367649	y6	588.3352	588.45	352012	y8	863.4621	863.63	225758		
				8	VVSVGDGIAR		71	971.5400	486.81	774.4104	y8	774.51	4716322	588.3100	588.43	2231936	b2	286.1761	286.28	2239301				
					TGSIVDPAGK		59	1042.5659	522.31	1399983	y7	685.3879	685.48	1494325	y6	586.3195	586.42	1196662	y4	372.2241	372.37	523597		
					AAELTTLLESR		78	1202.6506	602.49	1527160	y4	504.2776	504.39	254026	y7	819.4571	819.57	161281	y6	718.4094	718.53	123456		
					TAIAIDTILNQK		79	1299.7398	650.93	467695	y3	389.2143	389.32	191797	b9	912.5401	912.67	131823	y4	502.2984	502.46	64022		
					AILSTINPELQK		51	1325.7554	664.03	2081184	y6	728.3937	728.53	522600	y5	614.5508	614.45	397754	b7	696.3927	696.59	385051		
					VVDALGVPIQDK		76	1181.6656	592.00	3644103	y7	685.3879	685.48	1498485	y5	529.2980	529.47	1118528	y10	984.5360	984.66	558435		
					DNGMHALIYYDDLK	Ox-M	73	1719.8138	861.03	971020	y8	966.5142	966.67	88109	y9	1079.5893	1079.75	84054	y6	740.3461	740.48	79307		
34	TC278636	Mitochondrial processing			MTNFYTNFQVDEIGR	Ox-M	106	1849.8305	926.01	301443	y10	1178.5800	1178.76	61376	y5, y10++	589.294, 589.7937	589.37	33643	y11	1341.6434	1341.82	27550		
				2	LNPLVNEFDQIK		68	1428.7613	715.54	192951	y10++	601.8244	601.97	156524	y7	893.4363	893.55	80863	y10	1202.6416	1202.82	51763		
					AVDAITLADVSTVAEK		58	1601.8512	802.03	127952	y9	919.4731	919.62	27939	y6	634.3406	634.40	18608	y8	848.4360	848.59	18874		
	35	TC282024	Mitochondrial processing	3	LNPLVNEFDQIK		68	1428.7613	715.50	195444	y10++	601.8244	601.95	131874	y7	893.4363	893.54	62501	y10	1202.6416	1202.82	40786		
					AVDGITLADVSSVAEK		95	1573.8199	788.37	373815	y9	905.4575	905.59	126973	y8	834.4203	834.54	80065	y11	1119.5892	1119.75	98291		
					ELTSLATPGQVDQTQLDR		52	1970.9909	986.65	387306	y11	1256.6230	1256.78	501438	y12	1357.6706	1357.81	100284	y13	1428.7078	1428.89	64014		
	94	TC282611	Gamma carbonic anhydrase	1	LGSTIQGGLR		84	1000.5665	501.20	190520	y5	530.3045	530.28	227931	y4	402.2459	402.24	158531	y6	643.3886	643.32	77974		
	78	CA698948	Cytochrome oxidase VIB	3	FPTTNQTR		51	963.4774	482.83	259124	y6	720.3635	720.34	154070	y5	619.3158	619.29	91677	y7++	409.2118	409.25	85076		
					VPTLAEEYSLPPK		93	1442.7657	721.82	582914	y3	341.2183	341.23	98684	y9	1033.5201	1033.54	59918	y8	962.4829	962.48	50029		
					DTETSPADETAVAVEEK		94	1790.8058	896.22	158470	y12	1258.6161	1258.67	68980	y5	575.3035	575.30	24780	yO3	387.1874	387.21	11670		
91	CK197437	NADH-cytochrome b5 reductase		1	DYSQGEVTGLLK		53	1308.6561	655.33	377986	y8	816.4825	816.43	43658	y10	1031.5732	1031.53	23377	y4	430.3024	430.27	17078		
	106	TC286019	ATP synthase 24 kDa subunit	4	ADLLNDSQR		54	1030.5043	516.36	169747	y5	619.2794	619.29	257879	y6	732.3635	732.38	84997	y4	505.2365	505.30	42312		
					TYLDTLQQLR		70	1249.6666	625.88	400895	y8	986.5629	986.59	144031	y7	873.4789	873.49	109774	y4	544.3202	544.36	101736		
					NMNLLLAEFDK	Ox-M	82	1322.6540	662.36	227842	y6	722.3719	722.41	62325	y7	835.4560	835.48	59374	y5	609.2879	609.31	54502		
					IEENLEMELAK	Ox-M	57	1333.6435	667.85	631575	y9	1092.5242	1092.55	41468	y6	736.3546	736.37	37517	y8	963.4816	963.47	21524		
	106, 107	TC287957	ATP synthase 24 kDa subunit	4	EVVEAMEGQLK		70	1249.6666	625.88	400895	y8	986.5629	986.59	144031	y7	873.4789	873.49	109774	y4	544.3202	544.36	101736		
					TYLDTLQQLR	Ox-M	70	1249.6666	625.88	400895	y8	986.5629	986.59	144031	y7	873.4789	873.49	109774	y4	544.3202	544.36	101736		
					NMGLLLAEFDK	Ox-M	88	1265.6326	633.89	173905	y9, b9	1005.5615, 1005.5074	1005.57	39016	y7	835.4560	835.48	33737	y5	609.2879	609.29	32079		
					IEENLEMELAK	Ox-M	57	1333.6435	667.85	631575	y9	1092.5242	1092.55	41468	y6	736.3546	736.37	37517	y8	963.4816	963.47	21524		
					1 LTVNFVLPIK		82	1192.6856	597.42	231177	y3	407.2289	407.27	91861	y4	520.3130	520.36	75572	y8	979.5611	979.57	55651		
113, 114	CK194120	ATP synthase delta chain		1	ISTMTADEYFAK	Ox-M	70	1391.6279	696.79	1193961	y*10++	588.2499, 587.7579	587.77	46506	y6	772.3512	772.35	19016	y8	944.4360	944.48	18707		
	116	CK217579	ATP synthase D chain	1	ETTGIVGLDVPEAR		74	1554.8253	778.44	293300	y4	472.2514	472.30	102609	y9	955.5520	955.55	74233	b11	1084.5885	1084.63	48280		
	138	TC303680	Complex 1 subunit B13	1	L																			

Photorespiration	2, 3, 4, 147	TC283187	Glycine decarboxylase P	3 FEEDDLMLPK	Ox-M	76	1322.6064	662.49	867384	y9	1047.5027	1047.67	208988	y6	690.3491	690.46	166125	y8	918.4601	918.58	94398				
				GEDFPAENYIK		60	1380.6561	691.39	863744	y8	933.5040	933.63	208988	b08**	421.6694	421.29	50662	y7	836.4512	836.63	34932				
				IGVIFYQAGEYADK		59	1558.7668	780.51	221828	y10	1191.5317	1191.72	30361	y9	1044.4633	1044.64	19442	y6	682.3042	682.43	13742				
				3 VDDGYVINGNK		53	1134.5669	568.36	644.3726	y6	27028	644.46	27028	y5	545.3043	545.44	29391	y9	921.4789	921.56	34778				
				LFEIGAGTSEIR		72	1291.6772	646.97	81859	y8	790.4054	790.49	56750	y6	662.3468	662.43	35405	y7	733.3839	733.49	14745				
				MADMYTSLQSSR	2 x Ox	58	1420.5963	711.40	112572	y7	778.4054	778.50	16964	y6	677.3577	677.48	12688	y5	590.3257	590.35	8136				
				2 LFEIGAGTSEIR		73	1291.6772	646.87	295856	y8	790.4054	790.40	68270	y6	662.3468	662.34	40951	y9	903.4894	903.50	23931				
				DCAGVILFAAER	Carbai	67	1320.6496	660.82	819.4723	y7	819.4723	819.50	28598	y5	593.3042	593.33	26038	y6	706.3883	706.35	17453				
				2 AFGAQLVLTDPK		93	1329.7292	665.97	216133	y6	644.3614	644.46	58865	y7	743.4298	743.52	37431	y3	315.2027	315.29	32715				
				DTAAHLIGR		52	952.4454	477.23	458.3085	y4	53471	458.36	53471	y5	595.3675	595.48	28742	y5**	298.1874	298.28	15465				
Molecular Chaperones	131	CK215900	Glycine decarboxylase H	2 TPGVDDVSGEPLQR		88	1581.7999	791.96	543454	y5	626.3984	626.35	61977	y8	899.4945	899.46	56071	y7	812.4625	812.44	25893				
				96 TC283468	Adenylate kinase	110	1616.8410	809.24	133014	y8	809.24	809.24	133014	y5	626.3984	626.35	61977	b10	1072.5673	1072.54	27650	y4	546.2862	546.26	17348
				129	CK195103	Nucleoside diphosphate h	91	1595.155	799.99	236939	y5	626.3984	626.35	61977	y8	913.5102	913.47	48324	y11	912.6325	912.63	23153			
				169	TC34873	Aspartate aminotransferase	74	1637.6037	649.85	362386	y6	707.32	707.32	119326	y6	957.4190	957.42	119640	y7	870.4840	870.48	67042			
				169	TC34873	Aspartate aminotransferase	51	1309.6224	655.82	85758	y7	807.3917	807.38	29944	y8	878.4288	878.39	16518	y5	637.2862	637.29	10588			
				9	VDDVYGDR		56	936.4301	469.38	184060	y4	510.2307	510.33	681413	y6	723.3420	723.45	190935	y3	347.1674	347.29	164705			
				1	IAILNANYMAK		63	1220.6587	611.49	772785	y7	811.3767	811.51	722769	y8	924.4608	924.57	419207	y6	697.3338	697.48	203552			
				ITCADANIAEEAR	Carbai	107	1503.6987	752.96	714734	y5	575.2784	575.39	118922	y6	688.3624	688.46	83064	y10	1059.5065	1059.66	73636				
				LNATVEMMPVTDPK	Ox-M	83	1560.7528	781.50	580436	y9	1063.4799	1063.66	103151	y6	656.3614	656.48	86694	b12	1316.6018	1316.77	87633				
				LGTVTVQELPYFDTVK		88	1808.9560	905.55	747124	y7	869.4403	869.59	133297	y8	982.5244	982.69	47352	y10	1239.6256	1239.84	37591				
Antioxidant defense	121	TC277946	Chaperonin 20	ATAGIEPEDVAK		59	1199.6034	600.96	951510	y6	658.3406	658.42	29432	y7	787.3832	787.49	267007	b8, y073.3727, 769.3727			769.49	103084			
				GNINIEELR		62	1056.5563	529.02	1361286	y4	546.2882	546.45	424078	y6	773.4152	773.53	294447	b5	512.2827	512.35	185458				
				FCDALISIR	Carbai	70	1093.5590	547.92	1095708	y7	787.4672	787.57	1288599	y4	488.3191	488.47	3752288	y3	375.2350	375.34	445510				
				EYAAFPAAWLR		53	1293.6506	647.91	360607	y6	713.4093	713.50	399396	y7	860.4777	860.63	109173	b04	417.1769	417.32	101999				
				7 YSEGYPGAR		60	998.4457	500.37	709978	y4	400.2303	400.39	491768	y7	749.3577	749.48	523790	y6	620.5131	620.40	237697				
				GHVADFAAK		56	1310.5335	621.38	604411	y6	521.338	521.38	609462	y8	837.3989	837.42	339486	y9	904.3342	904.37	608962				
				LIVAGASAYAR		85	1090.8135	546.46	1215360	y7	695.3471	695.43	2967983	y9	865.4526	865.58	2756390	y5	766.3842	766.48	1509741				
				ALEAFNLDPEK		79	1245.6241	623.90	169585	y4	488.2351	488.24	52416	y3	373.2082	373.22	34594	y6	715.3621	715.33	28269				
				LDESTGLIDYDQLEK		78	1737.8309	870.05	2461139	y7	910.4153	910.53	304499	y8	1023.4993	1023.68	201581	y6	795.3883	795.51	105706				
				GYDIVSGGTDNHLVLNLIK		76	2013.0531	1007.57	413538	b14	1426.6754	1426.84	60682	y14	1466.7962	1466.99	56103	b16	1640.8279	1641.00	51645				
Metabolite Transport	50	TC289863	Aminomethyltransferase	YYGGNEYIDMAETLCQK	Carbai	77	2069.8710	1036.09	534220	y9	1111.4758	1111.65	271927	y5	649.3338	649.44	157150	y11	1387.6232	1387.80	124370				
				2 VGIFSQGPPIR		56	1153.6244	577.94	1939511	y5	523.2987	523.29	231527	y4	466.2772	466.40	206904	y7	738.3893	738.47	60024				
				DGTGSLTVFTNDK		81	1353.6413	678.01	802782	y6	624.2988	624.41	327712	y7	824.4149	824.53	240470	y4	477.2304	477.34	137687				
				1 VKPSPAPAELEGLLDSAK		133	1739.9305	871.01	1026451	y15	1513.7744	1513.81	128777	y12	1242.6576	1242.72	110404	y7	703.3985	703.45	45164				
				3 NTENDLSIK		52	1032.5087	517.31	120912	y7	818.4254	818.43	121416	y6	689.3828	689.40	95264	y4	462.2558	462.29	36467				
				76DEVLLVGMTR	Ox-M	68	1418.7076	709.93	441087	y5	537.2450	537.27	137728	b8	862.4815	862.49	11155	b7	749.3978	749.39	19678				
				VGQEVSEIFGK		54	1247.6761	625.34	355861	y9	8021.5564	8021.58	25803	y6	680.3614	680.37	27824	y7	774.4298	774.39	21609				
				1 SGGLSEAEIK		54	1035.5335	603.29	1093535	y4	804.4093	804.41	703441	y5	588.3342	588.34	334986	y4	717.37	717.37	30553				
				2 SGGLSESEIEK		65	1221.5724	611.82	389441	y7	821.3987	821.38	303417	y6	734.3567	734.36	58015	y5	605.3141	605.36	30264				
				NTADTTYSIEK		54	1354.6616	678.35	353353	y5	639.3348	639.36	62017	y9	1069.5412	1069.53	56504	y10	1140.5783	1140.62	50038				
Unknown	11	TC302569	Heat shock protein 60	14 LGADIIQK		54	856.5018	429.35	288527	y6	687.4036	687.50	166876	y7	744.4520	744.51	159082	y5	616.3665	616.48	48057				
				AALQAGVEK		53	885.4920	443.92	144134	y5	503.2824	503.36	511942	y6	631.3410	631.42	355237	y7	744.4250	744.52	304332				
				GIINVAIK		52	897.5647	449.87	529803	y7	728.4665	728.55	621025	y6	615.3824	615.48	299708	y4	402.2711	402.40	183605				
				VVNDGVTIAR		61	1042.5771	522.42	902621	y8	845.4476	845.56	308224	y4	460.2878	460.42	176969	y6	616.3777	616.47	92355				
				SIVEFENAR		63	1063.5298	532.97	553462	y7	864.4210	864.54	444696	y5	636.3100	636.42	369738	y6	765.3526	765.46	271400				
				LANAVGVTLGPR		77	1166.6772	584.42	1311322	y7	699.4148	699.53	239121	y5	543.3249	543.43	99230	y8	798.4832	798.60	85687				
				VGATTETELEDK		80	1319.6205	660.93	1328490	y6	762.3628	762.50	114560	y8	992.4531	992.62	92509	y7	891.4054	891.51	57123				
				GYISPOFVTNLEK		68	1494.7718	748.51	921833	y7	1075.5782	1075.70	396028	y10	1162.8103	1162.75	303865	y5	604.3301	604.46	114451				
				ELSEDTSDYSEK		52	1514.6624	758.48	692217	y8	956.4207	956.53	665323	y5	641.2777	641.36	63224	y9	1057.4684	1057.64	55965				
				GYISVTSGANPVSLEK		74	1943.5891	973.68	1943593	y10	973.5313	973.68	217501	y8	785.4516	785.48	127150	b11	1125.6150	1125.75	34111				
Antioxidant defense	13, 14, 15, 16, 148, 159	TC338148	Heat shock protein 60	TNDSAGDGTTCACVLLAR	Carbai	92	1708.7686	855.52	789744	y12	1221.5892	1221.81	16980	y8	891.4717	891.63	15110	y10	1049.5408	1049.72	11548				
				LIELANPMENAGAILIR	Ox-M	77	1768.9141	885.59	679012	y11	1158.5936	1158.78	217381	y12	1272.6365	1272.80	115199	y6	600.3828	600.53	44526				
				AVLQDIIVTGALEYALK		76	1773.9876	887.85	215609	y7	751.3985	751.51	815701	y8	852.4462	852.56	60431	y9	951.5146	951.66	48258				
				DLGLLVENATVDQLGTAR		81	1883.9953	943.09	186092	y7	760.3948	760.49	111311	b11	1125.6150	1125.75	34111	b14	1481.7846	1481.90	21317				
				8 AALQAGVEK		53	885.4920	443.92	144134	y5	503.2824	503.36	511942	y6	631.3410	631.42	355237	y7	744.4250	744.52	304332				
				VVNDGVTIAR		61	1042.5771	522.42	902621	y8	845.4476	845.56	308224	y4	460.2878	460.42	176969	y6	616.3777	616.47	92355				
				SIVEFENAR		63	1063.5298	532.97	553462	y7	864.4210	864.54	444696	y5	636.3100	636.42	369738	y6	765.3526	765.46	271400				
				LASAVGVTLGPR		93	1139.6663	570.95	1480046	b8, y7	699.4036, 699.4148	699.52	1135632	y3	329.1932	329.32	492245	y5	543.3249	543.48	357645				
				GYISPOFVTNLEK		68	1494.7718	748.51	921833	y7	1075.5782	1075.70	396028	y10	1162.8103	1162.75	303865	y5	604.3301	604.46	114451				
				LGILSVTSGANPVSLEK		74	1554.8981	778.59	1943593	y10	973.5313	973.68	217501	y8	785.4516	785.60	125785	y9	872.4836	872.63	110695				
Metabolite Transport	99, 100	TC277379	Outer mitochondrial memi	TNDSAGDGTTCACVLLAR	Carbai	92	1708.7686	855.52	789744	y12	1221.5892	1221.81	16980	y8	891.4717	891.63	15110	y10	1049.5408	1049.72	11548				
				LIELANPMENAGAILIR	Ox-M	77	1768.9141	885.59	679012	y11	1158.5936	1158.78	217381	y12	1272.6365	1272.80	115199	y6	600.3828	600.53	44526				
				10 VTDALNATK		73	931.4975	466.85	155034	y7	732.3586	732.50	511980	y8	546.3246	546.44	86018	b2	201.2324	201.14	20114				
				SVAAGNMNMDLR	2 x Ox	84	1266.5696	634.45	4																

Supplementary table 5

Detailed mass spectral information for the 51 peptides derived from 23 contaminating proteins confidently identified in this study (ions score >51). Spot number refers to Figure 1. Accession refers to the highest-scoring match in the wheat TC database (TaGI release 11). Protein descriptions were obtained by BLAST searching the matched TC sequence against Arabidopsis and rice, and selecting the most concise description of the closest homologue. Matched peptides is the number of peptides with ions score >51 matched to that accession. Ions score and predicted masses were determined by the Mascot search engine. Observed masses and intensities were extracted from raw peak list files. Table contains m/z values and peak intensities for precursor and the three most intense MS/MS fragment ions.

Funtional class	Spot number	Accession	Protein	# Matched peptides	Peptide sequence	Mods	Ions score	Mr	m/z	Precursor intensity	Fragment ion 1	Fragment 1 mass predicted	Fragment 1 mass observed	Intensity	Fragment	Fragment 2 predicted	Fragment 2 observed	Intensity	Fragment	Fragment 3 predicted	Fragment 3 observed	Intensity
Contaminants		6 TC309836	Transketolase		4 ESVLPEAVTAR	Carbami	60	1170.6244	586.44	1098332	y7	743.4046	743.51	1058339	y5	517.3093	517.46	65939	y8	856.4887	856.66	58894
					NLSQQCLNALAK		68	1358.6976	680.43	1015530	y10	1132.5779	1132.75	101959	y8	917.4873	917.62	71911	y7	789.4287	789.55	58582
		6 TC283917	Transketolase		EYGITAENVIAAAK	Ox-M	69	1448.7511	725.52	883810	y10	987.5469	987.69	402547	y9	886.4993	886.66	121982	y8	815.4621	815.57	90656
					VVPLGLIGGSADLASSNMTLLK		73	2058.1031	1030.21	217981	y8	909.4710	909.66	38847	y15	1480.7312	1480.94	20658	y9, y20++	980.5081	980.64	18290
		31, 33, 76, 86, 87, 134, 182 TC356437	RuBisCo large subun		2 EYGITAESVIAAAK		52	1421.7402	711.90	689307	y10	960.5360	960.69	102422	y9	859.4884	859.64	24713	y8	788.4512	788.58	15009
					ESVLPEAVTAR		60	1170.6244	586.44	1098332	y7	743.4046	743.51	1058339	y5	517.3093	517.46	65939	y8	856.4887	856.66	58894
					4 DTDILAAFR	Carbami	83	1020.5240	511.35	121396	y5	577.3457	577.29	321385	y4	464.2616	464.22	244614	y3	393.2245	393.20	117846
					VALEACVQAR		69	1115.5757	559.32	128141	y6	704.3508	704.49	56217	y5	633.3137	633.37	35967	y7	833.3934	833.52	26465
					DNGLLLHIHR		58	1186.6571	594.76	417513	y4	562.3208	562.29	86896	y5	675.4049	675.36	70695	y6	788.4890	788.46	61912
					EMTLGFVDLLR		Ox-M	59	1308.6748	655.37	839401	y7	819.4723	819.45	210289	y5	615.3824	615.34	118792	y4	516.3140	516.29
		51, 53 TC317220	RuBisCo activase		3 SFQCELVFAK	Carbami	56	1227.5958	614.98	151521	y7	866.4441	866.54	57808	y3	365.2183	365.30	54801	y4	464.2867	464.39	35015
					GLAYDISDDQQDITR		95	1708.7904	855.54	272222	y9	1077.4807	1077.64	87031	y8	990.4487	990.59	31003	y7	875.4217	875.52	28416
		68 TC283350	Fructose-bisphospha		MGINPIMMSAGELESGNAGEPAK	3 x Ox-IV	69	2351.0443	784.82	261742	b18++	926.3997	926.54	31681	b22++	1103.4767	1103.73	26206	y8	743.3682	743.45	27086
					1 AAQEALLLR		81	983.5763	492.90	217541	y3	401.2871	401.41	193210	y2	288.2030	288.28	136964	y4	514.3711	514.53	127438
		82 TC287942	Inorganic pyrophosph		2 IVAISLDDPK	3 x Ox-IV	58	1069.6019	535.82	388349	y8	858.4567	858.46	437404	y6	674.3355	674.33	179709	y7	787.4196	787.43	80669
					MEVATDEAYTPIK		89	1482.6912	742.41	157317	y10	1108.5521	1108.54	38963	y9	1037.5150	1037.54	16104	b3	376.1537	376.14	13651
103, 104	TC298182		Triosephosphate isor		1 TNVSDAVSTVR		99	1218.6204	610.25	97163	y9	905.4687	905.48	53526	y4	462.2671	462.29	33723	y5	533.3042	533.35	29502
		111, 112 TC278554	Peroxiredoxin		2 YPLVSDVTK		66	1020.5492	511.22	326341	y7	761.4403	761.47	219081	y6	648.3563	648.37	187041	y5	549.2879	549.33	115565
					AAAEYDLPLVGNK	66	1359.7034	680.76	108084	y6	627.3824	627.40	45021	y9	1018.5568	1018.60	30083	y8	855.4934	855.52	27633	
		126 CK216997	Cu/Zn superoxide dis		1 GGHELSTLTGNAGGR		51	1411.6804	706.43	103877	y8	719.3431	719.33	13405	y10	919.4592	919.40	13268	y7	632.3111	632.30	10688
					1 EHNSSPGYYDGR		74	1380.5694	691.32	874182	y7	827.3682	827.35	77206	y2	232.1404	232.09	18970	y10	1001.4323	1001.42	16321
		136 TC349826	RuBisCo small subur		1 GLLYLGMGVSGGEEGAR	Ox-M	54	1680.8141	841.37	525038	y8	762.3377	762.36	50662	y12	1122.4844	1122.48	38659	y7	675.3056	675.29	21787
					2 GFSSEGYIDK		65	1158.5193	580.28	179315	y9	955.4367	955.43	24503	y6	652.3301	652.44	20757	y8	868.4047	868.43	18048
		160 TC310800	6-phosphogluconate r		LLAGESGVGPIDR		58	1282.6881	642.38	671691	y5	557.3042	557.32	137994	y8	800.4261	800.39	64919	y4	500.2827	500.28	50733
					2 GFSSEGYIDK		65	1158.5193	580.28	179315	y9	955.4367	955.43	24503	y6	652.3301	652.44	20757	y8	868.4047	868.43	18048
		163 TC316257	3-oxoacyl synthase		ALESAGLALGSDAMAK	Ox-M	74	1519.7552	760.83	377959	y7, b08	695.3029	695.33	115252	y8, b09	808.3869	808.45	59959	y6	638.2814	638.29	39636
					1 AAPAAAAYPAYTR		52	1228.6564	615.38	151812	y11++	544.2984	544.30	77405	y6	706.3883	706.39	53347	y7	777.4254	777.43	41774
		175 TC281478	Fructose-bisphospha		1 LASIGLENTEANR		73	1386.7103	694.40	924232	y9	1003.4803	1003.45	98370	y7	833.3748	833.31	57694	y6	704.3322	704.31	26842
					2 LASIGLDNTEVNR		71	1400.7259	701.33	710328	y9	1017.4960	1017.52	36553	y7	847.3904	847.37	23184	y6	732.3635	732.30	8006
		176 TC342749	Fructose-bisphospha		GILAIDESSATCGK	Carbami	83	1420.6868	711.33	249066	y9	954.3833	954.34	34418	y10	1067.4674	1067.49	20936	y4	465.2126	465.24	16182
					5 VIAAGANPVQITR		89	1308.7514	655.51	547733	y6	713.4305	713.54	317657	y7	827.4734	827.59	179301	y9	955.5320	955.66	152275
13, 14	TC282663		Heat shock protein 6		NLIEAAEQDYEK		87	1421.6674	711.91	754249	y9	1082.4637	1082.60	214821	y8	953.4211	953.55	119626	y10	1195.5477	1195.73	106553
					GYISPYFVTDSEK		83	1504.7086	753.50	511128	y9	1085.5150	1085.69	313151	y10	1172.5470	1172.69	286257	y7	825.3989	825.53	58410
					ESTTIVGDGSTQEEVTK		67	1779.8374	890.49	640982	y11	1150.5222	1150.68	223951	y12	1249.5907	1249.75	141116	y9	978.4738	978.63	81069
					SSENNLYVVEGMQFER		Ox-M	56	1916.8574	959.52	720253	y8	1011.4564	1011.61	196502	y7	912.3880	912.52	149865	y9	1110.5248	1110.70
13, 14	TC323689		Heat shock protein 6		5 VEDALNATK		54	959.4924	480.86	429802	y7	732.3886	732.50	1137782	b2	229.1183	229.11	184120	y5	546.3246	546.45	130901
		LADLVGVTLGPK			54		1181.7020	592.02	1643797	y7	671.4087	671.51	463471	y8	770.4771	770.58	270719	b5	512.3079	512.44	149124	
					CCLLEHAASVAK	2 x Carb	58	1244.5642	623.42	443757	y7	683.3835	683.47	41029	y9	925.5102	925.64	32597	y6	546.3246	546.46	27950
					GYISPYFVTDSEK		83	1504.7086	753.50	511128	y9	1085.5150	1085.69	313151	y10	1172.5470	1172.69	286257	y7	825.3989	825.53	58410
		5 TC318499	Heat shock protein 7		AAVEEGIVVGGGCTLLR	Carbami	82	1699.8927	851.07	395992	y8	833.4298	833.55	171879	y10	1031.5666	1031.73	144094	y9	932.4982	932.64	72513
									2 NQADSVVYQTEK	68	1380.6521	691.46	115893	y5	668.3250	668.41	23158	y6	767.3934	767.44	18371	y10
		145 TC322003	Heat shock protein 9		IINEPTAASLAYGFEK		68	1722.8828	862.54	289807	y12	1254.6365	1254.83	83651	y8	914.4618	914.63	20139	y9	985.4989	985.73	16638
					1 ISDGALVAAAAASDR		85	1428.7572	715.35	540609	y8	774.4104	774.40	88683	y7	703.3733	703.41	49752	y6	632.3362	632.32	46725
15	TC299996		Heat shock protein 7		6 TPVDNSLR		60	900.4665	451.43	183456	y4	604.3049	604.41	289299	y6	703.3733	703.48	200476	y4	489.2780	489.37	143484
							IPAVQDLVK	77	981.5859	491.96	607814	y8++	435.2582	435.38	812059	y7	772.4563	772.56	374601	y6		
					EIDEVILVGGSTR		69	1386.7355	694.47	768667	y5	677.2416	677.34	248872	b8	911.5084	911.64	136546	y6	576.3100	576.41	98705
					NQAESVIYQTEK		69	1408.6834	705.53	149443	y10	1167.5892	1167.76	33716	y5	668.3250	668.39	21947	y6	781.4090	781.56	19484
					TGDGGDIVADFTDSN		60	1597.6380	799.93	636300	y8	884.3268	884.43	83008	b8	715.3257	715.40	45819	y6	698.2628	698.38	42601
					IINEPTAASLAYGFEK		68	1722.8828	862.54	289807	y12	1254.6365	1254.83	83651	y8	914.4618	914.63	20139	y9	985.4989	985.73	16638
146	TC287865		Heat shock protein 9		1 AIDLIDAGSR		72	1158.5880	580.20	289105	y6	634.2791	634.29	213554	y7	747.3632	747.34	118756	y9	975.4742	975.49	70615
		146 TC331352	Heat shock protein 9		63		1475.7773	738.86	211828	y5	617.3406	617.34	98912	y7	859.4672	859.47	57523	y6	730.4246	730.43	28392	

Supplementary Figure 1:

Supplementary Figure 1: DIGE images detailing protein spots that exhibited significant differences in abundance between varieties or treatments. The experiment compared protein abundance in mitochondria isolated from four experimental groupings: Wyalkatchem control, Janz control, Wyalkatchem salt, and Janz salt. Three biological replicates were performed. DIGE gels contained 50 μ g mitochondrial proteins labeled with Cy3 (green) and 50 μ g mitochondrial proteins labeled with Cy5 (red). Cy3 and Cy5 images were overlaid, such that protein spots equally abundant in the two samples are yellow, protein spots more abundant in Cy3 sample are green, and protein spots more abundant in Cy5 sample are red. Numbered protein spots showed significant difference in abundance between varieties or treatments ($p < 0.05$). For these spots, abundance data and protein identification details are shown in Table 1. Spot numbers follow the reference gel in Figure 1.

Supplementary Figure 2:

a) MS/MS spectrum of GDASAVVGLQSAIK peptide: only detected in W spot 191. Matched to gi19957070 (MOWSE score 84)

b) MS/MS spectrum of GDASVVHLQSAIK peptide: detected in W spot 193, and J spots 191 & 193. Matched to TC325434 (MOWSE score 6

c) MS/MS spectrum of ALEQLDAAASK peptide: detected only in W spot 191. Matched to qi19957070 (MOWSE score 61)

d) MS/MS spectrum of ALEQLDAVSK peptide: detected in W spot 193, and J spots 191 & 193. Matched to TC325434 (MOWSE score 76)

e) Sequence alignment of qi19957070 and TC325434

gi19957070	MRXHHQKHATYVANYNKALEQLDAAA SKGD ASAVVGLQSAIKFNGGGHVNH SIFWKNL K	60
TC325434	MRLHHQKHATYVANYNKALEQLDAAV SKGD ASAVVHLQSAIKFNGGGHVNH SIFWKNL K	60
	** *****	
gi19957070	PIS EGG EAPHGKLGWAIDEDFGSIEKLIK MNA E GAALQ SGSWVLALDKEAKRLSVET	120
TC325434	PIS EGG EP PH GKLGWAIDEDFGSIEKLIK MNA E GAALQ SGSWVLALDKEAKRLSVET	120

gi19957070	TPNQDPLVT KG SNLHPLLGIDVWEHAYYLQYKNVRPDYLTNIW VVN WKYAGEEY E KVLA	180
TC325434	TPNQDPLVT KG SNLYPLLGIDVWEHAYYLQYKNVRPDYLTNIW VVN WKYAGEEY E KVLA	180

Supplementary Figure 2: MS/MS spectra of Mn-SOD peptides detected only in Wyalkatchem spot 191 are shown in (a) and (c). MS/MS spectra of Mn-SOD peptides detected in Wyalkatchem spot 193 as well as Janz spots 191 and 193, are shown in (b) and (d). Detected ions matched to the theoretical fragment y-series and b-series ions masses by Mascot are annotated on the spectra. ClustalW sequence alignment of the two amino acid sequences (qi19957070 and TC325434) is shown in (e).

Supplementary Figure 3:

Spot	Abundance data	Description	Accession	MOWSE score	# Peptides
53		Rubisco activase	TC2798100	457	5
194		Photosystem 2 oxygen-evolving enhancer protein	TC277805	306	4
136		Rubisco small subunit	TC286624	62	1

Supplementary Figure 3: Changes in abundance and protein identification information for contaminating protein spots that displayed significant differences ($p < 0.05$) in abundance according to salt treatment in the DIGE experiment. All three spots are from proteins localised to the plastid. Spot numbers refer to supplementary Figure 1. Abundance data was calculated with Amersham DeCyder software, after measured spot intensity was normalised to the internal standard (pooled mixture of all 12 samples). W represents Wyalkatchem, J represents Janz, white bars represent control treatment, grey bars represent salinity treatment. Accession refers to the highest scoring match in the wheat TC database (TaGI release 11). MOWSE score is the probability-based score of match quality calculated by the Mascot search engine. Number of peptides refers to the number of matched peptides with ions score greater than 51 ($p < 0.05$).