

Comparative leaf proteomic profiling of salt-treated natural variants of *Imperata cylindrica*

Yun-Jhih SHIH^{1,5}, Hui-Chun CHANG^{1,5}, Min-Chieh TSAI^{1,5}, Ting-Ying WU², Tai-Chung WU³, Ping KAO², Wen-Yuan KAO³, Ing-Feng CHANG^{1,2,4*}

1. Institute of Plant Biology, National Taiwan University, Taipei, Taiwan.

2. Department of Life Science, National Taiwan University, Taipei, Taiwan.

3. Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei, Taiwan.

4. Genome and Systems Biology Degree Program, National Taiwan University and Academia Sinica, Taipei, Taiwan.

5. These people contributed equally to this work.

*Corresponding author's phone number: +886-2-33662534; Fax number: +886-2-23918940; E-mail: ifchang@ntu.edu.tw

(Manuscript received 1 February 2018; accepted 1 June 2018; online published 13 June 2018)

ABSTRACT: Cogon grass (*Imperata cylindrica* (L.) Beauv. var. *major* (Nees) Hubb.) is one of the top-ten weeds worldwide. It is also a C₄ medicinal plant. In particular, an ecotype from Chuwei (CW) mangrove forest was found to be salt tolerant. Comparative proteomic analysis using two-dimensional (2D)-difference in gel electrophoresis coupled with liquid chromatography-mass spectrometry (LC-MS) was carried out to identify responsive leaf proteins in the CW ecotype and salt-intolerant Sarlun (SL) population following three days of 150 mM sodium chloride salt stress treatment. We identified five photosynthesis proteins including Rubisco small subunit, uncharacterized protein LOC100194054, Cyt b6-f, oxygen-evolving enhancer 2, and photosystem I reaction center subunit IV which were significantly up- or down-regulated by salt stress in CW ecotype but not SL population. Gene ontology enrichment analysis showed that photosynthesis was over-represented. The mass spectrometry proteomics data were deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD008482. Taken together, our proteomic study identified differentially accumulated proteins which provide additional evidence of ecophysiological variation in two natural variants of *I. cylindrica*.

KEY WORDS: 2D-DIGE, C4 Plant, Cogon grass, Imperata cylindrica var. major, Photosynthesis, Salt stress.

INTRODUCTION

Abiotic stresses that include salt, heat, cold, and flooding all limit plant growth and reduce crop yields. Among these, salt stress affects plants the most because of two affective factors, osmotic stress and ion toxicity. Plants resolve the challenge of salt stress in different ways. One strategy is salt exclusion by reducing salt content in the cytosol through sodium proton antiporters. For example, Salt Overly Sensitive 1 (SOS1) transports sodium ions out of cells by the regulation of SOS2 and SOS3 (Zhu, 2003). Another strategy is to adjust osmotic potential by accumulation of compatible solutes *i.e.* proline (Slama et al., 2015). Plants also activate kinasemediated signal transduction pathways in response to salt stress. This usually accompanies downstream transcriptional activation of a series of stress-related genes (Shinozaki and Yamaguchi-Shinozaki, 2007). Moreover, antioxidants may play important roles in reactive oxygen species (ROS) homeostasis in halophytes (Bose et al., 2014).

Photosynthesis in C_4 plants differs greatly from that in C_3 plants in that the C_4 pathway (C_4 cycle) is also involved in photosynthesis. The C_4 pathway includes key enzymes phosphoenolpyruvate carboxylase (PEPC), malic enzyme, malate dehydrogenase, and pyruvate phosphate dikinase (PPDK) which increase the efficiency of photosynthesis in C₄ plants (Sage et al., 2012). A possible correlation between salt tolerance and the C₄ pathway was proposed (Bromham and Bennett, 2014); however, how C4 plants respond to salt stress is largely unknown. Studies have utilized a transcriptomic approach to identify salt-responsive genes and proteins in C₄ plants. For example, expressions of genes in response to salt stress changes in maize (Zea mays) kernels were profiled (Andjelkovic and Thompson, 2006). A late embryogenesis abundant (LEA) protein was up-regulated in response to dehydration. A transcriptomic study in Sorghum bicolor in response to dehydration, high salinity, and abscisic acid was carried out (Buchanan et al., 2005). They found clusters of genes with sequence similarity to dehydrins or LEA proteins were up regulated in response to abscisic acid (ABA), NaCl or polyethylene glycol (PEG). Expression of the gene for glycine-rich RNA binding protein is regulated by salinity in Sorghum bicolor (Aneeta et al., 2002).

In addition to studies on transcriptional regulation, many studies have used proteomic approach and identified proteins responsive to salt stress in C₄ plants (Zhao *et al.*, 2013a, 2013b). In maize, salt-responsive



proteins were identified using proteomic tools (Zörb et al., 2009, 2010). These include proteins involved in primary metabolism, energy, protein synthesis, secondary metabolism, disease/defence, and signal transduction. In Sorghum bicolor seedlings, a proteomic study found salt-responsive proteins (Ngara et al., 2012). In a C₄ dicot, Amaranthus cruentus, differentially accumulated proteins were identified in a proteomic study (Joaquin-Ramos et al., 2014). They found that A. cruentus var. Amaranteca could be better classified as a C3-C4 photosynthetic plant. A sensitive gel-based technique, 2D-difference in-gel electrophoresis (2D-DIGE), is based on labeling of two biologically different samples by Cy3 and Cy5 dyes individually, followed by combination of the samples for 2D-polyacrylamide gel electrophoresis (PAGE) analysis (Arruda et al., 2011; Nanjo et al., 2011). The differentially detected fluorescence of proteins indicates protein abundance in the two independent samples. The 2D-DIGE has been utilized in quantitative analysis of proteomes of saltstressed plants, including C₃ plants - Arabidopsis (Arabidopsis thaliana) (Ndimba et al., 2005), rice (Oryza sativa) (Song et al., 2011), and wheat (Triticum aestivum) (Gao et al., 2011), but not in C₄ plants.

Imperata cylindrica is a top-ten weed worldwide and a C₄ plant (Holm et al., 1977). It is widely used as a medicinal plant in Asia (Matsunaga et al., 1994; Kumar et al., 2011). The medical uses of I. cylindrica relies on its rhizomes (Sripanidkulchai et al., 2001; Yoon et al., 2006). Imperata cylindrica (L.) Beauv. var. major (Nees) Hubb. is widely distributed in Taiwan (Hsu, 1975) and also grows in the Chuwei (CW) mangrove salt marsh wetland. The leaf structure of I. cylindrica from CW examined by scanning electron microscopy (SEM) differed from other populations. The stele was empty and the surface of the lower stem was covered with epicuticular wax instead of trichomes (Cheng and Chou, 1997a). The polymorphism among populations was also analyzed by random amplified polymorphic DNA (RAPD) (Cheng and Chou, 1997b) and restriction fragment length polymorphism (RFLP) (Chou and Tsai, 1990) on ribosomal DNA (rDNA) (Chiang et al., 1998; Tsai and Chou, 1999). The CW population was therefore identified as a unique ecotype of I. cylindrica in Taiwan based on molecular classification. Moreover, the CW ecotype was shown to be salt and flood-tolerant in a hydroponic system (Chang and Chou, 2006). For unknown reasons, the population size of the CW ecotype was found to be decreasing (Kao et al., 2011). A proteomic approach showed that three proteins were differentially expressed in CW and a salt-intolerant Sarlun (SL) population: enolase, chloroplast ferredoxin-NADP(H) oxidoreductase, and mitochondrial malate dehydrogenase (Chang, 2008). However, the salt tolerance mechanism of the CW ecotype is unknown.

To date, proteomic studies of salt stress response in C_4 plants are limited. To investigate salt-responsive proteins in the salt-tolerant CW ecotype, proteomic analyses on salt-treated *I. cylindrica* were carried out in the present study. The CW ecotype and salt-intolerant SL population were used as plant materials for comparison. By use of 2D-DIGE, we identified several salt-responsive proteins. We found that the identified proteins are highly represented in the photosynthesis pathway.

MATERIALS AND METHODS

The study area: Sampling site and plant materials for salt stress treatment

Imperata cylindrica (L.) Beauv. var. major (Nees) Hubb, cogon grass, was used as plant materials in this study. The CW mangrove salt-marsh wetland in Taipei, Taiwan, was selected as the first sampling site. Imperata cylindrica collected from SL sandy beach in Taipei was used as a control. Plants collected from the field were grown in pots in a greenhouse. For hydroponic culture, plants were transplanted to Kimura's culture solution (Chang and Chou, 2006) aerated with an air pump for acclimation for 2 weeks. The culture solution was refreshed every week for hydroponic culture. After 2 weeks, salt treatment was conducted with fresh culture solution containing 150 mM sodium chloride (NaCl) for three days. As a control, no NaCl was added. Leaf tissues were harvested for further proteomic analyses. Four biological replicates (R1-R4) were prepared and analyzed for the CW ecotype and the SL population (Fig. 1).

Extraction of proteins

Proteins were extracted based on a phenol-based method as described by Torabi et al. (2009). One gram of leaf sample of I. cylindrica was ground to fine powder in liquid nitrogen with a mortar and pestle. The powder was resuspended directly in 2.5 mL of Tris pH 8.8 buffered phenol and an equal volume of extraction buffer containing 0.1 M Tris-HCl pH 8.8, 10 mM EDTA, 0.4% 2-mercaptoethanol, and 0.9 M sucrose. The homogenate was mixed for 30 min at 4°C and centrifuged afterwards at 5000 g at 4°C for 15 min. After removal of the phenol phase, proteins were precipitated with five volumes of ice-cold 0.1 M ammonium acetate in 100% methanol at -20°C overnight. The homogenate was centrifuged at 5000 g at 4°C for 10 min. The protein pellet was transferred into a 1.5-mL microfuge tube after washing twice in 5 mL of ice-cold 0.1 M ammonium acetate in 100% methanol. The protein pellet was further washed twice in 1 mL of 80% ice-cold acetone with 10 mM DTT and washed in 1 mL of 70% ethanol. Finally, the pellet was air-dried in a fume hood.



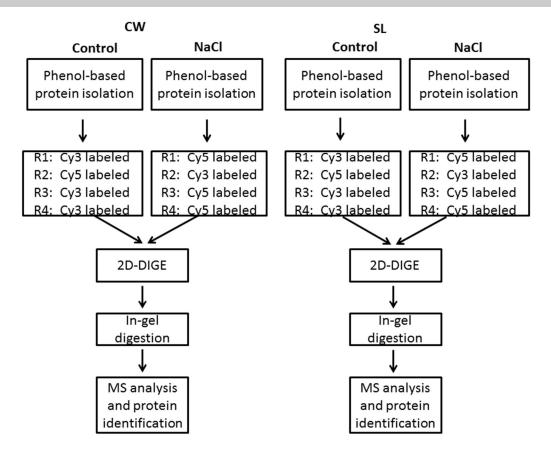


Fig. 1. Workflow of 2D-DIGE analysis of salt-stressed Imperata cylindrica leaf proteome.

Proteins labeling with cyanine dyes

A 1-mM stock of each CyDyesTM dye (GE Healthcare, USA) was diluted with anhydrous dimethylformamide to a working dye solution (400 pmol/ μ L) just prior to the labeling reaction. The extracted proteins were dissolved in lysis buffer containing 30 mM Tris pH 8.5, 7 M urea, 2 M thiourea, and 4% (w/v) CHAPS. Approximately 50 µg of proteins were mixed with 1 µL of Cy2, Cy3, or Cy5 (0.4 mM), vortexed, and incubated on ice for 30 min in darkness. The reactions were quenched by addition of 1 µL of 10 mM lysine, vortexed, and incubated on ice for 10 min in darkness.

Two-dimensional gel electrophoresis (2-DE)

After the protein samples were labeled by CyDye, an equal volume of 2× sample buffer containing 8 M urea, 130 mM DTT, 4% (w/v) CHAPS, and 2% (v/v) PharmalyteTM 3-10 was added and left on ice for 10 min. Three prepared protein samples were combined. The volume of the combined labeled sample was adjusted to 250 µL with standard rehydration buffer containing 8 M urea, 4% (w/v) CHAPS, and 1% (v/v) PharmalyteTM 3-10. For the first dimension, the adjusted labeled sample was subjected to isoelectric focusing (IEF) using a 13-cm IPG strip (pH 3–10 linear) in the IPGphorTM 3 system (GE Healthcare) with a total of 12,040 V h voltage-hours

applied. For the second dimension, the strip was equilibrated in the sodium dodecyl sulfate (SDS) equilibration buffer and resolved by 15% SDS-PAGE.

2D-DIGE imaging analysis

The Cy2-, Cy3-, and Cy5-labeled protein images were scanned by fluorescence scanner (Typhoon Trio+, GE Healthcare) using filters specific for each dye's excitation and emission wavelength. The excitation wavelengths were Cy2: 488 nm, Cy3: 532 nm, and Cy5: 633 nm; and corresponding emission wavelengths were 520 ± 20 , 580 ± 15 , and 670 ± 15 nm. The gel images were exported (in 16bit tagged image file TIFF format) for analysis. The gel images were submitted to REDFIN 2D Gel Image Analysis server (Ludesi, Malmo, Sweden, www.ludesi.com) for spot detection, matching, and analysis.

Gel-based mass spectrometry (MS) sample preparation

Protein spots excised from the stained 2D gels were subjected to in-gel digestion using MS-grade Trypsin Gold (Promega, Madison, WI, USA) overnight at 37°C. Tryptic digested fragments were extracted using 10 μ L of Milli-Q water initially, followed by two extractions with a total of 20 μ L of solution containing 50% acetonitrile/0.1% trifluoroacetic acid. The combined extracts were dried in a vacuum concentrator at room temperature.



MS analysis and protein identification

For protein spots excised from 2D gels, the ESI-MS/MS mass spectrometers utilized for peptide analysis were a Thermo LTQ-Velos or LTQ-Orbitrap (Thermo Scientific, USA) in Taiwan. Peptide samples prepared from the CW ecotype were analyzed by LTQ-Velos. The tryptic peptide mixtures were injected into a nano-flow high-performance liquid chromatography system (Agilent Technologies 1200 series, Waldbronn, Germany) coupled to an LTQ-Velos mass spectrometer (Thermo Electron, Thermo Scientific, Waltham, MA, USA). The tryptic peptides were separated on an Thermo C18 column (100 \times 0.075 mm, 2.1 µm particle size) with mobile phases of 0.1% formic acid in water (solvent A) and 0.1% formic acid in acetonitrile (solvent B) at a flow rate of 0.5 µL/min using a 30-min linear gradient of 5-35% solvent B. Peptide samples prepared from the SL population were analyzed by LTQ-Orbitrap. The tryptic peptide mixtures were injected into a nano-flow high-performance liquid chromatography system (Agilent Technologies 1200 series) coupled to an LTQ-Orbitrap Discovery[™] hybrid mass spectrometer with a nanoelectrospray ionization source (Thermo Electron). The tryptic peptides were processed as previous described separated on an Agilent C18 column (100 \times 0.075 mm, 3.5 μ m particle size) with mobile phases of 0.1% formic acid in water (solvent A) and 0.1% formic acid in acetonitrile (solvent B) at a flow rate of 0.5 µL/min using a 30-min linear gradient of 5% to 35% solvent B. On both mass spectrometers, following each full scan (m/z range of 200-2000), a data-dependent acquired MS/MS scan for a series of precursor ions was selected on the basis of the conventional MS spectra (Survey Scan) triggered at high resolution (M/DM, 60,000 full-width half-maximum). The former acquired the spectrum (CID or MS/MS spectra) for the fragment ions generated by CID, whereas the latter examined the accurate mass and the charge state of the selected precursor ion.

The MS/MS fragmentation pattern was analyzed using the MASCOT v2.5 search engine (www.matrixscience.com) (Perkins et al., 1999). The search parameters were defined as follows: Database, NCBInr 20150912; Taxonomy, Viridiplantae (Green Plants); Enzyme, Trypsin; Variable modifications, phosphorylation; Peptide MS tolerance, \pm 0.6 Da; Fragment MS tolerance, ± 0.6 Da and allowance of one missed cleavage site. Alternatively, CW- and SLspecific local databases (created by RNA-seq, data not shown) were also searched. Peptides were validated using Scaffold software (Proteome Software, USA). The mass spectrometry proteomics data were deposited in the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD008482.

Chlorophyll fluorescence measurement

To compare efficiency of excitation capture by open

photosystem II (the effective quantum yield of PSII or Y), we conducted chlorophyll fluorescence measurement with a portable, pulsed amplified modulation fluorometer (PAM-2000, Walz, Effeltrich, Germany) as described by Wu and Kao (2011). Before the measurement was taken, the plants were dark-adapted for 30 min. The Y was determined under steady-state illumination for 10 min: Y (Fm' – Ft)/Fm', where Fm' is maximal fluorescence and Ft is steady-state fluorescence of illuminated leaf.

RESULTS AND DISCUSSION

Five photosynthesis proteins were significantly up or down-regulated by salt stress in leaves of salt-treated CW ecotype, but not in SL population

A previous study showed that the CW ecotype was salt tolerant. In a hydroponic system, the CW ecotype survived but the SL population did not under 1% and 2% NaCl salt stress (Chang and Chou, 2006). Use of 1D gel-based analysis we identified Native three differentially expressed proteins among different I. cylindrica populations (Chang, 2008). However, the number of identified proteins remains limited. To systematically and quantitatively investigate the saltresponsive proteins, 2D-DIGE was introduced. We carried out salt treatment on the CW ecotype in 150 mM NaCl hydroponic culture for 3 days. Total proteins from the CW ecotype were isolated by phenol-based method. Proteins from control and salt-treated groups were labeled with either Cy3 or Cy5 dye. The mixture of the combined protein sample was subjected to 2DE followed by laser imaging. After analyses of gel images using REDFIN (Ludesi) software, fold change of protein spot intensity was calculated. By measuring Cy3-labled protein spot intensity, Cy5-labled protein spot intensity and each normalized to Cy2-labled protein spot intensity, we further took Cy5/Cy3 ratio as fold change (DIGE ratio). Protein spots with differential abundance were excised from the gel followed by in-gel digestion and liquid chromatography tandem mass spectrometry (LC-MS/MS) analyses (Fig. 1). A total of 26 protein spots showed differential abundance in response to salt stress (intensity fold change >1.65 or <0.60). The DIGE ratios are shown in Table S1. Of these 26 spots, 20 showed significant differential accumulation of proteins between CW and SL (ANOVA, p < 0.05). These spots were subjected to in-gel digestion followed by LC-MS/MS analyses. Among these protein spots, five proteins significantly up- or down-regulated by salt stress (t-test, p < 0.05) were successfully identified by MASCOT searching against the NCBI database (Fig. 2, Figure S1, Table 1 and 2). These included uncharacterized protein LOC100194054 (thylakoid lumenal 17.4-kDa protein, spots # 52 and 70), ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) small subunit (spot #



Table 1. Proteins identified in 2D-DIGE of leaf proteins isolated from salt-treated CW ecotype

Spot #	Protein name	Accession number	Experimental pl/MW	Theoretical pl/MW	Mascot score	Unique peptide #	Organism	Fold Change (p value 1, 2)
Metabo	lism							
178	Plastidic aspartate aminotransferase	gi 633095	6.32/42.97	8.62/50.48	1129	16	Panicum miliaceum	1.66 (0.07, 0.6)
Signali								
957	General regulatory factor (14-3-3)	gi 1345588	4.70/29.53	4.75/29.64	247	3	Zea mays	1.86 (0.28, 0.02)
Stress								
	Superoxide dismutase [Mn] 3.1, mitochondrial precursor	gi 134668	6.40/20.77	6.71/25.21	248	2	Zea mays	
93	Superoxide dismutase [Mn] 3.4, mitochondrial precursor	gi 212722004	6.03/23.89	6.71/25.21	157	4	Zea mays	5.16 (0.16, 0.045)
Photos	ynthesis							
	Ribulose-1, 5-							
61	bisphosphate carboxylase/oxygenase small subunit	gi 3914607	4.70/13.29	9.04/19.25	227	2	Sorghum bicolor	0.5 (0.003, 0.02)
11	Hypothetical protein SORBIDRAFT_02g002690 (OEE2)	gi 242047384	6.23/23.38	8.63/27.72	725	5	Sorghum bicolor	2.07 (0.03, 0.0005)
27	Hypothetical protein SORBIDRAFT_02g002690 (OEE2)	gi 242047384	5.60/23.65	8.63/27.72	529	5	Sorghum bicolor	2.48 (0.38, 0.34)
52	Uncharacterized protein LOC100194054	gi 212721648	4.54/17.68	7.44/24.15	1459	5	Zea mays	1.76 (0.003, 0.00005)
70	Uncharacterized protein LOC100194054	gi 212721648	3.78/7.18	7.44/24.15	181	3	Zea mays	0.51 (0.02, 0.002)
957	Chloroplast oxygen- evolving enhancer protein 1, OEE1	gi 383511664	4.70/29.53	5.59/34.78	1072	12	<i>Saccharum</i> hybrid cultivar	1.86 (0.28, 0.02)
199	Unknown (Cyt b6-f)	gi 194702912	5.30/20.50	6.41/21.03	917	6	Zea mays	0.59 (0.01, 0.02)
208	Unknown (Cyt b6-f)	gi 194702912	6.23/12.52	6.41/21.03	217	3	Zea mays	0.25 (0.005, 0.00004)
279	ATP synthase CF1 beta subunit	gi 227786	4.98/28.60	8.62/38.68	272	10	Sorghum bicolor	1.57 (0.55, 0.76)
470	Photosystem I reaction center subunit IV		7.01/16.36	9.82/15.45	131	3	Imperata cylindrica	2.03 (0.03, 0.009)
666	Photosystem I reaction center subunit VII		5.06/7.50	6.69/9.52	88	2	Imperata cylindrica	1.89 (0.33, 0.3)
Others							_ ·	
201	Cyclophilin	gi 242079005	4.24/41.25	4.83/46.69	497	14	Sorghum bicolor	1.77 (0.07, 0.03)

1. The first p value: p values of T-test for most proteins with significant differential abundance between control and salt-stressed plants are shown after fold change ratio.

2. The second p value: p values of ANOVA for proteins with significant differential abundance between CW ecotype and SL population are shown after fold change ratio.

61), photosystem I reaction center subunit IV (spot # 470), Cyt b6-f (spots # 199 and 208), and oxygenevolving enhancer 2 (OEE2) (spot # 11 and #27). The identified peptides are shown in Table S2.

In addition, we identified proteins with significant differences in DIGE ratio between CW and SL, but not significantly up- or down-regulated by salt stress in CW: Mn superoxide dismutase (Mn-SOD3.4) (spot # 93) and cyclophilin (spot # 201) (Table 1 and 3). Moreover, we identified proteins with no significant difference in DIGE ratio between CW and SL: aspartate aminotransferase (spot # 178), ATP synthase beta subunit (spot # 279), and photosystem I reaction center

subunit VII (spot # 666) (Table 1 and 4). The identified peptides are shown in Table S2. However, oxygenevolving enhancer 1 (OEE1) and 14-3-3 were identified in the same spot (# 957), and so the DIGE ratio is unknown for each protein. Both OEE2 and thylakoid lumenal 17.4-kDa protein were identified in two individual spots. However, spot # 70 appeared to be the degraded product of thylakoid lumenal 17.4-kDa protein. Photosystem I reaction center subunits IV (spot # 470) and VII (spot # 666) were identified by MASCOT searching against the local database. Interestingly, most of the proteins were in chloroplasts and involved in the photosynthesis pathway.



Spot # CW, SL	Protein name	Accession Number CW, SL	Mascot Score CW, SL	Unique peptide # CW, SL	Fold Change CW, SL (p value)
Photosynthesis					
61, 56	Ribulose-1, 5-bisphosphate carboxylase/oxygenase small subunit	gi 3914607, gi 164698711	227, 75	2, 2	0.5, 1.05 (0.02)
11	Hypothetical protein SORBIDRAFT_02g002690 (OEE2)	gi 242047384	725	5	2.07 (CW) (0.0005)
52, 755	Uncharacterized protein LOC100194054	gi 212721648, gi 212721648	1459, 213	5, 3	1.76, 1.18 (0.00005)
70	Uncharacterized protein LOC100194054	gi 212721648	181	3	0.51 (CW) (0.002)
199, 74	Unknown (Cyt b6-f)	gi 194702912, gi 194702912	917, 139	6, 4	0.59, 0.93 (0.02)
208	Unknown (Cyt b6-f)	gi 194702912	217	3	0.25 (CW) (0.00004)
470, 452	Photosystem I reaction center subunit IV		131, 177	3, 4	2.03, 0.99 (0.009)

Table 2. Salt-regulated proteins with significant differences between salt-treated CW ecotype and SL population.

P value: P values of ANOVA for proteins with significant differential abundance between CW ecotype and SL population are shown after fold change ratio.

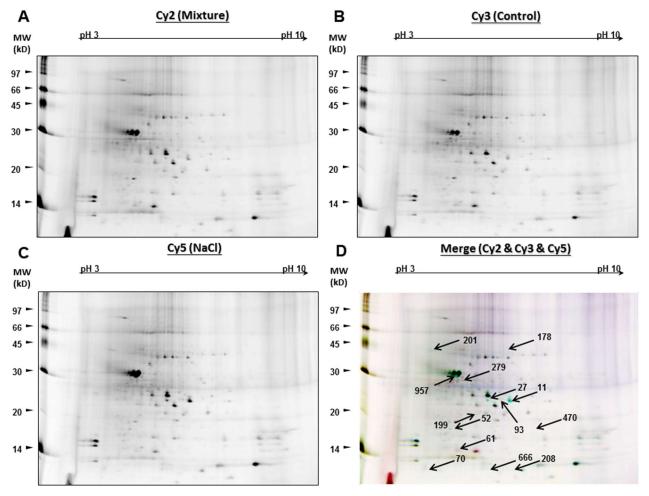


Fig. 2. Representative 2D-DIGE image of leaf proteins isolated from salt-treated CW ecotype. The gel image corresponds to one representative biological replicate. **A**, Loading control; **B**, control (no salt); **C**, salt-treated group; **D**, merged image. The image was analyzed using 2D gel image analysis software REDFIN.



Table 3. Proteins with significan	t differences between salt-	-treated CW ecotype ar	nd SL population but not re	equiated by salt stress

Spot # CW, SL	Protein name	Accession Number CW, SL	Mascot Score CW, SL	Unique peptide # CW, SL	Fold Change CW, SL (p value 1, 2)
Signaling					
957, 753	General regulatory factor (14-3-3)	gi 1345588, gi 242073380	247, 709	3, 36	1.86, 0.95 (0.02)
Metabolism	t	······································			
612	Fructose-bisphosphate aldolase	gi 242059597	245	12	0.89 (SL) (0.048)
Protein degradation					
415	Proteasome beta subunit	gi 242079721	317	5	0.83 (SL) (0.045)
Stress					
91	Superoxide dismutase [Cu/Zn]	gi 1568639	104	2	1.05 (SL) (0.01)
93	Superoxide dismutase [Mn] 3.4, mitochondrial precursor	gi 212722004	157	4	5.16 (CW) (0.045)
Photosynthesis	producer				
957, 753	Chloroplast oxygen- evolving enhancer protein 1, OEE1	gi 383511664, gi 383511664	1072, 477	12, 15	1.86, 0.95 (0.02)
470, 452	Photosystem I reaction center subunit IV		131, 177	3, 4	2.03, 0.99 (0.009)
Others					
201, 106	Cyclophilin	gi 242079005, gi 242079005	497, 304	14, 7	1.77, 0.96 (0.03)

P value: p values of ANOVA for proteins with significant differential abundance between CW ecotype and SL population are shown after fold change ratio.

Table 4. Proteins	with no significan	t differences betwee	n salt-treated CW	/ ecotype and SL	population

Spot # CW, SL	Protein name	Mascot Score CW, SL	Unique peptide # CW, SL	Fold Change CW, SL (p value)
178, 214	Plastidic aspartate aminotransferase	1129, 507	16, 8	1.66, 0.95 (0.6)
666, 173	Photosystem I reaction center subunit VII	88, 189	2, 2	1.89, 1.71 (0.3)

P value: p values of ANOVA for proteins with significant differential abundance between CW ecotype and SL population are shown after fold change ratio.

In addition, we identified Cyt b6-f in two separate protein spots with decreased fold change (spots # 199 and 208). However, spot # 208 appeared to be the degraded product of Cyt b6-f. In an independent 2D-DIGE analysis, we identified one more isoform, Mn-SOD3.1, in CW. However, only Mn-SOD3.4 showed consistent up-regulation in CW in response to salt stress. Functional categories of the identified proteins were metabolism, signaling, stress, photosynthesis and others. The identification of these proteins was validated using Scaffold software v4.3 at probability >95% (Figure S2).

With the same approach as used in analyzing the salttreated CW leaf proteome, we also aimed to identify saltresponsive proteins in the SL population (Fig. 1). A total of 26 protein spots corresponding to spots of the same position as in the CW protein gel were detected. These spots were subjected to in-gel digestion followed by LC-MS/MS analyses. The DIGE ratios are shown in Table S3. Of these spots, 20 showed differential accumulation of proteins between populations (significant difference between CW and SL, by ANOVA at p < 0.05). In these spots, eight proteins with significant difference in DIGE ratio between CW and SL were successfully identified by MASCOT searching against the NCBI database (Fig. 3, Figure S3, Table 2, 3 and 5). However, none of these proteins were significantly up- or down-regulated by salt stress (*t*-test, p < 0.05). These proteins were fructosebisphosphate aldolase (spot # 612), copper/zinc superoxide dismutase (Cu/Zn-SOD) (spot # 91), proteasome beta subunit (spot # 415), Cyt b6-f (spot # 74), Rubisco small subunit (spot # 452), uncharacterized protein LOC100194054 (thylakoid lumenal 17.4-kDa protein, spot # 755), and cyclophilin (spot # 106). The identified peptides are shown in Table S4.

In addition, we identified proteins with no significant difference in DIGE ratio between CW and SL: aspartate aminotransferase (spot # 214) and photosystem I reaction center subunit VII (spot # 173) (Table 4 and Table 5). OEE1 and 14-3-3 were identified in the same



Table 5. Proteins identified in 2D-DIGE of leaf proteins isolated from salt-treated SL population

Functional category	Spot #	Protein name	Accession number	Experime ntal pl/MW	Theoretic al pl/MW	Mascot score	Unique peptide #	Organism	Fold Change (p value 1, 2)
Metabolisr	n			•					
	214	Plastidic aspartate aminotransferase	gi 514719430	6.60/ 40.55	8.62/ 50.48	507	8	Setaria italica	0.95 (0.62, 0.6)
	612	Fructose-bisphosphate aldolase	gi 242059597	6.32/ 38.68	6.96/ 38.99	245	12	Sorghum bicolor	0.89 (0.83, 0.048)
Signaling									
	753	General regulatory factor (14-3-3)	gi 242073380	5.09/ 28.71	4.76/ 29.74	709	36	Sorghum bicolor	0.95 (0.97, 0.02)
Stress									
	91	Superoxide dismutase [Cu/Zn]	gi 1568639	4.96/ 16.24	5.35/ 20.42	104	2	Triticum aestivum	1.05 (0.85, 0.01)
Protein de	gradatio	n							
	415	Proteasome beta subunit	gi 242079721	6.36/ 19.81	5.71/ 26.31	317	5	Sorghum bicolor	0.83 (0.88, 0.045)
Photosynt	hesis								
	74	Unknown (Cyt b6-f)	gi 194702912	5.50/ 17.07	6.41/ 21.03	139	4	Zea mays	0.93 (0.68, 0.02)
	56	Ribulose-1, 5- bisphosphate carboxylase/oxygenase small subunit	gi 164698711	4.79/ 13.10	8.78/ 19.37	75	2	Miscanthus xgiganteus	1.05 (0.49, 0.02)
	173	Photosystem I reaction center subunit VII	gi 7524738	6.02/ 11.50	6.69/ 9.52	189	2	Pinus thunbergii	1.71 (0.43, 0.3)
	452	Photosystem I reaction center subunit IV		7.01/ 16.36	9.82/ 15.45	177	4	Imperata cylindrica	0.99 (0.49, 0.01)
	755	Uncharacterized protein LOC100194054	gi 212721648	4.78/ 15.91	7.44/ 24.15	213	3	Zea mays	1.18 (0.57, 0.00)
	753	Chloroplast oxygen- evolving enhancer protein 1, OEE1	gi 383511664	5.09/ 28.71	6.08/ 34.95	477	15	Saccharum hybrid cultivar	0.95 (0.97, 0.02)
Others								- .	
	106	Cyclophilin	gi 242079005	4.36/ 40.14	4.83/ 46.69	304	7	Sorghum bicolor	0.96 (0.46, 0.03)

1. The first p value: p values of T-test for most proteins with significant differential abundance between control and salt-stressed plants are shown after fold change ratio.

2. The second p value: p values of ANOVA for proteins with significant differential abundance between CW ecotype and SL population are shown after fold change ratio.

spot (# 753) and so the DIGE ratio is unknown for each protein. Photosystem I reaction center subunit IV (spot # 452) was identified by MASCOT searching against the local database. The identified peptides are shown in Table S4.

Interestingly, by use of the local database, more peptides were identified for 14-3-3 proteins (Table S4). In addition, two phosphopeptides of thylakoid phosphoprotein membrane 14-kDa protein (ATpSGGEGATEEVPEIVK) and a chloroplast a and b binding protein CP29 (NEPGAVIGpTRFESSDVK) were identified from the data set of our previous study (Wu et al., 2015). The phosphorylation sites are evolutionarily conserved compared with other plant species (Figure S4). These indicate that the local database helped improve peptide identification for I. cylindrica, a non-model organism with no genome sequence. Functional categories of the identified proteins were metabolism, stress, signaling, protein

photosynthesis, degradation, others. The and identification of these proteins was validated using Scaffold software v4.3 at probability >95% (Figure S5).

Gene ontology (GO) term enrichment analysis of the identified proteins

A total of five proteins were significantly up- or downregulated by salt stress in CW: Rubisco small subunit, uncharacterized protein LOC100194054, Cyt b6-f, oxygen-evolving enhancer 2, and photosystem I reaction center subunit IV. All five proteins were from the photosynthesis pathway; however, their DIGE ratios varied in CW and SL. In CW, three of the five proteins (with the exceptions of Cyt b6-f and Rubisco small subunit) showed increased abundance; however, in SL they all had no significant change of abundance. The GO term enrichment analysis was carried out by searching the PANTHER GO database (http://www.geneontology.org/). The GO biological process result showed that removal



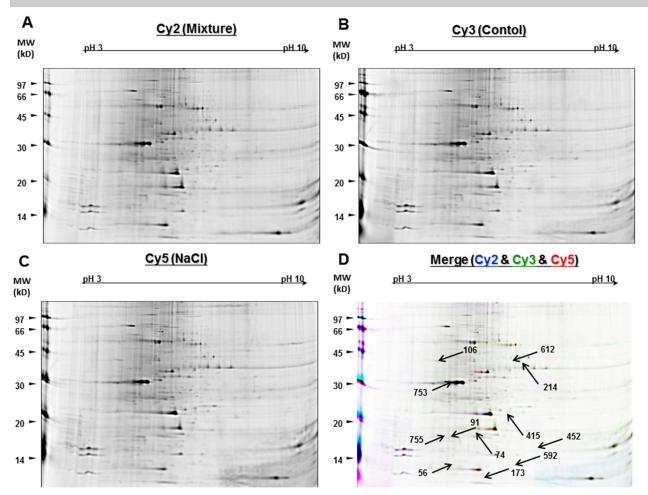


Fig. 3. Representative 2D-DIGE image of leaf proteins isolated from salt-treated SL population. The gel image corresponds to one representative biological replicate. **A**, Loading control; **B**, control (no salt); **C**, salt-treated group; **D**, merged image. The image was analyzed using 2D gel image analysis software REDFIN.

of superoxide radicals (p-value: 8.17E-03, fold enrichment > 100%) and photosynthesis were enriched (pvalue: 5.76E-07, fold enrichment > 100%). The GO cellular component result showed enrichment of photosystem I (p-value: 9.53E-04, fold enrichment >100%), thylakoid (p-value: 7.01E-05, fold enrichment 83.43%), and thylakoid membrane (p-value: 3.99E-03, fold enrichment 78.33%). Thus, GO term enrichment analysis showed that photosynthesis was over-represented.

Differentially accumulated photosynthesis proteins in salt stress response

Differentially accumulation of photosynthesis proteins under salt stress conditions have been reported in many plant proteomics studies (Zhang *et al.*, 2012; Kosová *et al.*, 2014; Nouri *et al.*, 2015; Silveira and Carvalho, 2016). A proteomic study showed that 20 chloroplast proteins were affected by salt stress treatment in the C₄ plant maize (Zörb *et al.*, 2009): 12 proteins increased their abundance and eight showed decreases. In our proteomic study, we identified five photosynthesis proteins with differential accumulation patterns in response to salt stress in CW and SL (Tables 1, 2, and 5) and the GO enrichment result confirmed this. Our results support Zörb's and others findings. The differential accumulation of photosynthesis proteins may be the major difference between CW and SL. In fact, differential phosphorylation of C4-specific enzymes in the CW ecotype and SL population was previously reported (Wu *et al.*, 2015). Our results suggest that CW and SL may differ in the C4 pathway in response to salt stress.

In particular in the present study, OEE2 (spots # 11 and 27) (Fig. 2) accumulated more in salt-treated plants than controls. The OEE2 is an extrinsic polypeptide in photosystem II involved in oxygen production (Seidler, 1996; Bricker *et al.*, 2012). Previous studies have shown a correlation between OEE abundance and salt stress. Abundance OEE1 or OEE2 were found to be changed in response to salt stress in *Bruguiera gymnorrhiza* (Sugihara *et al.*, 2000), maize (Zörb *et al.*, 2009), rice (Abbasi and Komatsu, 2004), cowpea (de Abreu *et al.*, 2014) tobacco, (Razavizadeh *et al.*, 2009), potato and



canola (Aghaei et al., 2008; Bandehagh et al., 2011), Brachypodium (Lv et al., 2014), and Kandelia candel (Wang et al., 2013). In mangrove species Bruguiera gymnorrhiza, OEE1 transcripts were enhanced by salt stress (Sugihara et al., 2000). In maize, OEE2 abundance increased after salt exposure (Zörb et al., 2009). In addition, OEE1 and OEE2 were found to be responsive to salt stress in rice leaf sheath (Abbasi and Komatsu, 2004). Moreover, there was increased abundance of OEE2 in a salt-tolerant cultivar of cowpea following salt exposure (de Abreu et al., 2014). In the present study, OEE2 was up-regulated in response to salt stress based on our 2D-DIGE results (spots #11 and 27). Overall, our results are consistent with these others. It appears that OEE2 abundance may affect the PSII activity under salt stress in plants.

In contrast, we found that Rubisco small subunit and Cyt b6-f showed significantly decreased abundance under 150-mM salt stress. Similar results were reported by other groups. In a C₄ halophyte *Aeluropus lagopoides*, Rubisco small subunit was down-regulated by salt stress at the protein level (Sobhanian *et al.*, 2010). However, a proteomic study found Cyt b6-f was gradually up-regulated by salt stress in wheat (Kamal *et al.*, 2012).

Since most of the identified photosynthesis proteins showed increased abundance in CW, it is possible that CW had higher photosynthesis efficiency than SL under salt stress. This may help in tolerance to local salt stress in the CW mangrove forest. In fact, we found the chlorophyll fluorescence value of salt-treated I. cylindrica (both populations) decreased with stress but slightly recovered after acclimation (Figure S6); however, the chlorophyll fluorescence value was higher for CW than SL. Our results suggest a higher photosynthetic efficiency for CW than SL under salt stress. This phenomenon was also observed in other plant species. In Arabidopsis transformed with a Lepidium crassifolium gene conferring salt tolerance, the Fv/Fm value was less affected than in Arabidopsis wild type (Rigó et al., 2016). Since our results showed that Rubisco protein abundance decreased in both populations with salt stress, this is highly possible due to differences in protein levels of photosystem components.

Identification of Mn-SOD

In addition to photosynthetic proteins, an antioxidant protein Mn-SOD was identified in spot # 93 (Fig. 2) in salt-treated CW leaves. Differential accumulation of ROS scavengers under salt stress has been reported in many plant proteomic studies (Zhang *et al.*, 2012; Kosová *et al.*, 2014). Abbasi and Komatsu (2004) showed that SOD increased in abundance in response to salt stress in rice leaf sheath. In *Suaeda aegyptiaca* leaves, Cu/Zn-SOD was responsive to salt stress in a proteomic study (Askari *et al.*, 2006). In pea, Cu/Zn-SOD increased in response to salt stress (Hernhdeza *et* *al.*, 1995). In rice, overexpression of yeast Mn-SOD and rice Cu/Zn-SOD increased salt tolerance (Tanaka *et al.*, 1999; Guan *et al.*, 2017). The increased abundance of SOD is believed to be a mechanism to deal with oxidative stress under salt stress conditions in plants. Our results concerning OEE2 and SOD are consistent with previous results. This suggests an evolutionarily conserved mechanism for salt stress response of these proteins. However, we did not identify the proteins in the SL population. Our results suggest that Mn-SOD may be involved in salt stress tolerance of CW as a ROS scavenger. Whether enzyme activity of Mn-SOD is consistently up-regulated in the CW ecotype under salt stress is unknown and requires further study.

Identification of cyclophilin

In leaves of CW and SL, cyclophilin was identified as a protein with differential DIGE ratio. Cyclophilin is encoded by a multigene family. It was reported that cyclophilin gene expression in bean (*Phaseolus vulgaris*) is differentially regulated by salt stress (Marivet *et al.*, 1994). A proteomic study identified a rice cyclophilin OsCYP2 and its overexpression increased salt tolerance (Ruan *et al.*, 2011). Moreover, overexpression of a pigeonpea cyclophilin gene increased salt tolerance of Arabidopsis (Sekhar *et al.*, 2010). Our findings suggest that cyclophilin may be involved in salt stress response in the CW ecotype but with an unknown mechanism.

Possible salt tolerance mechanism of CW ecotype

In summary, we identified differentially accumulated proteins in leaves of two natural variants of I. cylindrica in response to salt stress using 2D-DIGE. These proteins included SODs, cyclophilin, and many photosynthesis proteins, which suggests that the CW ecotype may have higher antioxidant activity and photosynthesis efficiency, and so can deal with oxidative stress damage and energy limitation resulting from salt stress in mangrove forest. Low accumulation of sodium in leaves of the CW ecotype under salt stress was previously reported (Chang and Chou, 2006). It is highly likely that an unknown transporter is involved in avoiding salt accumulation in leaves. This would prevent salt damage to enzyme stability and activity in leaves. However, determining which transporter may be involved will require further study.

ACKNOWLEDGEMENTS

We appreciate funding support from the Ministry of Science and Technology, Taiwan (MOST# 104-2311-B-002-034, MOST# 106-2313-B-002-014, and MOST# 106-2313-B-002-004) and the National Taiwan University (Grant # 105R892002). We thank Mr. C.S. Wang and Mr. C.H. Wang (Tamsui Farm) for help with *Imperata cylindrica* sampling. Many thanks to BioMed Proofreading, LLC for English editing. We appreciate the technical support from Visual Protein,



Taipei, Taiwan. We also thank Technology Commons, College of Life Science, National Taiwan University, for technical help.

LITERATURE CITED

- Abbasi, F.M. and S. Komatsu. 2004. A proteomic approach to analyze salt-responsive proteins in rice leaf sheath. Proteomics **4(7)**: 2072-2081.
- Aghaei, K., A.A. Ehsanpour and S. Komatsu. 2008. Proteome analysis of potato under salt stress. J. Proteome Res. 7(11): 4858-4868.
- Andjelkovic, V. and R. Thompson. 2006. Changes in gene expression in maize kernel in response to water and salt stress. Plant Cell Rep. 25(1): 71-79.
- Aneeta, N. Sanan-Mishra, N. Tuteja and S. Kumar Sopory. 2002. Salinity- and ABA-induced up-regulation and lightmediated modulation of mRNA encoding glycine-rich RNA-binding protein from *Sorghum bicolor*. Biochem. Biophys. Res. Commun. **296(5)**: 1063-1068.
- Arruda, S.C., S. Barbosa Hde, R.A. Azevedo and M.A. Arruda. 2011. Two-dimensional difference gel electrophoresis applied for analytical proteomics: Fundamentals and applications to the study of plant proteomics. Analyst 136(20): 4119-4126.
- Askari, H., J. Edqvist, M. Hajheidari, M. Kafi and G.H. Salekdeh. 2006. Effects of salinity levels on proteome of *Suaeda aegyptiaca* leaves. Proteomics 6(8): 2542-2554.
- Bandehagh, A., G.H. Salekdeh, M. Toorchi, A. Mohammadi and S. Komatsu. 2011. Comparative proteomic analysis of canola leaves under salinity stress. Proteomics 11(10): 1965-1975.
- Bose, J., A. Rodrigo-Moreno and S. Shabala. 2014. ROS homeostasis in halophytes in the context of salinity stress tolerance. J. Exp. Bot. 65(5): 1241-1257.
- Bricker, T.M., J.L. Roose, R.D. Fagerlund, L.K. Frankel and J.J. Eaton-Rye. 2012. The extrinsic proteins of photosystem II. Biochim. Biophys. Acta 1817(1): 121-142.
- Bromham, L. and T.H. Bennett. 2014. Salt tolerance evolves more frequently in C4 grass lineages. J. Evol. Biol. 27(3): 653-659.
- Buchanan, C.D., S. Lim, R.A. Salzman, I. Kagiampakis, D.T. Morishige, B.D. Weers, R.R. Klein, L.H. Pratt, M. M. Cordonnier-Pratt, P.E. Klein and J.E. Mullet. 2005. Sorghum bicolor's transcriptome response to dehydration, high salinity and ABA. Plant Mol. Biol. 58(5): 699-720.
- Chang, I.F. 2008. Ecotypic variation of a medicinal plant *Imperata cylindrica* populations in Taiwan: Mass spectrometry-based proteomic evidence. J. Med. Plants Res. 2: 71-76.
- Chang, I.F. and C.H. Chou. 2006. Ecotypic variation of *Imperata cylindrica* populations in Taiwan: II. Physiological and biochemical evidence. Bot. Stud. 47: 175-184.
- Cheng, K.T. and C.H. Chou. 1997a. Ecotypic variation of *Imperata cylindrica* populations in Taiwan: I. Morphological and molecular evidences. Bot. Bull. Acad. Sinica 38: 215-223.
- Cheng, K.T. and C.H. Chou. 1997b. Specific RAPD Markers of *Imperata cylindrica* populations in Taiwan. J. Genet. Mol. Biol. 8(3): 41-54.
- Chiang, Y. C., T.Y. Chiang, I.F. Chang and C.H. Chou. 1998. Sequence announcement: rDNA IGS of *Imperata*

cylindria (L.) Beauv. Var. *major* (Ness) C E Hubb. Plant Mol. Biol. **39:** 391-392.

- de Abreu, C.E., S. Araújo Gdos A.C. Monteiro-Moreira, J. H. Costa, B. Leite Hde, F. B. Moreno, J.T. Prisco and E. Gomes-Filho. 2014. Proteomic analysis of salt stress and recovery in leaves of Vigna unguiculate cultivars differing in salt tolerance. Plant Cell Rep. 33(8): 1289-1306.
- Gao, L., X. Yan, X. Li, G. Guo, Y. Hu, W. Ma and Y. Yan. 2011. Proteome analysis of wheat leaf under salt stress by two-dimensional difference gel electrophoresis (2D-DIGE). Phytochemistry 72(10): 1180-1191.
- Guan, Q., X. Liao, M. He, X. Li, Z. Wang, H. Ma, S. Yu and S. Liu. 2017. Tolerance analysis of chloroplast OsCu/Zn-SOD overexpressing rice under NaCl and NaHCO3stress. PlosOne 12(10): e0186052
- Hernández, J.A., E. Olmos, F.J. Corpas, F. Sevilla and L.A. del Río. 1995. Salt-induced oxidative stress in chloroplasts of pea plants. Plant Sci. 105: 151-167.
- Holm, L.G., D.L. Plucknett, J.V. Pancho and J.P. Herberger. 1977. The world's worst weeds: Distribution and biology. University Press, Honolulu, Hawaii. pp. 609.
- Hsu, C. C. 1975. Gramineae. In: Li, H. L. et al. (eds.), Flora of Taiwan, 661-662, Vol. 6, Taiwan. pp. 661-662.
- Joaquin-Ramos, A., J.A. Huerta-Ocampo, A. Barrera-Pacheco, A. De Leon-Rodriguez, S. Baginsky, S. and A.P. Barba de la Rosa. 2014. Comparative proteomic analysis of amaranth mesophyll and bundle sheath chloroplasts and their adaptation to salt stress. J. Plant Physiol. 171(15): 1423-1435.
- Kamal, A.H., K. Cho, D.E. Kim, N. Uozumi, K.Y. Chung, S.Y. Lee, J.S. Choi, S.W. Cho, C.S. Shin and S.H. Woo. 2012. Changes in physiology and protein abundance in salt-stressed wheat chloroplasts. Mol. Biol. Rep. 39(9): 9059-9074.
- Kao, P., T.Y. Wu, C.L. Chang, C.H. Chou and I.F. Chang. 2011. Decreasing of population size of *Imperata cylindrica* mangrove ecotype & sea-level rising. *In*: Casalegno, S. (ed.), Global warming impacts - case studies on the economy, human health, and on urban and natural environments. InTech.
- Kosová, K., P. Vitamvás and I.T. Prášil. 2014. Proteomics of stress responses in wheat and barley-search for potential protein markers of stress tolerance. Front. Plant Sci. 5: 711.
- Kumar, M., M.A. Sheikh and R.W. Bussmann. 2011. Ethnomedicinal and ecological status of plants in Garhwal Himalaya, India. J Ethnobiol. Ethnomed. 7(1): 32.
- Lv, D.W., S. Subburaj, M. Cao, X. Yan, X. Li, R. Appels, D. F. Sun, W. Ma and Y.M. Yan. 2014. Proteome and phosphoproteome characterization reveals new response and defense mechanisms of *Brachypodium distachyon* leaves under salt stress. Mol. Cell. Proteomics 13(2): 632-652.
- Marivet J., M. Margis-Pinheiro, P. Frendo and G. Burkard. 1994. Bean cyclophilin gene expression during plant development and stress conditions. Plant Mol. Biol. 26(4): 1181-1189.
- Matsunaga, K., M. Shibuya and Y. Ohizumi. 1994. Cylindrene, a novel sesquiterpenoid from *Imperata* cylindrica with inhibitory activity on contractions of vascular smooth muscle. J. Nat. Prod. 57(8): 1183-1184.
- Nanjo, Y., M.Z. Nouri and S. Komatsu. 2011. Quantitative proteomic analyses of crop seedlings subjected to stress



conditions; a commentary. Phytochemistry **72(10)**: 1263-1272.

- Ndimba, B.K., S. Chivasa, W.J. Simon and A.R. Slabas. 2005. Identification of Arabidopsis salt and osmotic stress responsive proteins using two-dimensional difference gel electrophoresis and mass spectrometry. Proteomics 5(16): 4185-4196.
- Ngara, R., R. Ndimba, J. Borch-Jensen, O.N. Jensen and B. Ndimba. 2012. Identification and profiling of salinity stress-responsive proteins in *Sorghum bicolor* seedlings. J. Proteomics 75(13): 4139-4150.
- Nouri, M. Z., A. Moumeni and S. Komatsu. 2015. Abiotic stresses: Insight into gene regulation and protein expression in photosynthetic pathways of plants. Int. J. Mol. Sci. 16(9): 20392-20416.
- Perkins, D.N., D.J.C. Pappin, D.M. Creasy and J.S. Cottrell. 1999. Probability-based protein identification by searching sequence databases using mass spectrometry data. Electrophoresis 20(18): 3551-3567.
- Razavizadeh, R., A.A. Ehsanpour, N. Ahsan and S. Komatsu. 2009. Proteome analysis of tobacco leaves under salt stress. Peptides 30: 1651-1659.
- Rigó, G., I. Valkai, D. Farago, E. Kiss, S. Van Houdt, N. Van de Steene, M.A. Hannah and L. Szabados, L. 2016. Gene mining in halophytes: Functional identification of stress tolerance genes in *Lepidium crassifolium*. Plant, Cell Environ. **39(9)**: 2074-2084.
- Ruan, S.L., H.S. Ma, S.H. Wang, Y.P. Fu, Y. Xin, W.Z. Liu, F. Wang, J.X. Tong, S.Z. Wang and H.Z. Chen. 2011. Proteomic identification of OsCYP2, a rice cyclophilin that confers salt tolerance in rice (*Oryza sativa* L.) seedlings when overexpressed. BMC Plant Biol. 11(1):34.
- Sage, R.F., T.L. Sage and F. Kocacinar. 2012. Photorespiration and the evolution of C4 photosynthesis. Annu. Rev. Plant Biol. 63(1): 19-47.
- Seidler, A. 1996. The extrinsic polypeptides of photosystem II. Biochim. Biophys. Acta 1277(1-2): 35-60.
- Sekhar, K., B. Priyanka, V.D. Reddy and K.V. Rao. 2010. Isolation and characterization of a pigeonpea cyclophilin (CcCYP) gene, and its over-expression in Arabidopsis confers multiple abiotic stress tolerance. Plant Cell Environ. 33: 1324-1338.
- Shinozaki, K. and K. Yamaguchi-Shinozaki. 2007. Gene networks involved in drought stress response and tolerance. J. Exp. Bot. 58(2): 221-227.
- Silveira, J.A.G. and F.E.L. Carvalho. 2016. Proteomics, photosynthesis and salt resistance in crops: An integrative view. J Proteomics 143: 24-35.
- Silveira, J. A.G., A.R.B. Melo, R.A. Viegas and J.T.A. Oliveira 2001. Salinity-induced effects on nitrogen assimilation related to growth in cowpea plants. Environ. Exp. Bot. 46(2): 171-179.
- Slama, I., C. Abdelly, A. Bouchereau, T. Flowers and A. Savoure. 2015. Diversity, distribution and roles of osmoprotective compounds accumulated in halophytes under abiotic stress. Ann. Bot. 115(3): 433-447.

Song, Y., C. Zhang, W. Ge, Y. Zhang, A.L. Burlingame and Y. Guo. 2011. Identification of NaCl stress-responsive apoplastic proteins in rice shoot stems by 2D-DIGE. J. Proteomics **74(7)**: 1045-1067.

- Sripanidkulchai, B., V. Wongpanich, P. Laupattarakasem, J. Suwansaksri and D. Jirakulsomcho. 2001. Diuretic effects of selected Thai indigenous medicinal plants in rats. J. Ethnopharmacol. 75(2-3): 185-190.
- Sugihara, K., N. Hanagata, Z. Dubinsky, S. Baba and I. Karube. 2000. Molecular characterization of cDNA encoding oxygen evolving enhancer protein 1 increased by salt treatment in the mangrove *Bruguiera gymnorrhiza*. Plant Cell Physiol. 41(11): 1279-1285.
- Tanaka, Y., T. Hibino, Y. Hayashi, A. Tanaka, S. Kishitani, T. Takabe, S. Yokota and T. Takabe. 1999. Salt tolerance of transgenic rice overexpressing yeast mitochondrial Mn-SOD in chloroplasts. Plant Sci. 148(2): 131-138.
- Torabi, S., M. Wissuwa, M. Heidari, M.R. Naghavi, K. Gilany, M.R. Hajirezaei, M. Omidi, B. Yazdi-Samadi, A.M. Ismail and G.H. Salekdeh. 2009. A comparative proteome approach to decipher the mechanism of rice adaptation to phosphorous deficiency. Proteomics 9(1): 159-170.
- Tsai, C.C. and C.H. Chou. 1999. Sequence of a 5.8s rRNA gene and internal transcribed spacer (ITS) from *Imperata* cylindrica var. major. J. Genet. Mol. Biol. 10(2): 41-47.
- Wadsworth, G.J. 1997. The plant aspartate aminotransferase gene family. Physiol. Plant. 100(4): 998-1006.
- Wang, L., W. Liang, J. Xing, F. Tan, Y. Chen, L. Huang, C.L. Cheng and W. Chen. 2013. Dynamics of chloroplast proteome in salt-stressed mangrove *Kandelia candel* (L.) Druce. J. Proteome Res. 12(11): 5124-5136.
- Wu, T.C. and W.Y. Kao. 2011. Ecophysiological traits of leaves of three *Marsilea* species distributed in different gengraphical regions. Taiwana 56(4): 279-286.
- Wu, T.Y., P. Kao, C.L. Chang, P.H. Hsu, C.H. Chou and I.F. Chang. 2015. Phosphoproteomic profiling of microsomal fractions in leaves of Cogon grass (*Imperata* cylindrica). Plant OMICS J. 8: 595-603.
- Yoon, J.S., M.K. Lee, S.H. Sung and Y.C. Kim. 2006. Neuroprotective 2-(2-phenylethyl) chromones of *Imperata cylindrica*. J. Nat. Prod. 69(2): 290-291.
- Zhang, H., B. Han, T. Wang, S. Chen, H. Li, Y. Zhang and S. Dai. 2012. Mechanisms of plant salt response: Insights from proteomics. J. Proteome Res. 11(1): 49-67.
- Zhao, Q., S. Chen and S. Dai. 2013a. C4 photosynthetic machinery: Insights from maize chloroplast proteomics. Front. Plant Sci. 4: 85.
- Zhao, Q., H. Zhang, T. Wang, S. Chen and S. Dai. 2013b. Proteomics-based investigation of salt-responsive mechanisms in plant roots. J. Proteomics 82: 230-253.
- Zhu, J.K. 2003. Regulation of ion homeostasis under salt stress. Curr. Opin. Plant Biol. 6: 441-445.
- Zörb, C., R. Herbst, C. Forreiter and S. Schubert. 2009. Short-term effects of salt exposure on the maize chloroplast protein pattern. Proteomics 9(17): 4209-4220.
- Zörb, C., S. Schmitt and K.H. Muhling. 2010. Proteomic changes in maize roots after short-term adjustment to saline growth conditions. Proteomics **10(24)**: 4441-4449.

More supplementary data is shown in electronic form.

DOI: 10.6165/tai.2018.63.171



SUPPLEMENTARY DATA

 Table S1. Proteins identified in 2D-DIGE of leaf proteins isolated from salt-treated CW ecotype.

-		Replicate	1		Replica	te 2		Replicate	3		Replicate	4	
Spot	R1	R1	R1	R2	R2	R2	R3	R3	R3	R4	R4	R4	Average
#	control	NaCl	DIGE Ratio	control	NaCl	DIGE Ratio	control	NaCl	DIGE Ratio	control	NaCl	DIGE Ratio	(p value)
													2.072666667
11	2606.12	9320.89	3.57653694	2505.63	1076.50	0.429632328	2352.45	5200.82	2.21080929	665.79	6901.60	10.3660937	(0.03, 0.0005)
27	821.23	3881.63	4.726616397	405.49	0.00	0	758.45	2068.46	2.72721881	33375.14	85737.34	2.56889782	2.484666667
													(0.38, 0.34)
52	1005.89	1783.18	1.772739447	941.56	1785.15	1.895952967	1149.32	1838.48	1.59961654				1.7563333333 (0.003,
													0.00005)
61	4259.56	1858.45	0.436301059	4295.43	2143.23	0.498957148	4830.62	2701.25	0.55919312				0.498
													(0.003, 0.02)
70	1460.09	1229.76	0.842248416	1313.71	348.11	0.264986932	1404.61	576.96	0.41076241	2186.77	811.89	0.37127478	0.506 (0.02, 0.002)
													0.3683333333
83	1159.00	634.04	0.547061952	1729.46	360.56	0.208482516	1351.63	473.04	0.34997824	2949.55	127.76	0.04331656	(0.04,
													0.0007)
93	77.24	1017.54	13.17312884	123.28	0.00	0	0.00	625.74	#DIV/0!	126.67	291.97	2.3049637	5.159321333 (0.16, 0.045)
													0.408
96	512.48	431.29	0.841573677	472.55	79.15	0.167500038	537.74	115.33	0.2144641				(0.11, 0.01)
123	1275.54	1210.83	0.94927326	1208.52	435.65	0.360481568	1185.15	486.64	0.41060907				0.573333333
													(0.18, 0.01)
125	907.20	682.71	0.752543401	1240.87	379.49	0.305824539	1210.90	628.78	0.51927092				0.526 (0.02, 0.04)
													0.3886666667
150	750.23	583.59	0.777887002	783.61	16.21	0.020683334	698.21	256.30	0.36707989				(0.11, 0.04)
178	210.54	300.12	1.42550449	298.99	454.40	1.519796246	217.59	444.61	2.04339308				1.663
													(0.07, 0.6) 7.5176666667
182	54.17	381.58	7.044460573	42.10	383.73	9.11431732	76.70	490.54	6.39518367				(0.01,
													<0.00001)
189	842.94	543.84	0.645165205	812.02	345.19	0.425095735	743.44	533.94	0.71820322	701.24	514.70	0.73397715	0.596
													(0.02, 0.004) 0.593
199	1196.38	882.06	0.737269475	1254.90	612.18	0.487830848	1414.56	784.06	0.55427769				(0.01, 0.02)
201	475.79	957.08	2.011559033	513.90	697.15	1.356598352	531.24	1025.51	1.93039639	960.51	1370.51	1.42686253	1.766
201	475.79	957.08	2.011559055	515.90	097.15	1.330396332	551.24	1025.51	1.93039039	900.51	1370.51	1.42000200	(0.07, 0.03)
208	765.84	214.23	0.279724954	739.35	153.81	0.208028923	729.38	194.08	0.26608334	773.44	465.19	0.60146081	0.2513333333
200	705.04	214.23	0.279724934	139.33	155.61	0.200020923	129.30	194.00	0.20008334	115.44	405.19	0.00140081	(0.005, 0.00004)
212	E42 22	252.22	0 466091271	710 14	202 71	0.426270762	500.41	254.24	0 42426912				0.4386666667
212	543.32	253.23	0.466081371	710.14	302.71	0.426270762	599.41	254.31	0.42426813				(0.01, 0.0007)
279	429.51	337.19	0.785057014	1308.12	3748.40	2.865481252	503.68	534.79	1.06176757				1.5706666667
													(0.55, 0.76) 2.858
315	270.59	293.51	1.084706513	74.14	455.15	6.139233109	262.75	354.77	1.35021193				(0.11, 0.05)
378	557.34	330.45	0.592896508	775.75	362.59	0.467407913	514.27	274.73	0.53421174				0.531333333
0/0	001.04	000.40	0.002000000	110.10	002.00	0.407407010	014.27	214.10	0.00421114				(0.06, 0.3)
440	261.50	1283.05	4.906401101	249.36	423.35	1.697775023	195.41	395.34	2.0231673				2.875666667 (0.25, 0.19)
													16.6615
441	11.80	82.34	6.976285896	5.29	139.43	26.34717534	0.00	1351.26	#DIV/0!				(0.34, 0.19)
470	454.16	820.49	1.806632791	491.52	793.84	1.615086394	402.62	1076.12	2.67280324				2.031333333
													(0.03, 0.009) 1.893
666	295.44	755.89	2.558539947	0.00	156.27		380.48	467.01	1.22742629				(0.33, 0.3)
0.57	1025.01	E600 00	0.007000540	2005 04	4040.00	0.000000077	4004.00	2400 75	4 74445000				1.8566666667
957	1935.94	5686.02	2.937080548	2005.21	1849.33	0.922262587	1864.68	3190.75	1.71115236				(0.28, 0.02)



Table S2. Proteins identified in 2D-DIGE of leaf proteins isolated from CW e	ecotype
---	---------

Spot #	Accession number	Experimental pl/MW	Theoretical pl/MW	Mascot score	Unique peptide #	Peptide score	Experimental pl/MW	Theoretical pl/MW	Peptide Sequence (Scaffold probability)
Metabolism 178	gi 633095	6.32/42.97	8.62/50.48	1129	20	46	888.4385	888.5181	LAAAFIQR (97%)
	ite aminotransfei		0.02,00.10			45	911.6042	911.46	LYDSISSK
						41	961.4454	961.5345	LNLGVGAYR (100%)
						69	971.5229	971.6015	ISLAGLSLAK (100%)
						28	1008.3218	1008.4182	AQSDNMTDK (99%)
						54	1079.318	1079.4375	QEMEEMAGR
						42	1095.8918	1095.4325	QEMEEMAGR.I + Oxidation (M)
						34	1337.5794	1337.7092	VLISSPTWGNHK (100%)
						90	1344.5218	1344.6384	
						30 90	1357.549 1360.479	1357.67 1360.6333	QIGMFSYTGLNK (99%) GMEVFVAQSYSK.N + Oxidation (M)
						90 50	1373.5414	1373.6649	QIGMFSYTGLNK + Oxidation (M)
						43	1463.6104	1463.766	EYLPIEGLAAFNK (100%)
						51	1500.615	1500.7395	RGMEVFVAQSYSK (100%)
						36	1516.5657	1516.7344	RGMEVFVAQSYSK.N + Oxidation (M)
						91	1523.7066	1523.8559	ATAELLLGADNPVIK (100%)
						85	1530.7016	1530.8293	TEELQPYVLNVVK (100%)
						75	1669.8254	1669.8457	IGAINVVCSAPEVADR.V +
									Carbamidomethyl (C)
						108	1686.8	1686.9265	QGLVATLQSLSGTGSLR (100%)
						103	1761.7211	1761.876	IVANVVGDPTMFGEWK (100%)
						37	1777.7211	1777.8709	IVANVVGDPTMFGEWK.Q + Oxidation (M
						78	1891.7951	1891.9679	GENKEYLPIEGLAAFNK AQSDNMTDKWHVYMTK
						16 65	1953.668	1953.8713	
							2099.8473	2100.0602	FEGVPMAPPDPILGVSEAFK (100%) FEGVPMAPPDPILGVSEAFK.A + Oxidati
						75	2115.832	2116.0551	(M)
						25	2839.0474	2839.2979	IVANVVGDPTMFGEWKQEMEEMAGR.I Oxidation (M)
ignaling 957	gi 1345588	4.70/29.53	4.75/29.64	247	5	45	817.39	817.4368	ICDGILK.L + Carbamidomethyl (C)
eneral regulato	ory factor (14-3-3	5)					906.4369	906.5174	NLLSVAYK (98%)
							1405.5048	1405.6573	TVDSEELTVEER (100%)
							1693.7479	1693.8886	LLESHLVPSSTAPESK (100%)
tress		•					1785.8167	1785.9737	AAQDIALAELAPTHPIR (100%)
uperoxide									
smutase [Mn]									
.1,	gi 134668	6.40/20.77	6.71/25.21	248	5	74	1316.6267	1316.6262	HHATYVANYNK (100%)
itochondrial	gi104000	0.40/20.11	0.7 1/20.21	240	5	/4	1010.0207	1010.0202	
recursor									
						43	1226.4512	1226.5819	YAGEVYENVLA (100%)
						66	1530.6674	1530.7943	NVRPDYLNNIWK (100%)
						26	1598.7729	1598.7743	FNGGGHVNHSIFWK (94%)
						64	1615.831	1615.8318	NLKPISEGGGEPPHGK (100%)
93	gi 212722004		6.71/25.21	157	6	74	1127.6175	1127.6186	ALEQLDAAVAK (100%)
uperoxide dism	utase [Mn] 3.4,	mitochondrial pre	cursor			96	1355.7405	1355.7409	GDASAVVQLQGAIK (100%)
						41	1530.7938	1530.7943	NVRPDYLNNIWK (100%)
						79	1614.8463	1614.8465	LSVETTANQDPLVTK (100%)
						33 113	1615.831 1742.9452	1615.8318 1742.9414	NLKPISEGGGEPPHGK
hotoovathooid		•				113	1742.9452	1742.9414	KLSVETTANQDPLVTK
hotosynthesis 61	gi 3914607	4.70/13.29	9.04/19.25	227	2	63	1447.4446	1447.5674	ENSTSPCYYDGR.Y + Carbamidomethy
	• •					05	0040.0000		
IDUIOSE-1, 5-DIS	sphosphate carb	oxylase/oxygena	se small subun	It		35	2018.9003	2019.0928	FETLSYLPPLTQEQLLK (100%)
11	gi 242047384	6.23/23.38	8.63/27.72	725	5	85 39	2147.0061 944.473	2147.1878 944.508	KFETLSYLPPLTQEQLLK (100%) EFPGQVLR (95%)
•••••••••••••••••••••••••••••••••••••••		FT 02g002690 (125		53	1229.6442	1229.6517	EREFPGQVLR (100%)
ypotrictical pro		1 1_029002030 (OLLZ)			80	1268.5908	1268.6725	HQLITATVSDGK (100%)
						80	2098.8688	2099.0131	TADGDEGGKHQLITATVSDGK (100%)
						125	2239.8898	2240.0597	YEDNFDANSNVSVIIQPTSK (100%)
						84	2500.0919	2500.2737	KTITEYGSPEEFLSQVDFLLGK (100%)
27	gi 242047384	5.60/23.65	8.63/27.72	529	6	38	790.9552	790.4589	VDFLLGK
		FT_02g002690 (34	944.4306	944.508	EFPGQVLR (99%)
		`				51	1229.6032	1229.6517	EREFPGQVLR (100%)
						54	1268.5737	1268.6725	HQLITATVSDGK (100%)
						90	2098.8606	2099.0131	TADGDEGGKHQLITATVSDGK (100%)
						62	2239.8467	2240.0597	YEDNFDANSNVSVIIQPTSK (100%)
						132	2372.2294	2372.1788	TITEYGSPEEFLSQVDFLLGK (100%)
50		4 5 4 14 7 00	7 44/04 15	4450	0	62	2500.0743	2500.2737	KTITEYGSPEEFLSQVDFLLGK (100%)
52	gi 212721648		7.44/24.15	1459	6	37	912.3221	912.4705	AYAVGASFK (96%)
nunaracterized	protein LOC100	194094				65 48	934.4428	934.5124	ADLTGAIFK (97%)
						48	1075.3442 1090.4656	1075.4281 1090.5692	FCDYTNEK.T + Carbamidomethyl (C)
						101 98	1090.4656	1090.5692	SLAAALMSEAK (100%)
						98 101	1207.5175	1207.5833	SLAAALMSEAK.F + Oxidation (M) GTDETNAVIDE (100%)
						92	1414.5043	1207.5655	GTDFTNAVIDR (100%) FDGADMSEVVMSK (100%)
						92 107	1430.5184	1430.6058	FDGADMSEVVMSK (100%) FDGADMSEVVMSK.A + Oxidation (M)
						80	1446.4746	1446.6007	FDGADMSEVVMSK.A + 2 Oxidation (M)
	gi 212721648	3.78/7.18	7.44/24.15	181	3	46	934.452	934.5124	ADLTGAIFK (100%)
70					J.		1090.4809	1090.5692	SLAAALMSEAK (100%)
70 ncharacterized		194054				64			
	protein LOC100	194054				64 89	1414.4982	1414.6109	FDGADMSEVVMSK (100%)



Table S2. continued

Spot	Accession	Experimental	Theoretical	Mascot	Unique	Peptide	Experimental		Peptide
#	number	pl/MW	pl/MW	score	peptide #	score	pl/MW	pl/MW	Sequence (Scaffold probability)
Chloroplast oxy	/gen-evolving enh	ancer protein 1,	OEE1			57	1095.4492	1095.5448	LTYDEIQSK(100%)
						49	1251.5808	1251.6459	RLTYDEIQSK (100%)
						69	1421.6535	1421.7588	KLCLEPTSFTVK.A + Carbamidomethyl (C)
						53	1430.5731	1430.6889	GDEEELQKENIK (100%)
						112 100	1462.6138 1561.6072	1462.7627 1561.7485	NAASSTGNITLSVTK (100%) GGSTGYDNAVALPAGGR (100%)
						77	1759.7137	1759.8741	DGIDYAAVTVQLPGGER (100%)
						48	1774.7089	1774.8711	GRGGSTGYDNAVALPAGGR (100%)
									GTGTANQCPTIDGGVESFPFK.A +
						114	2181.809	2182.0001	Carbamidomethyl (C)
						64	2249.0126	2249.1845	QLVATGKPESFGGPFLVPSYR (100%)
						69	2292.9453	2293.1226	FEEKDGIDYAAVTVQLPGGER (100%)
						60	2489.9193	2490.1623	GGSTGYDNAVALPAGGRGDEEELQK
						00	2409.9195	2490.1023	(100%)
						75	2575.0071	2575.229	SNPETGEVIGVFESVQPSDTDLGAK
									(100%)
199	gi 194702912	5.30/20.50	6.41/21.03	917	7	67	1088.3727	1088.4927	TGEDPWWKA (100%)
Unknown (Cyt	b6-f)					90	1362.5254	1362.6667	GDPTYLVVEQDK (100%)
						47	1413.6151	1413.7504	
						83	1506.6421	1506.7871	VLFVPWVETDFR (100%)
						61	1656.7038	1656.8723	
						121	1773.7377	1773.9261	GPAPLSLALVHADVDDGK (100%)
						52	1808.6325	1808.7723	FiCPCHGSQYNNQGK.V + 2
208	gi 194702912	6.23/12.52	6.41/21.03	217	3	83	1362.5067	1362.6667	Carbamidomethyl (C) GDPTYLVVEQDK (100%)
Unknown (Cyt		0.20/12.02	0.41/21.00	211		83	1506.6643	1502.0007	VLFVPWVETDFR (100%)
Ulikilowii (Cyt	50-1)					65	1773.745	1773.9261	GPAPLSLALVHADVDDGK (100%)
279	gi 227786	4.98/28.60	8.62/38.68	272	17	59	974.506	974.5549	IGLFGGAGVGK (100%)
	CF1 beta subunit		0.02,00.00			53	1031.4001	1031.5135	AINLEEESK (100%)
, ojnaldoo						37	1044.4845	1044.5968	VVDLLAPYR (100%)
						27	1172.5617	1172.6554	VVDLLAPYQR
						65	1190.4984	1190.6183	SAPAFIELDTK (100%)
						47	1221.4738	1221.5846	AVAMSATDGLMR (100%)
						27	1261.4943	1261.6336	TIAMDGTEGLVR
						33	1277.5054	1277.6286	TIAMDGTEGLVR.G + Oxidation (M)
						41	1327.5855	1327.6633	AHGGVSVFGGVGER (100%)
						29	1398.676	1398.762	VGLTGLTVAEHFR (100%)
						24	1408.648	1408.8038	VLNTGSPITVPVGR
						57	1415.5173	1415.6793	IVGNEHYETAQR (100%)
						47	1432.6444	1432.7344	MVQAGSEVSALLGR.M + Oxidation (M)
						94	1433.3454	1432.7674	FVQAGSEVSALLGR (100%)
						98 59	1470.6003	1470.7541	
						59 22	1486.6275	1486.749	VGLTALTMAEYFR.D + Oxidation (M)
						22	1491.6424 2059.8438	1491.7681 2060.0248	FTQANSEVSALLGR GIYPAVDPLDSTSTMLQPR (100%)
						42	2184.9207	2185.1379	IPSAVGYQPTLATDLGGLQER
						50	2280.9025	2281.0719	MPSAVGYQPTLSTEMGSLQER (100%)
									MPSAVGYQPTLSTEMGSLQER.I +
						21	2296.8617	2297.0668	Oxidation (M)
470		7.01/16.36	9.82/15.45	131	5	33	731.4335	731.433	YPVVVŘ
Photosystem I	reaction center su					103	1869.9116	1869.9108	VNYAGVSTNNYALDEIK
						20	1018.49	1018.5811	ADKPPPIGPK
						53	2083.817	2083.9909	ADEDATAEPAEGEGVVATKPK
						30	2425.8851	2426.1139	ESYWYNGIGNVVTVDQDPNTR
666		5.06/7.50	6.69/9.52	88	2	53	1054.3881	1054.5295	VYLSSETTR
Photosystem I	reaction center su	bunit VII				49	1540.4911	1540.665	CESACPTDFLSVR.V+ 2
		•				-			Carbamidomethyl (C)
Others	ail242070005	4.24/41.25	1 02/46 60	407	14	FO	700 4000	700 4000	
201 Cyclophilin	gi 242079005	4.24/41.25	4.83/46.69	497	14	59 52	788.4033	788.4028	ALDSVER (90%)
Cyclophilin							932.4961 986.5029	932.4967	YALPIDNK (100%) ANGEELLNK (100%)
						51 82	986.5029 1110.6626	986.5032 1110.6648	SLILAGLAEPK (100%)
						93	1126.6339	1126.6346	LAVGLEELQR (100%)
						53 54	1142.6033	1142.6043	RANGEELLOK (100%)
						79	1157.5164	1157.5175	FYDGMEIQR (100%)
						73	1285.6136	1285.6125	KFYDGMEIQR (100%)
						78	1315.6694	1315.6694	TVPLEIMVDGDK (100%)
						51	1377.5978	1377.5983	DNPNIEDCVFR.I + Carbamidomethyl (C)
						97	1425.6896	1425.6897	LPFNAFGTMAMAR (100%)
						101	1432.7199	1432.7198	APVYGETLEELGR (100%)
						88	1613.8525	1613.8512	EVQKPLEDITDSLK (100%)
						100	1614.7861	1614.7849	ESELTPSNANILDGR (100%)
						80	1618.7779	1618.7773	IKDNPNIEDCVFR.I + Carbamidomethyl (C)
						77	2490.1548	2490.1551	ADGFVVQTGDPEGPAEGFIDPSTGK (100%)



Table S3. DIGE ratio of leaf proteins identified from SL population

			•			om SL popu					Deall 1		
Spot		Replicate 1 R1	R1	R2	Replicate 2 R2	R2	R3	Replicate 3 R3	R3	R4	Replicate 4 R4	4 R4	Average
#	control	NaCl	DIGE Ratio	control	NaCl	Ratio	control	NaCl	Ratio	control	NaCl	Ratio	DIGE Ratio (p value)
99	611.93	791.15	1.29286605	353.57	260.24	0.736043932	320.74	264.40	0.824357642	2399.17	2969.42	1.237689567	0.951 (0.86, 0.0005)
434	286.87	248.87	0.8675393	348.20	467.06	1.341344649	440.07	273.06	0.620485774	698.41	535.44	0.766658886	0.943 (0.61, 0.34)
755	439.45	350.51	0.797619821	311.94	446.54	1.431503684	664.07	862.83	1.299315868				1.1763333333
56	5012.29	2860.57	0.570711131	2882.18	4881.42	1.693655994	4638.30	4088.68	0.881503202	5653.75	4224.53	0.747208497	(0.57, 0.00005) 1.049
537	82.19	88.90	1.081737604	11.33	25.13	2.217162584	14.01	32.49	2.318542424	968.04	868.38	0.897051182	(0.49, 0.02) 1.872666667
621	94.70	52.27	0.551984903	32.25	83.96	2.603565285	57.82	90.92	1.572624749	758.55	272.43	0.359145023	(0.96, 0.002) 1.576333333
415	19.84	23.51		9.46	4.49	0.474598047	18.21	15.13		119.66	152.22	1.272032526	(0.58, 0.0007) 0.830333333
			1.185487796						0.830943856				(0.88, 0.045) 1.051666667
91	1238.91	1331.20	1.074497183	1191.75	1317.68	1.105668386	1679.54	1637.11	0.974733919	542.84	622.83	1.147356479	(0.85, 0.01) 2.255
559	94.89	129.65	1.366343464	21.95	73.57	3.351283641	27.26	55.83	2.04771984	834.18	699.23	0.838226477	(0.99, 0.01) 0.889333333
59	3092.78	2744.38	0.887351632	2774.69	3042.02	1.096348687	3454.77	2377.93	0.688303204	901.60	677.44	0.751374516	(0.67, 0.04) 1.154247
272	53.49	57.70	1.078687883	0.00	1.37	#DIV/0!	34.56	29.64	0.857541269	437.68	667.78	1.525741155	(0.77, 0.04)
214	392.23	460.30	1.173539856	611.65	375.96	0.614670353	230.45	241.41	1.047563396	152.66	19.82	0.129849756	0.945666667 (0.62, 0.6)
723	0.23	0.23	0.998264708	8.64	27.60	3.194981229	3.38	6.84	2.024976031	29.61	113.49	3.832427833	2.072666667 (0.39, <0.00001)
656	248.05	72.13	0.290782993	126.88	331.57	2.613261045	229.21	202.03	0.88141365	469.61	568.23	1.210025421	1.261666667 (0.85, 0.004)
74	3120.87	2692.13	0.862620502	2707.27	3220.01	1.189391898	3408.23	2478.42	0.727185244	1342.26	1043.04	0.777072449	0.9263333333 (0.68, 0.02)
106	1093.39	1045.88	0.956545116	1125.58	1013.39	0.900332924	908.16	918.09	1.010934894	813.13	493.96	0.607478224	0.956 (0.46, 0.03)
592	195.16	7.82	0.040062163	163.55	273.89	1.674617947	315.09	306.39	0.972375913	394.09	196.81	0.499400819	0.895666667
504	418.48	259.78	0.620768697	452.61	262.97	0.580998543	462.54	484.40	1.047259974	471.62	247.89	0.525615438	0.7496666667 (0.09, 0.0007)
188	714.17	726.94	1.017881051	1449.85	1221.04	0.842184761	1273.66	1192.28	0.936101541	1019.65	1029.14	1.0093113	0.932
612	129.57	196.42	1.515956208	189.73	39.80	0.209761766	107.77	101.10	0.938176076	170.85	318.25	1.862713743	(0.73, 0.76) 0.888
589	425.10	546.59	1.285798279	325.77	659.46	2.024282133	631.50	1271.96	2.01420197	296.87	231.52	0.77985345	(0.83, 0.048) 1.775333333
427	188.80	192.41	1.019109661	536.96	645.53	1.202205019	202.29	177.30	0.876450833	93.82	199.04	2.12150493	(0.33, 0.3) 1.032333333
													(0.76, 0.19) 1.499333333
566	9.96	15.72	1.57864553	55.12	94.27	1.71004735	35.51	42.94	1.209140018	3.20	3.33	1.042782462	(0.6, 0.19) 0.993
452	484.67	403.76	0.833051921	423.09	303.30	0.716868564	535.51	765.16	1.428837611	214.69	553.75	2.579307044	(0.49, 0.009) 1.705
173	198.57	204.48	1.029798049	213.89	255.50	1.194542289	153.45	443.52	2.890235709	187.62	109.95	0.586006167	(0.43, 0.3) 0.948
753	4005.60	3138.37	0.783495357	2025.79	1966.88	0.970920806	2285.03	2490.18	1.089781756	3306.89	4121.66	1.246382791	(0.97, 0.02)
99	611.93	791.15	1.29286605	353.57	260.24	0.736043932	320.74	264.40	0.824357642	2399.17	2969.42	1.237689567	0.951 (0.86, 0.0005)
434	286.87	248.87	0.8675393	348.20	467.06	1.341344649	440.07	273.06	0.620485774	698.41	535.44	0.766658886	0.943 (0.61, 0.34)
755	439.45	350.51	0.797619821	311.94	446.54	1.431503684	664.07	862.83	1.299315868				1.1763333333 (0.57, 0.00005)
56	5012.29	2860.57	0.570711131	2882.18	4881.42	1.693655994	4638.30	4088.68	0.881503202	5653.75	4224.53	0.747208497	1.049 (0.49, 0.02)
537	82.19	88.90	1.081737604	11.33	25.13	2.217162584	14.01	32.49	2.318542424	968.04	868.38	0.897051182	1.872666667 (0.96, 0.002)
621	94.70	52.27	0.551984903	32.25	83.96	2.603565285	57.82	90.92	1.572624749	758.55	272.43	0.359145023	1.576333333 (0.58, 0.0007)
415	19.84	23.51	1.185487796	9.46	4.49	0.474598047	18.21	15.13	0.830943856	119.66	152.22	1.272032526	0.8303333333 (0.88, 0.045)
91	1238.91	1331.20	1.074497183	1191.75	1317.68	1.105668386	1679.54	1637.11	0.974733919	542.84	622.83	1.147356479	1.051666667
559	94.89	129.65	1.366343464	21.95	73.57	3.351283641	27.26	55.83	2.04771984	834.18	699.23	0.838226477	(0.85, 0.01) 2.255 (0.00, 0.01)
59	3092.78	2744.38	0.887351632		3042.02	1.096348687	3454.77	2377.93	0.688303204	901.60	677.44	0.751374516	(0.99, 0.01) 0.889333333 (0.07, 0.04)
272	53.49	57.70	1.078687883	0.00	1.37	#DIV/0!	34.56	29.64	0.857541269	437.68	667.78	1.525741155	(0.67, 0.04) 1.154247
212	392.23	460.30		611.65		0.614670353	230.45			152.66	19.82	0.129849756	(0.77, 0.04) 0.945666667
			1.173539856		375.96			241.41	1.047563396				(0.62, 0.6) 2.072666667
723	0.23	0.23	0.998264708	8.64	27.60	3.194981229	3.38	6.84	2.024976031	29.61	113.49	3.832427833	(0.39, <0.00001) 1.261666667
656	248.05	72.13	0.290782993	126.88	331.57	2.613261045	229.21	202.03	0.88141365	469.61	568.23	1.210025421	(0.85, 0.004) 0.926333333
74	3120.87	2692.13	0.862620502		3220.01	1.189391898	3408.23	2478.42	0.727185244	1342.26	1043.04	0.777072449	(0.68, 0.02)
106	1093.39	1045.88	0.956545116	1125.58	1013.39	0.900332924	908.16	918.09	1.010934894	813.13	493.96	0.607478224	0.956 (0.46, 0.03)
592	195.16	7.82	0.040062163	163.55	273.89	1.674617947	315.09	306.39	0.972375913	394.09	196.81	0.499400819	0.895666667 (0.44, 0.00004)



Table S3. Continued

		Replicate '	1		Replicate 2	2		Replicate 3			Replicate 4	1	
Spot	R1	R1	R1	R2	R2	R2	R3	R3	R3	R4	R4	R4	Average
#	control	NaCl	DIGE Ratio	control	NaCl	Ratio	control	NaCl	Ratio	control	NaCl	Ratio	DIGE Ratio (p value)
504	418.48	259.78	0.620768697	452.61	262.97	0.580998543	462.54	484.40	1.047259974	471.62	247.89	0.525615438	0.749666667 (0.09, 0.0007)
188	714.17	726.94	1.017881051	1449.85	1221.04	0.842184761	1273.66	1192.28	0.936101541	1019.65	1029.14	1.0093113	0.932 (0.73, 0.76)
612	129.57	196.42	1.515956208	189.73	39.80	0.209761766	107.77	101.10	0.938176076	170.85	318.25	1.862713743	0.888 (0.83, 0.048)
589	425.10	546.59	1.285798279	325.77	659.46	2.024282133	631.50	1271.96	2.01420197	296.87	231.52	0.77985345	1.7753333333 (0.33, 0.3)
427	188.80	192.41	1.019109661	536.96	645.53	1.202205019	202.29	177.30	0.876450833	93.82	199.04	2.12150493	1.032333333 (0.76, 0.19)
566	9.96	15.72	1.57864553	55.12	94.27	1.71004735	35.51	42.94	1.209140018	3.20	3.33	1.042782462	1.4993333333 (0.6, 0.19)
452	484.67	403.76	0.833051921	423.09	303.30	0.716868564	535.51	765.16	1.428837611	214.69	553.75	2.579307044	0.993 (0.49, 0.009)
173	198.57	204.48	1.029798049	213.89	255.50	1.194542289	153.45	443.52	2.890235709	187.62	109.95	0.586006167	1.705 (0.43, 0.3)
753	4005.60	3138.37	0.783495357	2025.79	1966.88	0.970920806	2285.03	2490.18	1.089781756	3306.89	4121.66	1.246382791	0.948 (0.97, 0.02)

The first p value: p values of T-test for most proteins with significant differential abundance between control and salt-stressed plants

are shown after fold change ratio. 2. The second p value: p values of ANOVA for proteins with significant differential abundance between CW ecotype and SL population are shown after fold change ratio.

Table S4.	Proteins identified in 2D-DIGE	of leaf proteins isolated fi	rom SL population
-----------	--------------------------------	------------------------------	-------------------

Spot	Accession	Experimental		Mascot			Experimental	Theoretical	Peptide
#	number	pl/MW	pl/MW	score	peptide #	score	pl/MW	pl/MW	Sequence (Scaffold probability)
Vetabolism					_				
214	gi 514719430	6.60/40.55	8.62/50.48	507	7	58	914.5345	914.5073	IADVIQEK (99%)
Plastidic aspa	rtate aminotransfe	erase				35	935.4753	935.4501	VPWSEYR
						34	950.5081	950.4821	NLGLYSER
						43	961.5606	961.5345	LNLGVGAYR (90%)
						63	971.6303	971.6015	ISLAGLSLAK (100%)
						91	1360.6502	1360.6333	GMEVFVAQSYSK.N + Oxidation (M)
						68	1523.8794	1523.8559	ATAELLLGADNPVIK (100%)
						99	1530.8434	1530.8293	TEELQPYVLNVVK (100%)
612	gi 242059597	6.32/38.68	6.96/38.99	245	15	43	647.3753	647.3755	AAFLAR
Fructose-bispl	hosphate aldolase	9				48	830.4861	830.4861	ALQASTLK (99%)
						41	989.5021	989.5029	GTIEVAGTDK
						55	990.5134	990.5134	NAAYIGTPGK (100%)
						47	1116.6174	1116.6179	DGKPFVDVLK (99%)
						43	1153.5617	1153.5615	ANSEATLGTYK (100%)
						51	1210.6914	1210.6921	EGGVLPGIKVDK (99%)
						59	1243.6596	1243.6561	AWAGKVENIEK (100%)
						78	1312.6268	1312.6259	GDAAADTESLHVK (100%)
						80	1331.6934	1331.6933	GILAADESTGTIGK (100%)
						67	1375.7326	1375.7347	VTPEVIAEYTVR (100%)
						73	1487.7956	1487.7944	GILAADESTGTIGKR (100%)
						66	1501.7371	1501.7372	LSSINVENVEENR (100%)
						42	1503.8318	1503.8297	
						42 27	1657.8404	1657.8383	KVTPEVIAEYTVR (97%) LSSINVENVEENRR
ignaling						21	1037.0404	1037.0303	LISSINVENVEENKK
753	qi 242073380	5.09/28.71	4.76/29.74	709	36	20	769.4015	769.401	YLAEFK
	atory factor (14-3-		4.70/29.74	109	30	20 50	815.4122	815.4137	LAEQAER (90%)
General regul	atory factor (14-3-	3)				40	817.4366	817.4368	ICDGILK.L + Carbamidomethyl (C) (81%)
						38	902.5083	902.5073	IVSSIEQK
						34	906.5177	906.5174	NLLSVAYK (100%)
						25	931.4229	931.4222	MKGDYYR
						14	1006.5824	1006.5811	VTLIKDYR
						29	1024.5918	1024.5917	LVPAAAAVDAK
						30	1143.6269	1143.6248	GNEDRVTLIK
						71	1188.6542	1188.6536	DSTLIMQLLR (100%)
						53	1194.6356	1194.6357	KNEEHVAQIK (98%)
						74	1199.5135	1199.5128	DAAESTMNAYK (100%)
						72	1204.6488	1204.6485	DSTLIMQLLR.D + Oxidation (M)
						76	1211.5496	1211.5492	DAAENTMVAYK (100%)
						33	1214.5508	1214.5489	ESAESTMVAYK
						49	1215.5078	1215.5077	DAAESTMNAYK.A + Oxidation (M)
						66	1327.6094	1327.6078	KDAAESTMNAYK (100%)
						34	1333.5566	1333.557	YEEMVEFMEK (99%)
						101	1339.6436	1339.6442	KDAAENTMVAYK
						48	1349.5507	1349.5519	YEEMVEFMEK.V + Oxidation (M)
						107	1355.6392	1355.6391	KDAAENTMVAYK.A + Oxidation (M)
						96	1387.7299	1387.7307	IISSIEQKEEGR
						77	1403.724	1403.7256	IVSSIEQKEESR
						90	1405.6573	1405.6573	TVDSEELTVEER
						71	1417.693	1417.6936	TVDVEELTVEER (100%)
						80	1426.7459	1426.7416	IVSSIEHKEETR (94%)
						80 71	1486.7779	1426.7416	VEAELSGICAGILR + Carbamidomethyl (C

S5



Table S4 Continued.

Spot #	Accession number	Experimental pl/MW	Theoretical pl/MW	Mascot score	Unique peptide #	score	Experimental pl/MW	Theoretical pl/MW	Peptide Sequence (Scaffold probability)
						33 106 20	1495.7125 1503.6801	1495.7127 1503.6801	EEGRGNEAHAASIR SAGGAGGGEELSVEER (100%)
						30 81	1516.8722 1573.8039	1516.8725 1573.8021	NLLSVAYKNVIGAR IEAELSNICDGILK + Carbamidomethyl (C) (100%)
						51 46	1637.9163 1653.8592	1636.9148 1653.8573	LLDDRLVPAAAAVDAK LLDSHLVPSSTAAESK (100%)
						70 68	1669.8534 1693.8908	1693.8886	LLDSHLVPSSTASESK
						21	1709.7929	1709.793	SPTEPTREESVYMAK (100%)
						56 100	1771.9583 1785.9738	1771.9581 1785.9737	AAQDIALADLAPTHPIR AAQDIALAELAPTHPIR (100%)
						85 36	1920.9446 2049.9794	1920.9429 2049.0378	DAADSTLAAYQAAQDIAVK KDAADSTLAAYQAAQDIAVK
Stress 91	gi 1568639	4.96/16.24	5.35/20.42	104	3	17	1098.61	1098.6107	LACGVVGLTPL + Carbamidomethyl (C)
	dismutase [Cu/Zn]					94 66.2	1411.6814 1086.53	1411.6804 1086.5378	GGHELSLSTGNAGGR (100%) EDGPTTVNVR (100%)
Protein degrad 415	gi 242079721	6.36/19.81	5.71/26.31	317	5	36	755.4887	755.4653	VAANLIR (90%)
Proteasome	Deta subunit					43 38	845.5052 1016.5606	845.4793 1016.5502	VVSLAMAR (99%) TVTINADGVK (98%)
						49 60	1098.5348	1098.5128	TSTGMYVANR (100%)
Dhataaunthaa	-					111	1114.5304 1567.7608	1114.5077 1567.7478	TSTGMYVANR.A + Oxidation (M) SGSAADTQVISDYVR (100%)
Photosynthes 74	is gi∣194702912 Unknown (Cyt b6-f)	5.50/17.07	6.41/21.03	139	3	66 79	1088.4925 1362.6678	1088.4927 1362.6667	TGEDPWWKA (100%) GDPTYLVVEQDK (100%)
	Olikilowii (Cyt bo-i,)				56	1808.7704	1808.7723	FICPCHGSQYNNQGK.V + 2 Carbamidomethy
56	gi 164698711	4.79/13.10	8.78/19.37	75	4	15	769.3757	769.3759	(C) (100%) EGFVYR
	, 5-bisphosphate ca					31	905.4966	905.4971	QVDYLLR NNWVPCLEFSK.E + Carbamidomethyl (C)
						22	1392.6498	1392.6496	(100%) ENSTSPCYYDGR.Y + Carbamidomethyl (C)
						48	1447.5664	1447.5674	(100%)
173 Photosystem	gi 7524738 I reaction center s	6.02/11.50 ubunit VII	6.69/9.52	189	3	23 61	967.3716 1540.6612	967.3739 1540.665	TEDCVGCK.R + 2 Carbamidomethyl (C) CESACPTDFLSVR.V + 2 Carbamidomethyl (C)
						90	1644.7068	1644.7059	(100%) IYDTCIGCTQCVR.A + 3 Carbamidomethyl (C)
452		7.01/16.36	9.82/15.45	177	3	27	731.4555	731.4330	(100%) YPVVVR
Photosystem	I reaction center s	ubunit IV				28 46	1018.6050 2054.0008	1018.5811 2053.9804	ADKPPPIGPK (91%) ADEDAAAEPAEGEGVVATKPK (100%)
755	gi 212721648	4.78/15.91	7.44/24.15	213	3	69	1090.5704	1090.5692	SLAAALMSEAK (100%)
Uncharacteri	zed protein LOC10	0194054				61 95	1106.5644 1207.5826	1106.5641 1207.5833	SLAAALMSEAK.F + Oxidation (M) GTDFTNAVIDR (100%)
						77	1446.5949	1446.6007	FDGADMSEVVMSK.A + 2 Oxidation (M)
753 Chloroplast c	gi 383511664 bxygen-evolving en	5.09/28.71 hancer protein 1	6.08/34.95 OFF1	477	19	24 26	849.427 929.4605	849.4232 929.4607	GSSFLDPK NAPPEFQK
			,			48	949.5638	949.5637	VPFLFTVK (98%)
						49 11	1095.5448 1219.6234	1095.5448 1219.6237	LTYDEIQSK (99%) IQGIWYAQLE
						54	1251.6462	1251.6459	RLTYDEIQSK (100%)
						72	1285.59	1285.5907	ANLGMEVMHER LCLEPTSFTVK.A + Carbamidomethyl (C)
						46	1293.6646	1293.6639	(100%)
						64 59	1301.5846 1313.7102	1301.5856 1313.7092	ANLGMEVMHER.N + Oxidation (M) VINTWADIINR
						76	1421.7594	1421.7588	KLCLEPTSFTVK.A + Carbamidomethyl (C) (100%)
						34	1427.6318	1427.614	FCDWITSTENR.L + Carbamidomethyl (C)
						59 59	1430.6904 1458.7256	1430.6889 1458.7255	GDEEELQKENIK LIFQYASFnNSR
						96	1462.7625	1462.7627	NAASSTGNITLSVTK (100%)
						58 81	1463.7504 1498.617	1463.8195 1498.6172	SVASSSGKITLSVTK (100%) ETTENESANEGYR
						74	1561.7509	1561.7485	GGSTGYDNAVALPAGGR (100%)
						83 95	1759.8731 1774.8731	1759.8741 1774.8711	.DGIDYAAVTVQLPGGER (100%) GRGGSTGYDNAVALPAGGR (100%)
						54	2491.1665	2491.1463	GGSTGYDNAVALPAGGRGDEEELEK
106 Cyclophillin	gi 242079005	4.36/40.14	4.83/46.69	304	13	20	630.334	630.3337	
Cyclophilin						52 49	788.4021 986.5035	788.4028 986.5032	ALDSVER (90%) ANGEELLNK (100%)
						58	1110.6648	1110.6648	SLILAGLAEPK (100%)
						73 43	1126.6378 1142.6036	1126.6346 1142.6043	LAVGLEELQR (100%) RANGEELLNK (98%)
						37	1157.5168	1157.5175	FYDGMEIQR (98%)
						67 60	1266.7644 1285.6138	1266.7659 1285.6125	SLILAGLAEPKR (100%) KFYDGMEIQR (100%)
						46	1315.6688	1315.6694	TVPLEIMVDĠDK
						19 64	1377.5966 1425.6902	1377.5983 1425.6897	DNPNLEDCVFR.I + Carbamidomethyl (C) LPFNAFGTMAMAR (100%)
						71	1613.8514	1613.8512	EVQKPLEDITDSLK (100%)
						61	1614.789	1614.7849	ESELTPSNANILDGR (100%)

 Table S5. MASCOT search results deposited to ProteomeXchange consortium.



Peak list file	Mascot search result file
12_final spot#11	F011716.dat
32_final spot#27	F011717.dat
52_final spot#61	F011718.dat
56	F011745.dat
58_final spot@52	F011719.dat
64_final spot#70	F011720.dat
97_final spot#93	F011721.dat
111_new spot#755	F011735.dat
112_final spot#957	F011722.dat
157_new spot#91	F011736.dat
157_new spot#91	F011737.dat
162_final spot#178	F011723.dat
165_final spot#199	F011724.dat
173	F011747.dat
183_final spot#208	F011725.dat
220_new spot#106	F011738.dat
220_new spot#106	F011739.dat
259_final spot#201	F011726.dat
284_new spot#74	F011740.dat
385_final spot#279	F011727.dat
415	F011746.dat
452	F011748.dat
457_new spot#612	F011741.dat
506_final spot#470	F011728.dat
515_final spot#666	F011731.dat
597_final spot#470	F011730.dat
707_new spot#173	F011742.dat
835_new spot#753	F011743.dat

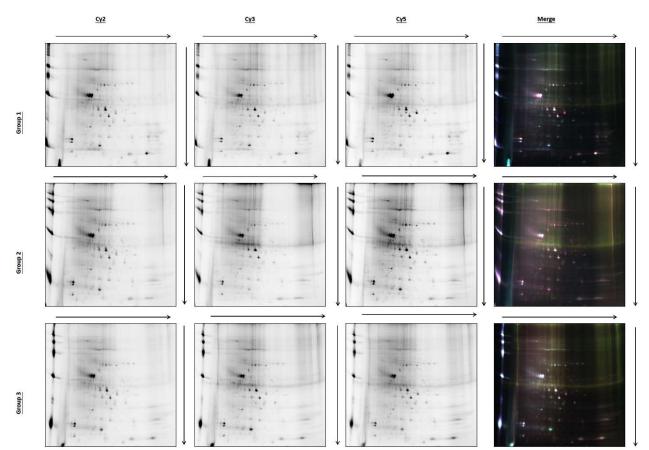


Fig. S1. 2D-DIGE images of leave proteins isolated from salt-treated CW ecotype. The gel images correspond to three representative biological replicates.



Taiwania

Spot # 11

Valid		Sequence	Prob	Masco	Maxo	. Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V 1	.0	(K)EREFPGQ¥LR(Y)	100%	54.0	51.6	8.8	2		410.89	1,229.64	3	-0.0075	-6.1	1190		5531	114	123	0		1231: Scan 7260 [.
V 1	.0	(K)EREFPGQVLR(Y)	100%	48.7	51.6	73	2		410.88	1,229.60	3	-0.047	-38	1220		2481	114	123	0		1261: Scan 7404 [.
V 1	.0	(R)EFPGOVLR(Y)	99%	39.2	52.5	8.4	2		473.24	944.47	2	-0.035	-37	2260		2005	116	123	0		2635: Scan 13802
V 1	.0	(R)EFPGOVLR(Y)	99%	33.3	52.5	13.0	2		473.24	944.46	2	-0.043	-46	2300		2595	116	123	0		2702: Sum of 2 sc.
1	.0	(R)EFPGQVLR(Y)	98%	36.4	52.5	13.4	2		473.22	944.42	2	-0.085	-90	1340		3173	116	123	0		1419: Sum of 2 sc.
1	.0	(R)EFPGQVLR(Y)	95%	29.5	52.5	2.0	2		473.22	944.43	2	-0.074	-78	1310		16540	116	123	0		1390: Scan 7974 [.
V 1	.0	(R)EFPGQVLR(Y)	95%	38.0	52.5	13.7	2		473.29	944.57	2	0.062	66	1270		1841	116	123	0		1328: Scan 7703 [.
		(R)EFPGOVLR(Y)	94%	28.8	52.5	2.1	2		473.23	944.44	2	-0.064	-68	2220		1704	116	123	0		2567: Scan 13551
1	.0	(R)EFPGQVLR(Y)	93%	28.6	52.5	2.0	2		473.24	944.47	2	-0.043	-45	2350		2149	116	123	0		2773: Scan 14347
V 1	.0	(R)EFPGQVLR(Y)	92%	28.4	52.5	1.9	2		473.23	944.45	2	-0.054	-58	2200		1739	116	123	0		2545: Scan 13478
V 1	.0	(R)EFPGOVLR(Y)	90%	27.8	52.5	2.2	2		473.24	944.47	2	-0.034	-35	2190		1640	116	123	0		2516: Scan 13372
V 1	.0	(R)EFPGQVLR(Y)	88%	27.2	52.5	2.0	2		473.24	944.46	2	-0.051	-54	2260		2092	116	123	0		2645: Scan 13837
		(R)EFPGOVLR(Y)	84%	26.5	52.5	2.1	2		473.23	944.45	2	-0.059	-62	2270		2106	116	123	0		2658: Scan 13887
V 1	.0	(R)EFPGQVLR(Y)	84%	26.5	52.5	2.1	2		473.23	944.45	2	-0.053	-56	2370		2086	116	123	0		2809: Scan 14493
		(R)YEDNFDANSNVSVIIOPTSK(K)	100%	125.5	49.9	31.7	2		1,120.95	2,239.89	2	-0.17	-76	1400		629.9	124	143	0		1497: Scan 8495 [.
1		(R)YEDNFDANSNVSVIIOPTSK(K)		85.1	49.9	10.5	2		747.64	2,239.91	3	-0.15	-68	1420		4084	124	143	0		1539: Scan 8667 [.
		(R)YEDNFDANSNVSVIIOPTSK(K)		51.9	49.9	11.4	2		747.64	2,239.90	3	-0.16	-71	1400		2343	124	143	0		1510: Scan 8539 [
V 1	.0	(R)YEDNFDANSNVSVIIOPTSK(K)	100%	44.1	50.0	20.0	2		747.63	2,239.86	3	-0.20	-88	1410		1298	124	143	0		1520: Scan 8582 [.
		(R)YEDNFDANSNVSVIIOPTSK(K)		37.2	50.0	12.5	2		747.63	2,239.87	3	-0.19	-85	1440		1235	124	143	0		1560: Scan 8748 [.
1		(K)KTITEYGSPEEFLSQVDFLLGK(84.0	49.9	44.1	2		834.37	2,500.09	3	-0.18	-73	1830		26160	144	165	0		2196: Sum of 10 s.
1		(K)KTITEYGSPEEFLSQVDFLLGK(59.1	49.9	33.6	2		834.37	2,500.09	3	-0.19	-75	1820		3418	144	165	0		2185: Sum of 2 sc.
1		(K)TITEYGSPEEFLSQVDFLLGK(Q		136.2	49.6	72.2	2		1,187.01	2,372.01	2	-0.17	-73	1840		9181	145	165	0		2215: Sum of 6 sc.
1		(K)TITEYGSPEEFLSOVDFLLGK(O		136.1	49.6	69.4	2		1,187.01	2,372.01	2	-0.17	-72	1850		7727	145	165	0		2219: Sum of 4 sc.
balled		(K)TITEYGSPEEFLSQVDFLLGK(Q		99.5	49.6	44.7	2		791.68	2,372.01	3	-0.17	-71	1840		161400	145	165	0		2210: Sum of 25 s.
baland		(K)TITEYGSPEEFLSQVDFLLGK(Q		93.3	49.6	38.2	2		791.68	2,372.01	3	-0.17	-70	1870		3910	145	165	0		2234: Sum of 2 sc.
		(K)TITEYGSPEEFLSQVDFLLGK(O		92.8	49.6	35.5	2		791.67	2,372.00	3	-0.18	-74	1860		7849	145	165	0		2226: Scan 11349
Same		(K)TITEYGSPEEFLSOVDFLLGK(O		52.4	49.6	23.9	2		1,187.01	2,372.00	2	-0.18	-74	1840		955.8	145	165	0		2213: Scan 11181
balant .		(K)TITEYGSPEEFLSQVDFLLGK(Q		48.5	49.6	14.8	2		1,187.00	2,371.99	2	-0.19	-81	1870		562.5	145	165	0		2236: Scan 11386
		(R)TADGDEGGKHOLITATVSDGK		80.5	50.0	0.0	2		700.63	2,098.87	3	-0.14	-69	1060		8635	210	230	0		1077: Scan 6455 [
-		(R)TADGDEGGKHOLITATVSDGK		46.7	50.0	0.0	2		700.63	2,098.86	3	-0.15	-71	1040		1282	210	230	0		1053: Scan 6335 [
Radual		(R)TADGDEGGKHOLITATVSDGK		35.8	50.0	0.0	2		700.62	2,098.84	3	-0.17	-80	2370		845.4	210	230	0		2813: Scan 14507
		(R)TADGDEGGKHOLITATVSDGK		33.3	50.0	0.0	2		700.62	2,098.84	3	-0.17	-81	1040		749.8	210	230	0		1049: Scan 6315 [
barred .		(K)HOLITATVSDGK(L)	100%	80.0	51.4	0.0	2		635.30	1.268.59	2	-0.082	-64	1080		2593	219	230	0		1106: Scan 6586 [
Line .		(K)HOLITATVSDGK(L)	100%	67.5	51.4	0.0	2		635.29	1,268.57	2	-0.10	-80	1090		1156	219	230	0		1117: Scan 6654 [
		(K)HQLITATVSDGK(L)	100%	63.0	51.4	0.0	2		635.30	1,268,58	2	-0.094	-74	2320		1188	219	230	0		2729: Scan 14172
1 m		(K)HQLITATVSDGK(L)	100%	61.9	51.4	0.0	2		635.30	1,268.60	2	-0.077	-61	2360		1247	219	230	0		2792: Scan 14431
		(K)HOLITATVSDGK(L)	100%	60.2	51.4	0.0	2		635.30	1,268.59	2	-0.078	-62	2350		1241	219	230	0		2781: Scan 14383
hand .		(K)HQLITATVSDGK(L)	100%	56.3	51.4	0.0	2		635.30	1,268.59	2	-0.081	-64	2240		1118	219	230	0		2612: Scan 13709
		(K)HOLITATVSDGK(L)	100%	56.2	51.4	0.0	2		635.30	1,268.59	2	-0.083	-65	2340		1113	219	230	ů.		2753: Scan 14278
		(K)HQLITATVSDGK(L)	100%	51.4	51.4	0.0	2		635.30	1,268.58	2	-0.093	-73	2200		932.3	219	230	0		2544: Scan 13475
time .		(K)HQLITATVSDGK(L)	100%	50.8	51.4	0.0	2		635.30	1,268.59	2	-0.085	-67	2390		1155	219	230	0		2834: Scan 14602
		(K)HQLITATVSDGK(L)	100%	46.7	51.4	0.0	2		635.30	1,268.59	2	-0.085	-67	2340		1213	219	230	0		2767: Scan 14328
		(K)HQLITATVSDGK(L)	100%	44.7	51.4	0.0	2		635.30	1,268.59	2	-0.088	-69	2370		1185	219	230	0		2808: Scan 14490
Second .		(K)HQLITATVSDGK(L)	100%	52.6	51.4	0.0	2		423.88	1,268.61	3	-0.059	-46	1080		2887	219	230	0		1103: Scan 6572 [.
builted		(K)HQLITATVSDGK(L)	100%	40.8	51.4	0.0	2		635.30	1,268.58	2	-0.091	-72	2310		1098	219	230	0		2716: Scan 14113
Line .		(K)HQLITATVSDGK(L)	100%	47.8	51.4	0.0	2		423.88	1,268.62	3	-0.051	-45	1050		5494	219	230	0		1072: Scan 6424 [
		(K)HQLITATVSDGK(L) (K)HQLITATVSDGK(L)	99%	47.0	51.4	0.0	2		423.00	1,268.65	3	-0.007	-45	1050		9256	219	230	0		1072: Scan 6424 [. 1083: Scan 6483 [.
			99%	45.0	51.4	0.0	2		635.31	1,268.60	2	-0.027	-21	2270		9230	219	230	0		2653: Scan 13864
		(K)HQLITATVSDGK(L)	99%	32.4	51.4	0.0	2		635.30	1,268.58	2	-0.074	-76	2270		1069	219	230	0		2000: Scan 13665
		(K)HQLITATVSDGK(L)	99%	34.3	51.4	0.0	2		635.30	1,268.58	2	-0.094	-/4	1120		586.1	219	230	0		2000: Scan 13005 1148: Scan 6841 [.
		(K)HQLITATVSDGK(L)		34.3	51.4	0.0	-		423.88		3	-0.10	-81	1120		2451	219	230	0		
v	.0	(K)HQLITATVSDGK(L)	90%	30.0	51.4	0.0	2		423.88	1,268.61	5	-0.062	-49	1050		2451	219	230	U		1060: Scan 6372 [

gi|242047384 (100%), 27,563.8 Da

hypothetical protein SORBIDRAFT_02g002690 [Sorghum bicolor]

7 exclusive unique peptides, 10 exclusive unique spectra, 51 total spectra, 73/261 amino acids (28% coverage)

MASTSCFLHQSTARLGASPRVAAAPRSAQLFVCKAQQKQQQDAAAVDQSDVSRRAALALFAGVAAVGAKVSPAAAAYGEAANVFGKPKTNTEYIAYNGDGFKLLIPSKWNPSKEREFPGQVLRYEDNFDANSNVSVIIQPTSKKTITEYGSPEEFLSQVDFLLGKQAFGGSTDSEGGFETGAVATANVLESSTPVVDGKQYYSVSVLTRTADGDEGGKHQLITATVSDGKLYICKAQAGDKRWFKGARKGVEKAAASFSVA

Spot # 61

gi|3914607 (100%), 19,036.4 Da

RecName: Full=Ribulose bisphosphate carboxylase small chain, chloroplastic; Short=RuBisCO small subunit; Flags: Precu 3 exclusive unique peptides, 5 exclusive unique spectra, 15 total spectra, 30/168 amino acids (18% coverage)

MALTVMASSA	TAAAPFQGLK	STASLPVARR	STTSLAKVSN	GGRIRCMQVW
PAYGNKKFET	LSYLPPLTQE	QLLK QVDYLL	RNNWVPCLEF	S K E G F V Y R E N
STSPCYYDGR	YWTMWKLPMF	GCTDASQVYK	ELQEAIASYP	ELRAILGFDN
IRQTQWLTFI	AYKPAGSE			



Yalid		Sequence	Pcob	Masco	Masco .	Masco	NII	Modifications	Observed	Actual Mass	Charge	Delta Ila	Delta	Retent	Intensity	ПС	Start	Stop	#Othe	Other Protei	Spectrum ID
1	10	(K)EREFFGQYLR (V)	100%	51.0	51.6	6 .8	2		410.68	1,229.60	3	-0.049	-39	1200		2659	114	123	D		1137: Scan 7298 [
2	10	(R)EFFGQVLR(Y)	99%	34.3	52.5	7.3	2		473.22	944.43	2	-0.077	-82	1250		4135	116	123	D		1206: Scan 7689 [
V	10	(R)YEDNFDANSNYSVIIQPISK(K)	100%	62.5	50.0	9.3	2		747.62	2,239.85	3	-0.21	-95	1410		1909	124	143	D		1382: Scan 8573 [
V	10	(K)KTHEYGSPEEFLSQVDFLLGK	100%	62.2	49.9	32.0	2		834.37	2,500.07	3	-0.20	-80	1840		2992	144	165	D		2076: Sum of 2 æ
V	1.0	(K)KTHEYGSPEEFLSQVDFLLGK	100%	47.5	49.9	23.0	2		834.37	2,500.09	3	-0.18	-73	1830		2585	144	165	D		2058: Sum of 2 x
V	10	(K)THTEYGSPEEFLSQVDFLLGK(C	100%	132.3	49.6	64.9	2		1,187.12	2,372.23	2	0.050	21	1850		2964	145	165	D		2091 : Sum of 3 x
V	10	(K)THEYGSPEEFLSQVDFLLGK(C	100%	111.5	49.6	51.9	2		1,187.01	2,372.00	2	-0.18	-76	1840		1349	145	165	D		2077: Sum of 2 x
V	10	(K)THEYGSPEEFLSQVDFLLGK(C	100%	111.1	49.6	57.7	2		1,187.01	2,372.00	2	-0.18	-76	1850		4634	145	165	D		2094: Sum of 4 x
V	10	(K)THEYGSPEEFLSQVDFLLGK(C	100%	109.1	49.6	43.0	2		791.68	2,372.00	3	-0.18	-74	1850		77560	145	165	D		2098: Sum of 21 s
7	1.0	(K)THEYGSPEEFLSQVDFLLGK(C	100%	BQ.4	49.6	35.9	2		791.69	2,372.01	3	-0.17	-73	1840		3886	145	165	D		2073: Sum of 2 x
V	10	(K)THEYGSPEEFLSQVDFLLGK(C	100%	59.7	49.6	8.9	2		791.68	2,372.00	3	-0.18	•74	1840		2825	145	165	D		2083: Scan 11227
2	10	(K)THEYGSPEEFLSQVDFLLGK(C	100%	40.3	49.6	19.5	2		791.57	2,372.00	3	-0.18	-76	1870		1100	145	165	D		2107: Scan 11392
V	10	(R)TADGDEGGKHQLITATVSDGB	100%	90.2	50.0	0.0	2		700.63	2,098.86	3	-0.15	-73	1070		4332	210	230	D		1011 : Scan 6504 [
1	10	(R)TADGDEGGKHQLITATVSDGB	100%	75.3	50.0	0.0	2		700.62	2,098.84	3	-0.17	-B3	1050		2957	210	230	D		993: Scan 6419 🗊
V	10	(R)TADGDEGGKHQLITATVSDGB	100%	55.7	50.0	0.0	2		700.63	2,098.86	3	-0.15	-73	1090		565.3	210	230	D		1024: Scan 6578 [
V	10	(R)TADGDEGGKHQLITATVSDGB	97%	38 O	50.0	0.0	2		700.62	2,098.83	3	-0.18	•86	1040		889.8	210	230	D		976: Scan 6335 [D
V	10	(K)HQLJIATVSDGK(L)	100%	53.6	51.4	0.0	2		635.29	1,268.57	2	-0.099	-78	1040		1465	219	230	D		981 : Storn of 2 sca
V	10	(K)HQLITATVSDGK(L)	100%	43.5	51.4	0.0	2		423.88	1,268.60	3	-0.069	-55	1070		3156	219	230	0		1018: Sum of 2 æ
2	1.0	(K)HQLJIA TVSDGK(L)	98%	38.6	51,4	0.0	2		423.88	1,268.60	3	-0.069	-53	1040		1261	219	230	D		977:Scan 6347 [D
V	10	(K)HQLITATVSDGK(L)	97%	30.9	51.4	0.0	2		635.30	1,268.59	2	-0.084	-66	2330		710.7	219	230	D		2630: Scan 14294
V	10	(K)HQLITATVSDGK(L)	97%	30.2	51.4	0.0	2		635.30	1,268.58	2	-0.092	-72	2350		602.7	219	230	D		2665: Scen 14455
V	10	(K)HQLITATVSDGK(L)	96%	36.2	51.4	0.0	2		423.88	1,268.63	3	-0.044	-35	1050		3074	219	230	D		996: Scan 6432 [D

gi|242047384 (100%), 27,563.8 Da hypothetical protein SORBIDRAFT_02g002690 [Sorghum bicolor] 7 exclusive unique peptides, 9 exclusive unique spectra, 22 total spectra, 73/261 amino acids (28% coverage)

MASTSCFLHQ	STARLGASPR VAAAPRSAQL	FVCKAQQKQQ QDAAAVDQSD	VSRRAALALF
AGVAAVGAKV	SPAAAAYGEA ANVFGKPKTM	TEYIAYNGDG FKLLIPSKWN	PSKEREFPGQ
VLRYEDNFDA	NSNVSVIIQP TSKKTITEYG	SPEEFLSQVD FLLGKQAFGG	STDSEGGFET
GAVATANVLE	SSTPVVDGKQ YYSVSVLTRI	ADGDEGGKHQ LITATVSDGK	LYICKAQAGD
KRWFKGARKG	VEKAAASFSV A		

Spot # 52

Valid	H 3	Sequence	Frob	Masco.	Mano.				Observed	Actual Mass	Charge	Delts Da			Interstity	TC	Start	Stop		Other Protei	
		(R) FCDY TNEK(T)	99%	48.2	52.1	16.7	2	Carbamidomethyi	539.69	1,075.34	2	-0.094	-78	005		9379	105	112	0		826: Scan 5433 [D
1	.0	(R)FCDYTNEK(I)	97%	37.8	52.1	3.9	2	Carbamidomethyl	538,67	1,075.33	2	-0.094	-87	914		1458	105	112	0		857: Scan 5609 [D
		(R)FCDYTNEK(I)	95%	32.2	52.1	2.3	2	Carbamidomethyl	538.09	1,075.36	3	-0.064	-59	2350		1373	105	112	0		2760 Scan 14416
		(R)FCDYTNEK(I)	94%	31.6	52.1	0.0	2	Cerbamidomethod	538.69	1,075 37	2	-0.059	-55	2310		1405	105	112	0		2594 Sens 14135
		(R)FCDYTNEK(I)	92%	34.8	52.1	0,7	2	Carbamidomethyi .,	539.57	1,075.32	2	-0.11	-100			2284	105	112	0		941: Scan 5539 (D
		(R)PCDYTNEK(I)	87%	29.1	52.1	7.0	2	Carbamido methyl	538.68	1,075.35	2	-0.076	-71	2340		1372	105	112	0		2740 Scan 14340
		(K)SLAAALMEEAK(F)	100%	101.4	52.2	60.6	2	- Ageneration and Sec.	546.24	1,090 47	2	-0.10	-95	1430		11360	119	129	0		1479 Sean 8707 [
		(K)SLAAAL MSEAK (F)	100%	97.5	52.0	60.1	2	Oxidation (+16)	554.23	1,105 45	2	-0.12	-110	1260		7120	119	129	0		1260 Sean 7674 [
		(K)SLAAALMSEAK (F)	100%	97 A	52.0	61.0	2	Osidation (+16)	554.24	1,106.47	2	-0.092	-03	1230		4650	119	129	0		1222: Som 7519 [
		(K)SLAAALMSEAK(F)	100%	96 S	52.3	579	2		546.25	1,090 49	3	-0.078	-71	1410		2239	119	129	0		1458 Scan 8620 [
		(K)SLAAALMSEAK(F)	100%	75.5	52.2	37.6	2		546.25	1,090 49	2	-0.075	-69	2350		1192	119	129	0		2765 Sean 14442
		(K)SLAAALMSEAK(F)	100%	73 1	52.2	41.2	2		546.25	1,090.49	2	-0.077	-70	2370		1107	119	129	0		2790 Sean 14551
		(K)SLAAALMSEAK(F)	100%	74.4	52.2	38.0	2		546.25	1,090.48	2	-0.091	-83	2340		1227	119	129	0		2742 Scan 14346
		(K)SLAAALMSEAK(F)	100%	71.3	52.3	37.9	2		546.25	1,090.48	2	-0.086	-78	1470		1824	119	129	0		1534 Scan 8945 [
		(K)SLAAALMEEAK(F)	100%	70.4	52.2 52.2		2		546.25	1,090.49	2	-0.081	-74	2220				129	0		2562 Sean 13626
		(K)SLAAALMSEAK(F)	100%	66.9		36.4	2	2012/06/10/07 10:00	546.25	1,090.49	2	-0.080		1490		1290	119	129	0		1563 Sem 9044 [
		(K)SLAAALMSEAK(F)	100%	63.3	52.0	325	2	Oxidation (+16)	554.24	1,106.46	2	-0.10	-93 -78	1270		995.4	119	129	0		1284. Scan 7768 [
1		(K)SLAAALMSEAK(F)	100%	61.3	52.2	28.5	2		546.25	1,090.48		-0.085		2390		1111	119	129	0		2810 Scan 14635
		(K)SLAAALMSEAK(F)	100%	57.8	52.2	23.4	2	A 11 2 1 1 1 A	546.25	1,090.48	2	-0.086	-79	2270		1202	119	129	0		2030 Sean 13903
		(k)FDGADMSEVVMSK(A)	100%	107.1	51.6		2	Oxidation (+16)	716.27	1,430.52		-0.067	-61	1100			130	142	0		1074 Sean 6714 [
		(K)FDGADMSEVVMSK(A)	100%		51.5	73.6	2	100 - 100 -		1,414.50	2	-0.11				1455	130	142	0		1345 Scan 8115 [
12		(K)FDGADMSEVVMSK(A)	100%	88.6	51.5	68.5		A 12 / 100	708.27	1,414.52	8	-0.069	-63	2360		B14.4	130	L42	0		2800 Scan 14595
		(K)FDGADM(SEYVMSK(A)	100%	79.7	51.7	62.4	2	Oxidation (+16),	724.24	1,446.47	×	-0.13	-87	978		2254	130	142	0		934: Scan 5990 [D
		(R)FDGADMSEVVMSE(A)	100%	71.7	51.6	12.9	2	Ostidation (+16)	716.27	1,430.53	2	-0.074	-52	2390		573.7	130	142	0		2009: Sonn 14632
		(K)FDGADMSEVVMSK(A)	100%	69.6	51,6	39.3	2	Oxidation (+16)	716.27	1,430.53	2	-0.060	-56	1230		969.5	1.90	142	0		1220 Scan 7507 [
	0	(K)FDOADMSEVVMSK(A)	100%	69.5 64.2	51.5	52.8	2		708.27	1,414.53	3	-0.077	-54	2340		764.5	130	142	0		2750 Scan 14372
	0	(E)FDGADMSEVVMSE(A)	100%		51.5	46.9	2	0.13.1. 6.10	208.27	1,414.53	2	-0.082		2290		712.0	130	142	0		2569 Sem 14018
		(K)FDGADMSEVVMSE(A)	100%	63.9	51.6	14.6	2	Oxidation (+16)	716.27	1,430.52	2	-0.097	-61	2320		673.9	130	142			2715: Som 14224
		(K)FDGADMSEYVMSE(A)	100%	69.4	51.7	40.9	- 2	Oxidation (+16),	724.24	1,446.46	2	-0.14		951		967.4	1,30	142	0		910: Scan 5890 [D
		(K)FDGADMSEVVMSE(A)	100%	68.5	51.8	41.4	<u>X</u>	Oxidation (+15),	724.23	1,446.45	3	-0.16	-110	969		1292	130	L42	0		921: Scan 5941 [D
		(K)FDGADMSEVVMSK(A)	100%	62.5	51.5	39.9	· 2		208.27	1,414.52	×	-0.094	-67	2310		736.5	130	142			2706 Scan 14197
		(K)FDGADMSEVVMSK(A)	100%	57.2	51.5	35.0	2		709.27	1,414.52	2	-0.095	-67	2260		859.1	130	142	0		2533: Soan 13074
		(K)FDGADMSEVVMSK(A)	100%	53.7	51.5	39.0	2		708.27	1,414.53	- 2	-0.076	-54	1400		664.1	130	142	0		1444 Scan 8554 [
		(K)FDJADMSEVVMSK(A)	100%		51,5	31.6	2	(10) 10 10 10 10 10 10 10 10 10 10 10 10 10	473.51	1,414.49	3	-0.12	-82	1300		1980	130		0		1384 Scan 8307 [
		(K)FDOADMSEVVMSR(A)		53 8 46 9	51.6	30.5	2	Omidation (+15)	477.B4	1,430.51	-	-0.095	-64	1250		1313 521.4	130	142	0		1265 Sean 7701 [
		(R)FDGADMSEVVMSK(A)	100%	40.9	51.6 51.5	30.6 31.3	2	Oxidation (+15)	716.26	1,430.51	2		-04			792.7		142	0		1296 Sean 7836 [
		(K)FDGADMSEVVMSK(A)	96%	410	52.5	10.3	2	Oxidation (+16)	708.25	1,430 37		-0.11	-170	1390		659.4	130	142	0		1421: Som 0455 [2773 Som 14475
		(K)FDGADMSEVVMSK(A)	93%	41.0	52.5	2.6	2	Oxidation (+15)	716.19	1,430.57	3	-0.04	-170	2350		659.4	1.81	142	0		2757 Sem 14405
		(K)FDJADMSEVVMSK(A)	80%	30.5	51.5	13.7		O STOR MORE (+10)	472.51	1,414.51	2	-0.10	-72	1350		1712	130	142	0		1369 Sens 8243 [
		(K)FDGADMEEVVMSK(A)	92%	37.3	51.3	4.7	2		457.17	912.32	2	-0.15	-160	1150		3999	143	151	0		1130: Som 7010 [
		(K)AVAVGASFR(G)	91%	29.4	51.3	7.1	- 2		457.22	912.42	2	-0.049	-54	2260		1855	143	151	0		2523 Scan 13841
		(K)AVAVGASFK (G)	100%	101.3	51.5	0.0	2		004.77	1,207.52	2	-0.049	-55	1250		39100	143	102	0		1251 Sum of 2 sc
		(K)GIDFINAVIDR (V)	100%	101.3	51.6	0.0	- 8		604.76	1,207 51	0	-0.077	-64	1270		5209	152	162			1275 Scan 7733 [
		(K)GIDFINAVIDR(V) (K)GIDFINAVIDR(V)	100%	93.0	51.6	0.0	2		604.76	1,207 50	2	-0.080	-66	2310		1796	152	162	0		2702: Sena 14169
		(K)GIDFINAVIDR(Y)	100%	91.0	51.6	0.0			604.75	1,207.50	2	-0.058	-73	2250		1500	152	162	0		2675 Scan 14055
		(K)GIDFINAVIDR(V)	100%	90.0	51.0	8.0	7		004.75	1,207.51	2	-0.072	-60	2350		1207	1.52	162	0		2821 Scan 14085
		(KIGIDFINAVIDE(V)	100%	86.3	51.6	0.0			604.76	1,207 51		-0.072	-64	2240		1620	152	162	0		2500 Sean 13763
		(K)GIDFINAVIDR(7)	100%	85.1	51.6	0.0	2		604.76	1,207 50	2	-0.091	-67	2200		1394	152	162	0		2525: Som 13495
		(K)GIDFINAVIDR(Y)	100%	817	51.6	0.0	2		604.76	1,207 51	2	-0.077	-64	2370		1994	1.52	162	ň		2762 Scan 14515
		(KIGIDFINAVIDE(7)	100%	85 1	51.6	0.0	2		604.75	1,307.49	2	-0.071	-75	2340		1780	1.52	162	ň		2741 Scan 14343
		(K)GIDFINAVIDR(V)	100%	85.0	51.6	0.0	2		604.75	1,207.49	2	-0.096	-80	2330		1290	152	162	0		2724 Scan 14268
		(K)GIDFINAVIDR(?)	100%	79.2	51.6	0.0	2		604.76	1,207 51	2	-0.070	-58	2290		1703	152	162	0		2658 : Soon 13961
		KIG IDFINAVIDR (7)	100%	76.7	51.6	0.0	2		604.76	1,207 50	2	-0.083	-69	2170		1119	1.52	162	0		2485 Scan 13344
		(K)CIDFINAVIDE(7)	100%	72.6	51.6	0.0	2		604.76	1,207.50	2	-0.087	-72	2220		1413	152	162	ñ		2553 Scan 13596
		(KIGIDFINAVIDROV)	100%	53.1	51.6	0.0	- 2		604.76	1,207.50	2	-0.090	-65	1320		1299	152	162	Ő		1333 Sean 8061 [
		(KIG IDFINAVIDR(7)	100%	45.9	51.6	0.0	2		604.76	1,207 51	2	-0.070	-59	1340		1279	152	162	0		1359 : Som 8185 [
		(K)GIDFINAVIDR(Y)	100%	53.5	51.6	0.0	2		403.52	1,207 52		-0.059	-49	1250		2093	152	162	ŏ		1245 Scan 7613 [
		(K)OIDFINAVIDE (7)	99%	417	51.6	0.0	3		403.52	1,207 55	3	-0.031	-25	1240		1,591	152	162	Ū.		1231 Scan 7961 [
		INIADL TOAIFK IN)	100%	65.3	52.7	12.3	2		468.23	03444	2	-0.070	-75	1300		30340	169	176	Ď		1430 Sum of 2 se
		(K)ADLTGAIFK(N)	100%	35.5	52.7	0.2	2		935.44	934 44	1	-0.077	-83	1390		1728	169	176	0		1432 Sean 8505 [
		(K)ADLTGAIFK (N)	100%	52.5	52.7	7.4	3		468.24	934 46	2	-0.054	-56	1420		5460	169	176	0		1471 Swn of 2 ac
		(K) ADL TOAIFK (N)	100%	50.0	52.7	8.0	3		468.24	934.47	2	-0.045	- 4 B	2200		1680	168	176	D		2535 Scan 13526
		(K)ADLTGAIFK (N)	100%	48.4	52.7	3.1	2		408.23	934.45	2	-0.050	-65	2320		1021	168	176	0		2720 Sean 14245
		(E)ADLTGAIFE (N)	100%	47.2	52.7	0.0	2		468.24	934 47	2	-0.043	-45	2390		1944	169	176	0		2306 Sem 14616
		(K)ADLTGAIFK (N)	100%	46.3	52.7	0.0	2		468.24	934.47	2	-0.039	-42	2190		1,550	163	176	0		2510 Scan 13431
		(K)ADLTGAIFK (N)	100%	44.3	52.7	0.0	2		468.34	934.47	2	-0.045	-48	2210		1847	163	176	ň		2549 Scan 13578
		(K)ADLTOAIFK(N)	100%	28.9	52.7	-2.8	2		935.44	934.44	1	-0.077	-82	1380		P28.7	168	176	ő		1412 Scan 8422 [
		(K)ADLTGAIFK (N)	100%	43.0	52.7	0.0	2		458.24	934 46	2	-0.055	-59	1370		2261	169	176	0		1400 Scan 8376 [
		(K)ADLTGAIFK (N)	99%	39.7	52.7	2.4	2		468.24	934.46	2	-0.052	-55	1450		1426	160	176	0		1559 Scan 9030 [
		(K)ADLTOAIFK (N)	99%	39.2	52.7	0.0	2		468.24	934 46	2	-0.052	-56	2340		1782	163	176	0		27.38 Scan 14334
	ñ	(K)ADLTGAIFK (N)	98%	35.6	52.7	11	2		458.25	934 49	2	-0.027	-70	2270		1672	168	176			2548 Scan 13930
121		unnear to an capa							- Contraction								and the second sec				and the second second second second

 Image: Note of the control o

MASSSCLASP	SGATLCRPRR	PRCRVACSAA	DAGGSTGPAW	AKGAGRLACG	VLAAWSVASA
SNPVIAASQR	LPPLSTEPNR	CERAFVGNTI	GQANGVYDKP	L D L R F C D Y T N	EKTNLKGK <mark>SL</mark>
AAALMSEAKF	DGADMSEVVM	SKAYAVGASF	KGTDFTNAVI	DRVNFEKADL	TGAIFKNTVL
SGSTFDDAKM	DDVVFEDTII	GYIDLQKLCT	NTSISPDARL	ELGCR	



Valid .	., Sequence	Prob	Masso.	. Marco	Masco	NII	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
1	0 (K)SLAAALMSEAK(F)	100%	63.9	52.2	31.3	2		546.25	1,090.48	2	-0.088	-81	1460		1175	119	129	0		1416: Scan 8846 [
1.	0 (K)SLAAALMSEAK(F)	100%	59,4	52.2	32.6	2		546.25	1,090.48	2	-0.087	-80	1450		1164	119	129	Û		1406: Scan 8796 [
7 1.	0 (K)SLAAALMSEAK(F)	100%	58.3	52.2	16.9	2		546.25	1,090.49	2	-0.079	-72	1430		1098	119	129	0		1388: Scan 8682 [
7 1.	0 (K)SLAAALMSEAK(F)	100%	57.2	52.2	265	2		546.25	1,090.49	2	-0.083	-76	1440		1193	119	129	0		1398: Scan 8744 [
V 1.	0 (K)FDGADMSEVVMSK(A)	100%	8B.7	51.5	68.4	2		708.26	1,414.50	2	-0.11	-80	1360		651.7	130	142	0		1306: Scan 8252 [
7 1.	0 (K)FDGADMSEYYMSK(A)	100%	68.8	51.5	52.7	2		708.26	1,414.50	2	-0.11	-81	1370		722.5	130	142	0		1314: Scan 8297 [
🔽 i.	0 (K)ADLIGAIFK(N)	100%	45.3	52.7	2.1	2		468.23	934.45	2	-0.061	-65	1400		1601	168	176	0		1348: Scan 8494 [

gi|212721648 (100%), 23,654.3 Da

uncharacterized protein LOC100194054 [Zea mays]

3 exclusive unique peptides, 3 exclusive unique spectra, 7 total spectra, 33/225 amino acids (15% coverage)

MASSSCLASP	SGATLCRPRR	PRCRVACSAA	DAGGSTGPAW	AKGAGRLACG	VLAAWSVASA
SNPVIAASQR	LPPLSTEPNR	CERAFVGNTI	GQANGVYDKP	LDLRFCDYTN	EKTNLKGK <mark>SL</mark>
AAALMSEAKF	DGADMSEVVM	SK AYAVGASF	KGTDFTNAVI	DRVNFEK <mark>ADL</mark>	TGAIFK NTVL
SGSTFDDAKM	DDVVFEDTII	GYIDLQKLCT	NTSISPDARL	ELGCR	

Spot # 93

Valid .	. Sequence	Prob	Maxo	Masco	Mesco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	#Othe	Other Protei	Spectrum ID
V 1) (K)ALEQUDAAYAK(G)	100%	77.1	51.5	16.5	2		564.76	1,127.50	2	-0.12	-100	1250		4959	72	82	0		1212: Scan 7572 [.
V 11) (K)ALEQIDAAYAK(G)	99%	32.5	51.5	10.2	2		564.74	1,127,48	2	-0.14	-130	2390		473.0	72	82	0		2719: Scan 14576
V 1) (K)GDASAYYQLQGAIK(F)	100%	98.4	51.3	49.8	2		678.82	1,355.62	2	-0.12	-89	1370		1418	83	96	0		1349: Span 8315 [.
V 1)) (K)LSVETLANQDFLVTK(G)	100%	63.2	50.9	0.0	2		808.35	1,614.69	2	-0.15	-94	1260		823.8	169	183	0		1228: Scan 7656 [.
V 11) (K)LSVETIANQDPLVTK(G)	100%	51.8	50.9	0.0	2		539.22	1,614.65	3	-0.20	-120	1270		1354	169	183	0		1239: Stan 7717 [.
V 1) (K)LSVETIANQDPLVTK(G)	87%	29.0	50.9	0.0	2		539.23	1,614.68	3	-0.17	-100	1250		992.1	169	183	0		1218: Scan 7608 [
V 1) (K)NYRPDYLNNIWK(V)	100%	43.4	51.1	8.4	2		511.23	1,530.67	3	-0.13	-83	1480		1889	206	217	0		1496: Scan 8949 [,
1) (K)YAGEVYENYLA(-)	100%	36.8	51.5	15.2	2		614.23	1,226.45	2	-0.13	-110	1420		992.7	223	233	0		1414: Scan 8594 [
V 1) (K)YAGEVYENYLA(·)	97%	30.1	51.5	14.2	2		614.22	1,226.42	2	-0.16	-130	1400		693.9	223	233	0		1391: Span 8479 [.

gi|1174391 (100%), 25,239.0 Da

RecName: Full=Superoxide dismutase [Mn] 3.4, mitochondrial; Flags: Precursor

5 exclusive unique peptides, 6 exclusive unique spectra, 9 total spectra, 63/233 amino acids (27% coverage)

MALRTLASKN	ALSFALGGAA	RPSAASARGV	TTVALPDLSY	DFGALEPAIS	GEIMRLHHQK
HHATYVGNYN	KALEQLDAAV	AKGDASAVVQ	LQGAIKFNGG	GHVNHSIFWK	NLKPISEGGG
EPPHGKLGWA	IDEDFGSFEA	LVKRMNAEGA	ALQGSGWVWL	A L D K E P K K L S	VETTANQDPL
VTKGASLVPL	LGIDVWEHAY	Y L Q Y K <mark>N V R P D</mark>	YLNNIWK VMN	WK YAGEVYEN	VLA



| 10 (K)ODPIVLVVEQDE(I)
 | 100% | 50.4
 | 51.6 | Masso. NT
DO 2 | T Motifications | Observed
682.27
 | Actual Mass
1,362.53 | Charge Deha D
3 -014 | -100 3 | 260 | tic
1535
 | Start
99 | Stop
[]] | 0
 | . Other Prote | 2460 Scar |
|---
--|---
--	--	--
---	--	--
--	---	---
--		
 (X)3DF1YLY7EQDE(I) (X)3DF1YLY7EQDE(I) 		
 | 100% | 50.2
67.8
 | 51.6
51.6 | 00 2 | I. | 683.27
683.26
 | 1,362.53
1,362.51 | 3 -0.13
2 -0.15 | | 250
400 | 1540
1980
 | 99
99 | 110 |
 | | 2440 Scar
2653 Scar |
| 10 (K)GDPIVLYYEQDK(I)
10 (K)GDPIVLYYEQDK(I)
 | 100% | 86.9
86.5
 | 51.6
51.8 | 00 2 | | 682.27
682.20
 | 1,362.52 | 2 -0.15 | | 280
220 | 1984
1451
 | 99
99 | 110 |
 | | 1192 Scar
2402 Scar |
| 1.0 (K)GDPIVLVVEQDE(I)
 | 100% | 76.6
76.5
 | 51.6
51.6 | 00 2 | | 682 28
682 28
 | L,362.55 | 2 -012 | -68 3 | 220.
330 | 1305
1522
 | 99
99 | 110 | 0
 | | 2391 Scar
2562 Scar |
| 10 (K)GDPIVL VYEQDK (I)
10 (K)GDPIVL VYEQDK (I)
 | 100% | 75.4
 | 51.6 | 00 2 | | 682.27
 | 1,362.53 | 2 -0.14 | -100 | 290 | 1579
 | 99 | 110 |
 | | 2496 Scar |
| 1.0 (K)GDPIVLVVEQDK(I)
1.0 (K)GDPIVLVVEQDK(I)
 | 100% | 74.9
73.2
 | 51.6
51.6 | 00 2 | | 682.27
682.27
 | 1,362.52
1,362.52 | 2 -0.15 | | 270
360 | 1547
1859
 | 99
99 | 110 |
 | | 2468: Scar
2600: Scar |
| 1.0 (K)GDPTVLYYEQDK(T)
1.0 (K)GDPTVLYYEQDK(T)
 | 100% | 71.1
 | 51.6
51.6 | 0.0 2 | | 682.27
 | 1,362.52
1,362.53 | 2 -0.14 | | 290
340 | 1596
 | 99
99 | 110 |
 | | 2510 Star
1250 Star |
| 1.0 (K)GDPIVLVVEQDK(I)
 | 100% | 66.3
 | 51.6 | 0.0 2 | i i i i i i i i i i i i i i i i i i i | 682.27
 | 1,362.53 | 2 -0.14 | -100 | 340 | 1862
 | 99 | 110 | 0
 | | 2580. Star |
| 1.0 (K)GDPTVLYVEQDK(T)
1.0 (K)GDPTVLYVEQDK(T)
 | 100% | 66.1
61.9
 | 51.6
51.6 | 00 2 | | 682.27
682.29
 | 1,362.53
1,362.55 | 2 -0.14 | | 250
240 | 1537
1424
 | 99
99 | 110 |
 | | 2445: Scar
2425: Scar |
| 1.0 (K)GDPTVL VYEQDK (T)
 | 100% | 61.0
46.6
 | 51.6
51.6 | 00 2 | | 682.27
682.27
 | 1,362.53
1,362.53 | 2 -0.14 | | 200
370 | 1375
 | 99
99 | 110 |
 | | 2365: Ster
2614: Ster |
| 1.0 (K)GDPTVLVVEQDK(T)
 | 100% | 45.2
 | 51.6 | 0.0 2 | i | 682.27
 | 1,362.52 | 2 -0.15 | -110 1 | 530 | 960.8
 | 99 | 110 | 1 0
 | | 1507: Sum |
| 10 (KARDBIATAARODK(L)
10 (KARDBIATAARODK(L)
 | 100% | 40.1 33.6
 | 51.6
51.6 | 00 2 | | 682.30
 | 1,362.59 | 2 -0.087 2 -0.16 | | 920
390 | 865.8
 | 99 | 110 |
 | | 2121 Ster
1297 Ster |
| 1.0 (K)GDPTVLVVEQDK(T)
 | 98% | 32.4
28.8
 | 51.6
51.6 | DO 2 | | 682.27
682.27
 | 1,362.53 | 2 -0.14 | | 470
390 | 592.2
1134
 | 99
99 | 110 |
 | | 1422 Scen
2644 Scen |
| 7 INFICECHIGSOVIDIOGE(V)
 | 100% | 51.5
 | 52.1 | 0.0 2 | Carbamidomethyl | 905.32
 | L,888.63 | 2 -0.14 | -77 | 61 | 692.0
 | 137 | 1.51 | 2
 | giB2651843 | 3 853 Scan |
| 0.7 (K)FICPCHGSQVIINQGK(Y)
0.7 (K)FICPCHGSQVIINQGK(Y)
 | 98% | 32.3
32.4
 | 52.0
52.0 | 00 2 | Carbemidomethyl
Carbemidomethyl | 905.33
603.90
 | 1,809.65 | 2 -0.12
3 -0.10 | | 956
956 | 421.4
6535
 | 137 | 151 | 2
 | giB2651843
giB2651843 | |
| 17 (K)FICPCHGSQVIINQ3E(Y)
 | 89% | 33.6
120.9
 | 52.0
50.9 | DO 2 | Carbonidomethyl | 985.40
987.89
 | 1,908.78 | 2 0.0064 | | 778
500 | 1298
2045
 | 137 | 1.51 | 2
 | giB2651843
giB2651843 | |
| 3.7 (R)SPAPLSCALVHADVDDGK(V)
3.7 (R)SPAPLSCALVHADVDDGK(V)
 | 100% | 118.8
 | 51.0 | 36.7 2 | Ŭ. | 887.84
 | 1,773.67 | 2 -0.26 | -150 1 | 510 | 2789
 | 155 | 170 | 2
 | giB9651843 | 3. 1486 Scen |
| 0.7 (R)3PAPLSLALVHADVDDOK(V)
0.7 (R)3PAPLSLALVHADVDDOK(V)
 | 100% | 71.0
67.0
 | 50.9
50.9 | 19.7 2
12.7 2 | | 592-26
592-26
 | 1,773.75 | 3 -0.18 | | 500
540 | 17160
25790
 | 155
155 | 175 |
 | ai89651843
ai89651843 | |
| 0.7 (R)3PAPLELALVHADVDDOK(V)
 | 100% | 57.8
56.0
 | 50.0
50.0 | 12.2 2
16.0 2 | | 502.26
502.27
 | 1,773.77 | 3 -0.16
3 -0.15 | | 580
250 | 60120
2067
 | 155
155 | 170 |
 | aB2651843
aB2651843 | |
| (R)3PAPLSLALVHADVDDOK(V) (R)3PAPLSLALVHADVDDGE(V)
 | 100% | 54.3
 | .90.9 | 21.9 2 | | 592.27
 | L,773.79
L,773.75 | 3 -0.14 | -79 | 210 | 1795
 | 155 | 175 | 1 2
 | giB2651843 | 3. 2387 Scan |
| 0.7 (R)GPAPLSLALVHADVDDGE(V)
0.7 (R)GPAPLSLALVHADVDDGE(V)
 | 100% | 56.9
51.3
 | 50.9
50.9 | 16.9 2
12.4 2 | | 592.26
592.27
 | L,773.75
L,773.77 | 3 -0.17 | | 550
280 | 3414
1738
 | 155 | 17: |
 | giB2651843
giB2651843 | |
| 0.7 (R)GPAPLSLALVHADVDDGK(V)
 | 100% | 48.5
 | 50.9 | 12.4 2 | 1 | 592.27
 | 1,773.78 | 3 -0.15 | -85 3 | 260 | 1961
 | 155 | 172 | 2
 | giB2651843 | 3 2461 : Star |
| 0.7 (R)GPAFLSLALVHADVDDGK(V)
0.7 (R)GPAFLSLALVHADVDDGK(V)
 | 100% | 48.2
45.0
 | 50.9
50.9 | 3.8 2
6.7 2 | | 592.26
592.27
 | L,773.77
L,773.79 | 3 -0.15
3 -0.14 | -77 3 | 390
200 | 1834
1557
 | 155
155 | 172 | 2
 | giB2651643 | |
| 0.7 (R)GPAPLSLALVHADVDDGK(V)
 | 100% | 44.9
44.6
 | 50.9
50.9 | 10.1 2
10.0 2 | | 592.27
592.27
 | L,773.79
L,773.79 | 3 -0.L3
3 -0.L4 | | 220
320 | 1736
1901
 | 155
155 | 172 | 1 2
 | gil/2651843 | |
| 0.7 (R)GPAPLELALVHADVDDGK(V)
 | 100% | 43.7
 | 50.9 | 16.7 2 | | 592.26
 | 1,773.77 | 3 -0.16 | -91 3 | 350 | 1809
 | 155 | 172 | 1 2
 | gil/2651043 | 3 2593: Scan |
| 0.7 (R)SPAPLELALVHADVDDOK(V)
0.7 (R)SPAPLELALVHADVDDOK(V)
 | 100% | 40.9
 | 50.9
50.9 | 98 2
00 2 | B. | 592.27
592.27
 | 1,773.79 | 3 -0.15 | | 230
210 | 1769
1630
 | 155
155 | 173 |
 | giB2651943
giB2651943 | |
| 7 (R) SPAPESLALVHADVDDGK(V)
 | 100% | 40.4
 | 50.9
50.9 | 10.3 2
9.1 2 | 1 | 592.27
592.27
 | 1,773,79
1,773,79 | 3 -0.15 | -62 1 | 560
300 | 2239
1749
 | 155 | 175 | 2
 | giB265184.
giB265184. | 3. 1547: Star |
| 17 (RX3PAPLSLALVHADVDDOE(V)
(RX3PAPLSLALVHADVDDOE(V)
 | 100% | 29.9
 | .50.9 | 86 2 | | 592.27
 | 1,773.79 | 3 -0.15 | -82 3 | 270 | 1994
 | 155 | 175 | 2
 | giB2651843 | 3. 2469 Scen |
| 7 (R)3PAPLSLALVHADVDDOK(V)
17 (R)3PAPLSLALVHADVDDOK(V)
 | 100% | 39.9
39.7
 | 50.9
50.9 | 50 2
B3 2 | 1 | 592.27
592.27
 | 1,773.80 | 3 -0.13
3 -0.15 | | 220
310 | 1671
1906
 | 155
155 | 175 |
 | giB2651843
giB2651843 | |
| 7 (R)3PAPLSLALVHADVDD0K(V)
 | 100% | 43.0
 | 50.9
50.9 | 16 2 | | 592.25
592.27
 | 1,773.76 | 3 -0.17 | -96 3 | 260
190 | 1950
 | 155 | 175 | 2
 | aB2651843 | 3 2452 Scar |
| 17 (R)3PAPLSLALVHADVDDOK(V)
17 (R)3PAPLSLALVHADVDDOK(V)
 | 100% | 30.6
 | 50.9 | 10.3 2 | | 592.26
 | 1,77370
1,77377 | 3 -0.16 | -90 5 | 240 | 1938
 | 155 | 172 | 1 2
 | giB2651843 | 3. 2434 Scar |
| 17 (R)3PAFLSLALVHADVDDOK(V)
17 (R)3PAFLSLALVHADVDDOK(V)
 | 100% | 39.1
30.2
 | 50.9
50.9 | 5.1 2
79 2 | 1 <u></u> | 592.27
592.27
 | L,773.78
L,773.79 | 3 -0.15
3 -0.13 | | 180 | 2813
 | 155 | 172 |
 | 282651843
262651843 | |
| 7 (R) 3PAPLSLALVHADVDDOK(V)
 | 99% | 38.9
 | 50.9 | 10.4 2 | | 593.20
 | 1,773.75 | 3 -0.18 | | 390 | 1701
 | 155 | 172 | 1 2
 | HB2651843 | 3. 2040 Scen |
| (R)3FAFLSLALVHADVDDOK(V) (R)3FAFLSLALVHADVDDOK(V)
 | 99% | 35.3
33.9
 | 50.9
50.9 | 95 2
02 2 | K
E | 593 27
593 27
 | L,773.78
L,773.78 | 3 -015 | | 360
570 | 1831
1597
 | 155
155 | 172 | 3
 | giB2651843
giB2651843 | |
| 7 (R)SPAPLSLALVHADVDDOE(V)
 | 96% | 34.0
33.6
 | 50.9
50.9 | 59 2
90 2 | 1 | 592.26
592.26
 | L 773 76
L 773 74 | 3 -0.17
3 -0.18 | | 980
370 | 1248
1772
 | 155
155 | 172 | 3
 | giB2651843
giB2651843 | |
| 17 (R)GPAPLSLALVHADVDDGE(V)
17 (R)GPAPLSLALVHADVDDGE(V)
 | 95% | 33.1
 | .50.9 | 10.5 2 | | 592.25
 | 1,773.76 | 3 -0.17 | -95 ; | 380 | 1777
 | 155 | 173 | 0 10
 | giB2651843 | 3. 2615 Scar |
| (R)GPAPLSLALVHADVDDGE(V) (K)VLFVPWVE7DFR(T)
 | 88% | 28.6
52.7
 | 50.9
51.3 | 4.3 2
DO 2 | l.
R | 592.27
754.33
 | 1,773.77
1,506.64 | 3 -0.15 | | 180 | 1423
181.30
 | 155 | 17. |
 | giB2651843 | 3 2325 Star
1968 Star |
| (K)YLFYPWVETDPR(T)
 | 100% | 74.9
 | 51.3 | 0.0 2 | | 754.33
 | 1,506.65 | 2 -0.14 | | 6.30 | 6262
 | 173 | 184 |
 | | 1976. Sum |
|
 | |
 | | | | |
 | 1,000,00 | | | |
 | | |
 | | |
|
 | 100% | 55.0
64.1
 | 51.3
51.3 | 00 2 | | 754,33
 | 1,505.64 | 2 -0.15 | -99 1 | 790
810 | 3390
4879
 | 173 | 184 | 0
 | | 1915; Scan |
| 1.0 (K)YLFYFWVETDFR(T)
1.0 (K)YLFYFWVETDFR(T)
 | 100% | 64.1
63.3
 | 51.3
51.3 | 00 2 | | 754,33
503,21
503,22
 | L,506.64
L,506.62
L,506.63 | 2 -0.15
3 -0.17
3 -0.15 | -99 1
-110 1
-100 1 | 790
610
620 | 3398
4879
9576
 | 173
173
173 | 184
184
194 |
 | | 1915 Star
1957 Star
1963 Sum |
| 0 (K)YLPYPWVETDPR(T)
0 (K)YLPYPWVETDPR(T)
0 (K)YLPYPWVETDPR(T)
1 (K)YLPYPWVETDPR(T)
 | 100%
100%
100% | 64.1
63.3
50.6
36.0
 | 51.3
51.3
51.3
51.3 | 00 2
00 2
00 2
00 2 | | 754,33
503,21
503,22
503,22
503,22
754,34
 | 1,506.64
1,506.63
1,506.63
1,506.65
1,506.66 | 2 -0.15
3 -0.17
3 -0.15
3 -0.14
2 -0.13 | -99 1
-110 1
-100 1
-90 1
-96 1 | 790
6L0
620
600
630 | 3390
4879
9576
6146
1366
 | 173
173
173
173
173
173 | 184
184
194
194 |
 | | 1915 Star
1957 Star
1963 Sum
1943 Sum
1990 Star |
| (X)YLFYPWVETDFR(T) (X)YLFYPWVETDFR(T) (X)YLFYPWVETDFR(T) (X)YLFYPWVETDFR(T) (X)YLFYPWVETDFR(T) (X)YLFYPWVETDFR(T) (X)YLFYPWVETDFR(T)
 | 100%
100% | 64.1
63.3
59.6
 | 51.3
51.3
51.3 | 00 2 | | 754,33
503,21
503,22
503,22
 | 1,506.64
1,506.62
1,506.63
1,506.65 | 2 -0.15
3 -0.17
3 -0.15
3 -0.14 | -99 1
-110 1
-100 1
-90 1
-96 1
-110 1 | 790
610
620
600 | 3398
4879
9576
6146
 | 173
173
173
173 | 184
184
194 |
 | | 1915: Scar
1957: Scar
1963: Sum
1943: Sum |
| (x) YL PY P WVETDPR(T) (x) YGEDP WWK(c)
 | 100%
100%
100%
99%
97%
98% | 64.1
63.3
50.6
36.0
38.9
35.3
32.2
 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3 | 00 2
00 2
00 2
00 2
00 2
00 2
00 2
-2.4 2 | | 754,33
503,21
503,22
503,22
754,34
503,22
503,22
503,22
509,69
 | 1,505.64
1,505.62
1,505.63
1,505.65
1,505.65
1,505.63
1,505.63
1,505.63 | 2 -0.15
3 -0.17
3 -0.15
3 -0.14
2 -0.13
3 -0.14
3 -0.13
3 -0.15
2 -0.096 | -599 1
-110 1
-100 1
-90 1
-96 1
-110 1
-100 1
-85 1 | 790
610
620
620
620
920
620
920
920
920 | 3398
4879
9576
6146
1366
2049
2667
768.9
 | 173
173
173
173
173
173
173
173
173
185 | 184
184
194
194
194
194
194
194 |
 | | 1915. Stau
1957. Stau
1963. Sum
1943. Sum
1943. Stau
1950. Stau
1924. Stau
1936. Stau
1316. Stau |
| (X)YLPY1WVETDPR(T) (X)YLPY1WVETDPR(T) (X)YLPY1WVETDPR(T) (X)YLPY1WVETDPR(T) (X)YLPY1WVETDPR(T) (X)YLPY1WVETDPR(T) (X)YLPY1WVETDPR(T) (X)TGEDPWWKA() (X)TGEDPWWKA() (X)TGEDPWWKA() (X)TGEDPWWKA()
 | 100%
100%
100%
100%
99%
97% | 64.1
63.3
50.6
36.0
38.9
25.3
32.2
31.6
66.5
 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
52.3
52.3
52.3
51.9 | D0 2 38 2 32.1 2 | | 754.33
503.21
503.22
754.34
503.22
503.22
503.22
509.69
509.69
509.69
 | L,506.64
L,506.63
L,506.65
L,506.66
L,506.66
L,506.63
L,506.63
L,506.63
L,506.63
L,506.63
L,507.37 | 2 -0.15
3 -0.17
3 -0.17
3 -0.14
2 -0.13
3 -0.16
3 -0.16
3 -0.16
2 -0.086
2 -0.086
2 -0.11
2 -0.12 | -99 1
-110 1
-100 1
-90 1
-100 1
-100 1
-100 1
-100 1
-110 1 | 790
610
620
600
600
600
900
900
900
900
900
900
90 | 3390
4879
9576
6146
1366
2049
2667
768.9
875.1
3363
 | 173
173
173
173
173
173
173
173
185
185
185 | 184
184
194
194
194
194
195
195
195 |
 | | 1915 Stan
1957 Stan
1963 Sum
1963 Sum
1990 Stan
1996 Stan
1996 Stan
1316 Stan
2560 Stan
1307 Stan |
| 10 (KYLLPY FWY CTOPR(1)
10 (KYLLPY FWY CTOPR(
 | 100%
100%
100%
99%
97%
98%
97%
100%
100%
3.4 Da | 64.1
53.3
50.6
360,6
380,9
383,9
35.3
322,2
31.6
56,5
55,7 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
 | 00 2
00 2
00 2
00 2
00 2
00 2
-2.4 2
381 2
32.1 2
36.9 2 | tra, 73 total spe | 754.33
503.21
503.22
503.22
754.34
503.22
503.22
503.22
509.69
509.69
509.68
545.19
545.20 | L,506.64
L,506.63
L,506.65
L,506.65
L,506.63
L,506.63
L,506.63
L,506.63
L,506.63
L,507.37
L,017.37
L,019.97
L,019.97
 | 2 -0.15
3 -0.15
3 -0.15
3 -0.14
2 -0.14
3 -0.16
3 -0.16
3 -0.16
2 -0.066
2 -0.16
2 -0.12
2 -0.12
2 -0.12 | -59
-110 1
-100 1
-50 1
-50 1
-100 1
-100 1
-100 1
-110 5
-110 1 | 790
600
600
600
600
600
900
900
900
900
9 | 3396
4879
9576
6146
1366
2049
2667
768.9
875.1 | 173
173
173
173
173
173
173
173
173
185
185
 | 184
184
194
194
194
194
194
194
194 | | | 1915. Stan
1957. Stan
1963. Sum
1963. Sum
1943. Sum
1990. Stan
1924. Stan
1936. Stan
1316. Stan
2560. Stan
 |
| 10 (KVILPP WEIDBER)
10 (KVILP
 | 100%
100%
100%
99%
99%
97%
100%
3.4 Da
3.4 Da
3.4 Da
V C
D K
N G
W K
6 Da | 64.1
98.6
98.6
98.6
98.6
98.6
98.6
98.2
98.2
98.2
98.2
98.2
98.2
98.2
98.2 |
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | 00 2
00 2
00 2
00 2
00 2
00 2
-2.4 2
381 2
32.1 2
36.9 2 | DRVPE
AWLN1 |
774.33
593.32
593.32
593.32
593.32
593.32
593.32
593.32
593.32
593.32
593.32
593.32
593.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
594.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
595.59
59 | L30664
L50663
L50663
L50665
L50665
L50665
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50664
L50663
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50663
L50664
L50663
L50664
L50663
L50664
L50663
L50664
L50663
L50664
L50663
L50664
L50663
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L5 | 2 -0.15
3 -0.15
3 -0.15
3 -0.14
2 -0.14
3 -0.16
3 -0.16
3 -0.16
2 -0.066
2 -0.16
2 -0.12
2 -0.12
2 -0.12 | | 790
60
60
600
600
900
900
900
900
 | 3390
4879
9576
6146
1366
2049
2667
768.9
875.1
3363 | 173
173
173
173
173
173
173
185
185
185
185
185
185 | 184
184
184
184
184
184
184
195
195
195 | со с
 | LAT | 1915 Stan
1957 Stan
1963 Sum
1963 Sum
1990 Stan
1996 Stan
1996 Stan
1316 Stan
2560 Stan
1307 Stan | | | | | | | | | | | | | | | |
| 0 CVLPP PW 2009601 10 CVLPP PW 2009601 11 A G G G T Y A K 11 A G G G T Y A K 11 A G C C V V PW | 1005
1005
1005
1005
997
997
1005
3.4 Da
s, 5 ехс
D K
N G
W K
6 Da
protein
ss, 2 ех | 64.1
53.3
90.6
38.9
38.9
35.3
34.6
65.7
Clusive
Q A A
L G N
A E N
A E N
A GF14
Clusive | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | 000 2
000 2
0
000 2
0
0
0
0 | DRVPE
AWLN]
<mark>CHGS(</mark>
tra, 10 total spe | 77433
50331
50332
50322
75434
50322
75434
50322
50322
50322
50322
504540
54540
54540
54540
0 M E K
F H G P
Q Y N N | L30634
L30643
L50643
L50643
L50643
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L50644
L506444
L506444
L506444
L506444
L506444
L506444
L506444
L506444
L506444 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
2 - 0.066
2 - 0.11
2 - 0.12
2 - 0.12
0 - 0.12
2 - 0.12
0 - 0.15
2 - 0 | | 790
60
620
620
620
620
620
620
790
620
790
790
790
790
790
790
790
790
790
79 | 3380
4579
9576
5146
1366
2049
2561
7563
9
7683
9
7683
9
7683
9
7683
9
7683
9
2049
2049
2049
2049
2049
2049
2049
20 | 179
178
178
179
179
179
179
179
179
179
179
179
179 | 1001
1001
1001
1001
1001
1001
1001
100 | а
а
а
а
а
а
а
а
а
а
а
а
а
а | L A T
<mark>K V L</mark> | 1915 Злат
1937 Злат
1937 Злат
1938 |
| 0 CONTRACTOR OF CONSIGNATION OF CONSIC | 1000k
1000k
1000k
997k
977k
977k
1000k
977k
1000k
977k
1000k
977k
1000k
977k
1000k
000k
000k
N G
W K
6 Da
protein
protein
N ∨ V | 64.1
53.3
90.6
38.9
38.0
38.9
38.0
38.9
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0
38.0 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | D0 2
D0 2
D0 2
D0 2
D0 2
D0 2
D0 2
244 2
36.9 2
32.1 2
36.9 2
H S A
T V E
I C P | DRVPE
AWLNI
<mark>Chgs</mark> | 7764.33
503.33
503.32
503.32
503.32
754.34
503.32
503.32
503.32
503.32
503.54
503.54
503.54
503.54
504
504
504
504
504
504
504
504
504
5 | L305663
L50663
L50663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L506663
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L50665
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L505
L50 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
2 - 0.086
2 - 0.11
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
X - 0.12
2 - 0.12
2 - 0.12
X - 0.15
X - 0 | | 790
60
60
60
60
60
60
60
60
60
6 | 3380
4879
9576
5146
1366
2049
2261
9751
3363
2261
3363
2261
2261
2261 | 6 M
6 K
7 | 10-10-10-10-10-10-10-10-10-10-10-10-10-1 | E S S S S S S S S S S S S S S S S S S S | LAT
KVL | 1915 Зек
1947 Зек
1943 Sum
1943 Sum
1943 Sum
1944 Sec
1945 Sum
1946 Sec
1946 Sec
19 |
| 0 CONTRACTOR 10 CONTRACTOR 11 CONTRACTOR 12 CONTRACTOR 13 CONTRACTOR 14 CONTRACTOR 15 CONTRACTOR 16 CONTRACTOR 17 CONTRACTOR 18 CONTRACTOR 19 CONTRACTOR 10 CONTRACTOR 11 CONTRACTOR 11 CONTRACTOR 11 CONTRACTOR 11 CONTRACTOR 12 CONTRACTOR 13 CONTRACTOR 14 CONTRACTOR 14 CONTRACTOR 15 CONTRACTOR 15 CONTRACTOR 16 CONTRACTOR 17 CONTRACTOR 18 | 1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005 | 64.1
63.3
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
52.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | 000 2
000 2
00 | DRVPC
AWLNT
<mark>CHGSC</mark>
tra, 10 total spe
AERYE | 77433
50331
50332
50332
75434
50322
75434
50322
50352
504532
504532
504532
504532
504532
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
504542
5045555555555 | L30564
L50564
L50663
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L50666
L5066
L5066
L5066
L5066
L5066
L5066
L5066
L5066
L5066
L5066
L5066
L5066
L506
L50 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
2 - 0.12
2 - 0.12
2 - 0.12
12 - 0.12
13 - 0.12
13 - 0.12
14 - 0.12
15 - 0.12 | | 790
60
60
60
600
600
90
90
90
90
90
90
90
90
90 | 3380
4879
9576
5146
1366
2049
2267
1367
2267
1363
2261
2261
2261
2261 | G M
E R
L K | 100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00
100-00 | в в в
в в в в | LAT
KVL
VAY
HLV | 1915 Злат
1937 Злат
1933 Злат
1933 Злат
1934 Злат
1934 Злат
1934 Злат
1934 Злат
1934 Злат
1936 Злат
1937 |
| 0 CONTRACTOR 10 CONTRACTOR 11 CONTRACTOR 12 CONTRACTOR 13 CONTRACTOR 14 CONTRACTOR 15 CONTRACTOR 16 CONTRACTOR 17 CONTRACTOR 18 CONTRACTOR 19 CONTRACTOR 10 CONTRACTOR 11 CONTRACTOR 11 CONTRACTOR 11 CONTRACTOR 11 CONTRACTOR 12 CONTRACTOR 13 CONTRACTOR 14 CONTRACTOR 14 CONTRACTOR 15 CONTRACTOR 15 CONTRACTOR 16 CONTRACTOR 17 CONTRACTOR 18 | 1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005 | 64.1
63.3
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3 | 000 2
000 2
0
00 2
0
00 2
0
00 2
0
0
0 2
0
0
0 2
0
0
0 2
0
0
0 2
0
0
0 2
0
0
0
0 | DRVPD
AWLNT
<mark>CHGS(</mark>
tra, 10 total spe
AERYE
NEDRV | 77433
50333
50333
50323
75434
50323
75434
50323
50323
50066
50066
50066
50066
50066
50066
50066
50066
50066
0 M E K
□ H G P
2 Y N N
2 Y N N | L30564
L50563
L50563
L50563
L50563
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.16
2 - 0.16
2 - 0.16
2 - 0.16
2 - 0.12
2 - 0.12
0 - 0.12
- | | 790
60
60
60
600
600
900
900
900 | 3380
4879
9576
6146
1366
2249
2261
7768
9
7768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
7
7
8
4
9
7
6
8
4
9
7
7
8
4
9
7
7
8
4
9
7
7
8
9
7
7
8
4
9
7
7
8
14
7
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
1
9
7
8
9
7
8
1
9
7
8
1
9
7
8
9
7
8
1
9
7
8
1
9
7
8
9
1
9
1
9
1
9
1
9
1
9
1
1
8
1
9
1
1
1
8
1
1
1
1 | E R
L K
A E | L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0 | P Y
K T
D G | LAT
KVL
VAY
HLV
HPI | E915 3.ea
1937 3.ea
1933 3.ea
1933 3.ea
1934 3.ea
1937 3.ea |
| 0 CONTRACTOR CODECO 0 F 0 F 0 F 0 F 0 F 0 F 0< | 10005
10005
10005
10005
9975
9975
10005
9975
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
9775
10005
10005
9775
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
9775
10005
10005
9775
10005
10005
9775
10005
10005
9775
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
1000000
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
100000000 | 64.1
63.3
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6
90.6 | 51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | 000 2
000 2
00 | DRVPC
AWLNT
CHGSC
tra, 10 total spe
AERYE
NEDRY
FKTGA | 77433
50333
50333
50323
75434
50323
75434
50323
50323
50066
50066
50066
50066
50066
50066
50066
50066
0 M E K
□ H G P
2 Y N N
2 Y N N | L30564
L50563
L50563
L50563
L50563
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.16
2 - 0.006
2 - 0.10
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
0 0 acids (34
K V V R C
K V V R C
V V R C
V V R C
V R C I
A E N T M | | 790
60
60
60
600
600
900
900
900 | 3380
4879
9576
6146
1366
2249
2261
7768
9
7768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
768
9
7
7
8
4
9
7
6
8
4
9
7
7
8
4
9
7
7
8
4
9
7
7
8
9
7
7
8
4
9
7
7
8
14
7
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
14
9
7
8
1
9
7
8
9
7
8
1
9
7
8
1
9
7
8
9
7
8
1
9
7
8
1
9
7
8
9
1
9
1
9
1
9
1
9
1
9
1
1
8
1
9
1
1
1
8
1
1
1
1 | E R
L K
A E | L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0 | P Y
K T
D G | LAT
KVL
VAY
HLV
HPI | 1915 3.ex 1937 3.ex <td< td=""></td<> |
| 10 CONTRACTORNO 11 CONTRACTORNO 12 CONTRACTORNO 13 CONTRACTORNO 14 CONTRACTORNO 15 CONTRACTORNO 16 CONTRACTORNO 17 CONTRACTORNO 18 CONTRACTORNO 19 CONTRACTORNO 11 CONTRACTORNO 11 CONTRACTORNO 11 CONTRACTORNO 11 CONTRACTORNO 11 CO | 10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10005
10 | 64.1
63.3
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790.6
790. | 313
313
313
313
313
313
313
313 | 000 2
000 2
0
000 2
0
000 2
0
000 2
0
0
0
0 | DRVPE
AWLNT
CHGSC
Tra, 10 total spe
AERYE
NEDRV
FKTGA
AKQAF
Q | 77433
50331
50332
50323
75434
50323
75434
50323
50323
503669
54539
54539
54530
0 M E K
Γ H G P
2 Y N N
2 Y N N
2 Y N N | L30564
L50563
L50563
L50563
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L50564
L5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
2 - 0.066
2 - 0.11
2 - 0.12
2 - 0.15
2 - 0 | | 790
60
60
600
600
600
900
900
900 | 3380
4379
9576
6146
1366
2049
2561
7563
9754
2049
2561
2049
2563
2049
2563
2049
2563
2049
2563
2049
2563
2049
2049
2049
2049
2049
2049
2049
2049 | E R
L K
A E | L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0
L00-0 | в в
в в
в в
в в
в в
в в
в в
в в | LAT
KVL
VAY
HLV
HPI
NLT | 1915 3.ex 1937 3.ex <td< td=""></td<> |
| 10 CVLPP PW 21098(0) 11 A G G G T Y A K 11 A G G G T Y A K 11 A G G G T Y A K 11 A G G G T Y A K 11 A G G G T Y A K 11 A G G G T Y A K 11 A S C L S R E E 11 A S A E L S R E E< | 1005
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006 | 64.1
50.6
53.3
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6
50.6 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | 000 2
000 2
0
000 2
0
000 2
0
0
0 2
0
0
0 2
0
0
0
0 | DRVPE
AWLNT
CHGSC
Tra, 10 total spec
AERYE
NEDRV
FKTGA
AKQAF
Q
Moliticators | 776133
50333
50333
50333
50333
751333
50333
50333
50333
50333
50333
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504535
504533
504535
504535
504535
504535
504535
504535
504535
504535
504535
504535
504535
504555
504555
504555
5045555
5045555
50455555
504555555
50455555555 | L30564
L50563
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L50663
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L5065
L505
L50 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.15
2 - 0.000
2 - 0.12
2 - 0.12
10 acids (34
L M N L L
R T L A C
K V V R C
K V V R C
M E K V A
Y R G K I
A E N T M
E L D T L
Charge Delba Da | -99 -10 -100 1 -100 1 -100 1 -00 | 790 790 60 600 6200 600 6300 990 6300 990 6300 990 6300 990 6300 990 6300 990 6300 990 6300 990 6300 990 770 990 6300 970 770 970 640 97 770 710 770 711 | 3380
4379
9576
6146
1366
2049
2561
7563
9754
9754
9754
9363
2261
2261
2261
2261
2261
2261
2261
2 | 1777
1777
1777
1777
1777
1777
1777
177 | 100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10
100-10 | в в в в в в в в в в в в в в в в в в в | LAT
KVL
VAY
HLV
HPI
NLT | L915 3.ca
L937 3.ca
L937 3.ca
L938 3.ca
L936 5.ca
L936 5.ca
L936 5.ca
L936 5.ca
L937 3.ca
L937 3.ca |
| 10 COLLEPT PRETORE(0) 11 COLLEPT PRETORE(0) 12 COLLEPT PRETORE(0) 13 COLLEPT PRETORE(0) 10 COLLEPT PRETORE(0) 11 COLLEPT PRETORE(0) 12 COLLEPT PRETORE(0) 13 COLLEPT PRETORE(0) 10 COLLEPT PRETORE(0) 11 COLLEPT PRETORE(0) 12 COLLEPT PRETORE(0) 13 COLLEPT PRETORE(0) 13 COLLEPT PRETORE(0) 13 COLLEPT PRETORE(0) 13 COLLEPT PRETORE(0) 14 G C C V V P W 14 G C C V V P W 14 F S C D P W 14 S C D P W 14 S E D P A E E I R 15 S E
 | 1005
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006 | 64.1
63.3
50.6
33.9
34.9
35.3
32.2
66.5
6.5
Clusive
Q A A
L G N
A E N
A E N
A E N
A E N
A Clusive
Y M /
E Q Y
P K H
//accord
 | 51.3
51.3
51.3
51.3
51.3
51.3
51.6
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.4
51.4
51.4
51.4
51.4
51.4
51.4
51.4
51.4
51.4
51.4
51.9
51.4
51.4
51.9
51.4
51.9
51.4
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9 | 000 2
000 2
0
00 2
0
00 2
0
0
0 2
0
0
0 2
0
0
0
0 | DRVPE
AWLNT
CHGSC
tra, 10 total spe
AERYE
NEDRV
FKTGA
AKQAF
Q
Molifications | 77433
50331
50332
50323
50323
77434
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
80322
8032
803
 | L30564
L30564
L50663
L50663
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L50664
L5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.16
2 - 0.13
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
no acids (34
L M N L L
R T L A C
K V V R C
K V V R C
M E K V A
Y R G K I
A E N T M
E L D T L
Charge Deba Da
2 - 0.15 | | 780 780 610 620 620 780 630 780 640 780 630 780 640 780 650 780 660 780 670 780 680 780 680 780 690 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 780 | 3380
4479
9576
5146
1366
2249
2261
2249
2261
2241
2241
2261
2201
2201
2201
2201
2201
2201
220 | E R
L K
M Q
Skert
37
 | 100-0 100-0 </td <td>E S P T H D C F</td> <td>LAT
KVL
VAY
HLV
HPI
NLT</td> <td>1915 Ster 1937 Ster 1937 Ster 1937 Ster 1933 Star 1933 Star 1933 Star 1933 Star 1934 Star 1937 Star 1937 Star 1937 Star 1937 Star 1937 Star 1937 Star</td> | E S P T H D C F | LAT
KVL
VAY
HLV
HPI
NLT | 1915 Ster 1937 Ster 1937 Ster 1937 Ster 1933 Star 1933 Star 1933 Star 1933 Star 1934 Star 1937 Star 1937 Star 1937 Star 1937 Star 1937 Star 1937 Star
 |
| 10 CONTRACTOR NOTICE CONT | 10054
1006
1006
1006
1006
1006
1006
1006
100 | 64.1 63.3 50.6 53.3 760.7 36.0 38.9 36.0 38.9 36.1 38.9 35.3 32.2 6.5 Clusive 65.7 Clusive 6.5 Clusive 6.5 Clusive 7 A A Clusive 7 Y M Y M Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y | 513
513
513
513
513
513
513
513
519
519
519
519
519
519
519
519
519
519 | 000 2 | DRVPE
AWLNT
CHGSC
tra, 10 total spe
AERYE
NEDRV
FKTGA
AKQAF
Q | 77433
50331
50332
50332
75434
50323
75434
50323
50323
50323
50323
50323
504530
0 M E K
F H G P
Q Y N N
E E M V
/ T L I
A E R K
F D E A
Dbarned
703.76 | L,506.64
L,506.63
L,506.63
L,506.63
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,506.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74
L,505.74L,505.74
L,505.74
L,505.74L,5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
3 - 0.16
3 - 0.16
2 - 0.16
2 - 0.16
2 - 0.15
2 - 0.15
2 - 0.15
2 - 0.15
2 - 0.15
2 - 0.15
2 - 0.15
3 - 0.15
3 - 0.15
- | -99 1 -110 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 -100 1 | 790 790 610 620 6200 620 630 790 930 930 930 | 3380
4479
9576
5146
1366
2049
2667
1751
3063
2261
2261
2261
1063
1063
1064
1064
1064
1064
1064
1064
1064
1064 | 1793
1793
1793
1793
1793
1793
1793
1793 | 100 100 100 | в в в
в в в в | LAT
KVL
VAY
HLV
HPI
NLT | 1915 Ster 1937 Ster 1937 Ster 1933 Star 1933 Star 1933 Star 1934 Star 1935 Star 1935 Star 1943 Star 1944 Star 1945 Star |
| 10 CONTRACTORNO 11 CONTRACTORNO 12 CONTRACTORNO 13 CONTRACTORNO 14 CONTRACTORNO 15 CONTRACTORNO 16 CONTRACTORNO 17 CONTRACTORNO 18 CONTRACTORNO 19 CONTRACTORNO 10 CONTRACTORNO 11 CONTRACTORNO 12 CONTRACTORNO 13 CONTRACTORNO 14 CONTRACTORNO 15 CONTRACTORNO 16 CONTRACTORNO 17 CONTRACTORNO 11 A G G G T Y A K 14 H L G C V V P W 15 CONTRACTORNO 13 CONTRACTORNO 14
 | 1005
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006 | 64.1 64.3 50.6 53.3 50.6 53.3 36.0 36.3 36.2 65.3 36.2 66.5 66.5 66.5 66.7 66.5 66.7 66.7 66.7 66.7 66.7 66.7 66.7 70.0 79.0 79.0
 | 51.3
51.3
51.3
51.3
51.3
51.3
51.3
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.9
51.4
51.4
51.4
51.4 | 000 2 | DRVPC
AWLNT
CHGSC
Tra, 10 total spec
AERYE
NERYE
FKTGA
AKQAF
Q
Molifications | 77433
50331
50332
50323
75434
50323
75434
50323
50323
50323
50066
50066
50066
50066
50066
54519
54519
54530
0 M E K
F H G P
Q Y N N
C T L I
A E R K
F D E A
005ervel
703.76
703.76
703.76
 | L:306.64
L:506.63
L:506.63
L:506.63
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:506.74
L:5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.16
3 - 0.16
2 - 0.16
2 - 0.16
2 - 0.16
Charge Deba Da
2 - 0.15
2 - 0.13
2 - 0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.13
0.15
0.15
0.13
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15
0.15 | | 790 790 610 620 6200 620 6200 620 6200 790 6200 790 6200 790 6200 790 6200 790 6200 790 6200 790 6200 790 6200 790 6200 70 6200 70 6200 71 6200 71 6200 71 6200 71 6200 71 6200 71 6200 71 6200 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 | 3380
4879
9576
6146
1366
22449
2267
13284
2249
2267
1353
2249
2267
1353
2261
14
V H
V H
V H
V H
C
C
 | 1793
1793
1793
1793
1793
1793
1793
1793 | Line
Line
Line
Line
Line
Line
Line
Line | в в в
в в в в | LAT
KVL
VAY
HLV
HPI
NLT | E 1915 Steer
1937 Steer
1937 Steer
1938 Steer
1938 Steer
1938 Steer
1934 Steer
1934 Steer
1934 Steer
1934 Steer
1934 Steer
1934 Steer
1937 Steer
1937 Steer
F V P
Y G I I
F V P V
P S S
R L G
L W T
Spectrum ID
1055 Steer
1055
 |
10 CONTRACTORNO 11 CONTRACTORNO 11 CONTRACTORNO 12 CONTRACTORNO 13 CONTRACTORNO 14 G G G T Y A K 14 G G C T Y A K 14 G C C V V P W 15 F T G E D P W 14 4557 1345588 (100%), 29,637.6 14 S C P Y L K M 15 S C N F Y L K M 16	100% 100% 100% 100% 100% 100% 100% 100%	64.1 50.6 53.3 50.6	51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.9 51.4	000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 01 2 01 2 01 2 01 2 01 2 01 2 01 2 01 2 01 2 01 2	DRVPE AWLNT CHGSC Tra, 10 total spec AERYE NEDRV FKTGA AKQAF Q	7764.33 503.33 503.33 503.33 503.33 503.33 503.33 503.33 504.34 504.545	L30564 L50563 L5065 L5065 L505 L50	2 - 0.15 3 - 0.17 3 - 0.15 3 - 0.16 3 - 0.16 3 - 0.16 3 - 0.16 2 - 0.16 2 - 0.12 10 acids (34 L M N L L R T L A C K V V R C M E K V A Y R G K I A E N T M Y R G K I A E N T M Charge Delta Da 2 - 0.15 2 - 0.081 2		790 790 60 600 600 600 600 990 600 990 600 990 600 990 600 990 600 990 600 990 600 990 600 990 600 990 600 990 600 990 600 970 600 970 700 700 700 700 700 700	3380 4879 9576 6146 1366 20449 2567 72049 2768 72049 2768 72049 2768 72049 2768 72049 2768 72049 2768 72049 2049 2049 2049 2049 2049 2049 2049	1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1793 1855 1855 1855 <td>00 00 100 00 <</td> <td>E S P T H D G G</td> <td>LAT KVL VAY HLV HPI NLT</td> <td>L915 3.cm 1937 3.cm 1937 3.cm 1933 3.cm 1943 3.cm 1943 3.cm 1944 3.cm 1944 3.cm 1944 3.cm 1945 3.cm 1946 3.cm 1946 3.cm 1946 3.cm 1947 3.cm 1947 3.cm 1947 3.cm 1947 3.cm 1948 3</td>	00 00 100 00 <	E S P T H D G G	LAT KVL VAY HLV HPI NLT	L915 3.cm 1937 3.cm 1937 3.cm 1933 3.cm 1943 3.cm 1943 3.cm 1944 3.cm 1944 3.cm 1944 3.cm 1945 3.cm 1946 3.cm 1946 3.cm 1946 3.cm 1947 3.cm 1947 3.cm 1947 3.cm 1947 3.cm 1948 3
10 GC/12727942109600 10 GC/12727942109600 10 GC/12727942109601 10 GC/12727942109601 10 GC/12727942109601 10 GC/1272942109601 10 GC/127294210 11 GC/GC V V PW 12 GC/C V V PW 13 GC/SS8 (100%), 29,637.6 13 GC/SS8 (100%), 29,637.6 13 GC/SS8 (100%), 29,637.4 13 SE D P A 13 SE S K V F Y L K 14 S A E L S R E E 15 S C D P A E E I R	100% 10% 1	64.1 63.3 50.6 53.3 38.0 38.0 38.1 35.3 38.2 66.5 66.5 63.7 Clusive 66.5 GGF14 Clusive A E Y M F Q Y M P K M P P K Maxco 1 90.7 86.5 35.0 30.1	51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.9 51.9 51.9 51.9 51.9 12 e unique 4. K L K Y R Y R A K L E Y Y D R A K L 51.4 51.4 51.4 51.4 51.4 51.4	000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2	DRVPE AWLNT CHGSC Tra, 10 total spe AERYE NEDRV FKTGA AKQAF Q Molifications	7764.33 503.33 503.33 503.33 503.33 7764.34 503.32 503.32 503.54 5045.02 5005.02 5005.02 5000	L305643 L50643 L50663 L50663 L50664 L	2 - 0.15 3 - 0.17 3 - 0.17 3 - 0.15 3 - 0.15 2 - 0.12 2 - 0.12 2 - 0.12 2 - 0.12 0 acids (23? M E K V A Y R G K I A E N T M E L D T L Charge Debala 2 - 0.15 2 - 0.13 2 - 0.076 (2 - 0.076) (2 - 0		780 780 610 620 6200 680 680 780 680 780 680 780 680 780 680 780 680 780 680 780 680 780 680 780 680 780 780	3380 4479 9576 8146 1366 2249 2249 2249 2249 2249 2249 2249 22	1793 1793 1793 1793 1793 1793 1793 1793	Loc	Image: 100 minipage Image: 100 minipage Image: 100 minipage Image: 100 minipage <td>LAT KVL VAY HLV HPI NLT</td> <td>L915 3.5ee L937 3.5ee L938 3.5ee L938 3.5ee L939 3.5ee F V P S R L G L V P S S R L G L V T S S L G L S S S S S L G L S S S L S S S S S</td>	LAT KVL VAY HLV HPI NLT	L915 3.5ee L937 3.5ee L938 3.5ee L938 3.5ee L939 3.5ee F V P S R L G L V P S S R L G L V T S S L G L S S S S S L G L S S S L S S S S S
10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699821096801 10 6001497699871096801 10 6001497699871096801 10 6001497699871096801 10 6001497699871096801 10 60014976998781096801 10 60014976998787606 10 600149789881000%1, 20,637.46 1345588 (100%1, 29,637.46 CName: Full=14.3.3.1ike xclusive unique peptide A S A E L S R E E R R A S W R I I S E S K V F Y L K M N F S V F Y E I S E D P A E E I R Sequence 10 (c)(TVISSELTVEER(0) 18 (c)(LISVAYK0) 1	1005 1006 1006 1006 1006 1006 1006 1007 1005 1005 1005 1005 1005 1005 1005 1005 1005 1005 1005 1005 1005 1005 1006	64.1 63.3 50.6 53.3 760.7 36.0 38.9 36.0 38.9 36.0 38.9 36.0 38.9 36.0 38.9 36.0 38.9 36.0 46.5 65.7 Clusive 45.7 GGF14 A A E A E A Clusive Y M Y S Y N S P Y N S P 90.7 86.6 79.0 35.0 30.1 45.3	51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.8 52.3 51.9 S1.9 S1.9 S1.4 S1.4 S1.4 S1.4 S2.4 S2.4 S2.4 S2.9	000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 00 2 00 2 00 2 00 2 000 2 000 2 001 2 000 2 000 2 000 2 000 2 000 2 000 2	DRVPE AWLNT CHGSC Tra, 10 total spe AERYE NEDRV FKTGA AKQAF Q Molifications	77433 50331 50333 50333 50333 75434 50333 75434 50353 50353 504533 704533 704533 70376 70376 70376 70376 70376 70376 70376 70376 70376 70376	L,506.64 L,506.63 L,506.63 L,506.63 L,506.64 L,506.75 L,5	2 - 0.15 3 - 0.17 3 - 0.15 3 - 0.15 3 - 0.15 2 - 0.06 2 - 0.12 2 - 0.12 2 - 0.12 2 - 0.12 Charge Delta Da 2 - 0.015 2 - 0.015 2 - 0.017 2 - 0.017 - 0.		790 790 610 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 790 6200 790 6200 790 6200 790 6200 790 6200 790 6200 790 6200 70 6200 70 6200 70 6200 70 6200 70 6200 70 6200 70 6200 70 6200 70 6200 70 6200 70	3380 4879 9976 8146 1366 2049 2049 2049 2049 2049 2049 2049 2049	1793 1793 1793 1793 1793 1793 1793 1793	Lièce Lièce	E S C S C S C S C S C S C S C S C S C S	LAT KVL VAY HLV HPI NLT	E 19 3 Steer 1937 Steer 1933 Star 1938 Star 1938 Star 1938 Star 1934 Star 1934 Star 1934 Star 1934 Star 1934 Star 1937 St
10 CALLEY EVELOPE (1) 11 CALLEY EVELOPE (1) 12 CALLEY EVELOPE (1) 13 CALLEY EVELOPE (1) 14 CALLEY EVELOPE (1) 15 CALLEY EVELOPE (1) 16 CALLEY EVELOPE (1) 17 CALLEY EVELOPE (1) 16 CALLEY EVELOPE (1) 17 CALLEY EVELOPE (1) 16 CALLEY EVELOPE (1) 16 CALLEY EVELOPE (1) 16 CALLEY EVELOPE (1) 16 CALLEY EVELOPE (1) 11 A G G G T Y A K 12 A G G G T Y A K 13 A G G G T Y A K 14 A G G G T Y A K 13 A G G C D Y W 14 A S A E L S R E E 13 A S W F Y L K M N F S V F Y Y E I </td <td>1005k 1</td> <td>64.1 64.3 50.6 53.3 50.6 53.3 36.0 36.0 36.2 66.5 66.5 66.5 66.7 66.7 66.6 79.0 90.7 80.6 90.7 90.7 90.7 90.7 90.7 90.0 30.1 45.3 47.8 47.8</td> <td>31.3 31.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$2.4 \$2.4 \$2.07 \$0.7</td> <td>000 2 000</td> <td>DRVPE AWLNT CHGSC AERYE AERYE NEDRY FKTGA AKQAF Q Moliŭestos</td> <td>77433 50331 50332 50323 50323 75434 50323 75434 50323 50323 50323 50323 50323 50324 50324 50324 504549 54519 54519 54519 54519 54519 54519 54519 54519 54519 54519 54519 54519 54519 70376 70377 45423</td> <td>L:306.64 L:506.63 L:506.63 L:506.63 L:506.64 L:506.75 L:506.64 L:506.75 L:506.64 L:506.75 L:5</td> <td>2 -0.15 3 -0.17 3 -0.15 3 -0.15 3 -0.16 3 -0.16 2 -0.16 2 -0.17 2 -0.12 2 -0.17 K V V R C K V V R C K V V R C K V V R C Charge Delta Da 2 -0.015 2 -0.013 2 -0.014 Charge 2 -0.15 2 -0.014 2 -0.014 2																
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.</td> <td></td> <td>780 780 610 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720</td> <td>3380
4879
9576
5146
1366
20449
2667
1752
2049
2667
1752
2049
2267
1753
2049
2267
1753
2049
2267
1753
2049
2267
1753
1762
1782
1782
1782
1782
1782
1782
1782
178</td> <td>1793
1793
1793
1793
1793
1793
1793
1793</td> <td>00 00 100 100 100 100 100 100</td> <td>в в в
в в в в</td> <td>LAT
KVL
VAY
HLV
HPI
NLT</td> <td>1915 Ster 1937 Ster 1937 Ster 1938 Star 1938 Star 1939 Ster 1934 Star 1937 Star 1937 Star 1938 Star 1937 Star 1937 Star 1935 Star 1945 Star 1947 Star 1947 Star 1948 Star 1948 Star 1949 Star 1949 Star 1949 Star 1953 Star 1953 Star 1999 Star 1188 Star</td> | 1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1005k
1 | 64.1 64.3 50.6 53.3 50.6 53.3 36.0 36.0 36.2 66.5 66.5 66.5 66.7 66.7 66.6 79.0 90.7 80.6 90.7 90.7 90.7 90.7 90.7 90.0 30.1 45.3 47.8 47.8
 | 31.3 31.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.3 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$1.4 \$2.4 \$2.4 \$2.07 \$0.7 | 000 2 000 | DRVPE
AWLNT
CHGSC
AERYE
AERYE
NEDRY
FKTGA
AKQAF
Q
Moliŭestos | 77433
50331
50332
50323
50323
75434
50323
75434
50323
50323
50323
50323
50323
50324
50324
50324
504549
54519
54519
54519
54519
54519
54519
54519
54519
54519
54519
54519
54519
54519
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376
70377
45423
 | L:306.64
L:506.63
L:506.63
L:506.63
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.64
L:506.75
L:506.64
L:506.75
L:506.64
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:506.75
L:5 | 2 -0.15
3 -0.17
3 -0.15
3 -0.15
3 -0.16
3 -0.16
2 -0.16
2 -0.17
2 -0.12
2 -0.17
K V V R C
K V V R C
K V V R C
K V V R C
Charge Delta Da
2 -0.015
2 -0.013
2 -0.014
Charge 2 -0.15
2 -0.014
2 -0.014
2 -0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0.014
-0. | | 780 780 610 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 620 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 6200 720 | 3380
4879
9576
5146
1366
20449
2667
1752
2049
2667
1752
2049
2267
1753
2049
2267
1753
2049
2267
1753
2049
2267
1753
1762
1782
1782
1782
1782
1782
1782
1782
178 | 1793
1793
1793
1793
1793
1793
1793
1793
 | 00 00 100 100 100 100 100 100 | в в в
в в в в | LAT
KVL
VAY
HLV
HPI
NLT | 1915 Ster 1937 Ster 1937 Ster 1938 Star 1938 Star 1939 Ster 1934 Star 1937 Star 1937 Star 1938 Star 1937 Star 1937 Star 1935 Star 1945 Star 1947 Star 1947 Star 1948 Star 1948 Star 1949 Star 1949 Star
 1949 Star 1953 Star 1953 Star 1999 Star 1188 Star |
| 10 CONTRACTORNO 11 CONTRACTORNO 11 CONTRACTORNO 12 CONTRACTORNO 13 CONTRACTORNO 14 G G G T Y A K 14 G G C T Y A K 14 G C C V V P W 15 F T G E D P W 14 4557 1345588 (100%), 29,637.6 14 S C P Y L K M 15 S C N F Y L K M 16 | 1005
1006
1006
1006
1006
1006
1006
1007
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1005
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006
1006 | 64.1 63.3 50.6 53.3 760.7 36.0 38.9 36.0 38.9 36.0 38.9 36.0 38.9 36.0 38.9 36.0 38.9 36.0 46.5 65.7 Clusive 45.7 GGF14 A A E A E A Clusive Y M Y S Y N S P Y N S P 90.7 86.6 79.0 35.0 30.1 45.3 | 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.8 52.3 51.9 S1.9 S1.9 S1.4 S1.4 S1.4 S1.4 S2.4 S2.4 S2.4 S2.9 | 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 000 2 00 2 00 2 00 2 00 2 000 2 000 2 001 2 000 2 000 2 000 2 000 2 000 2 000 2 | DRVPE
AWLNT
CHGSC
AWLNT
CHGSC
AWLSC
CHGSC
AWLSC
AWLSC
AWLSC
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Contemport
Conte | 77433
50331
50333
50333
50333
75434
50333
75434
50353
50353
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
504533
704533
704533
70376
70376
70376
70376
70376
70376
70376
70376
70376
70376 | L,506.64
L,506.63
L,506.63
L,506.63
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.64
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,506.75
L,5 | 2 - 0.15
3 - 0.17
3 - 0.15
3 - 0.15
3 - 0.15
2 - 0.06
2 - 0.12
2 - 0.12
2 - 0.12
2 - 0.12
Charge Delta Da
2 - 0.015
2 - 0.015
2 - 0.017
2 - 0.017
- 0. | | 780 780 610 620 620 620 620 620 620 780 | 3380
4879
9976
8146
1366
2049
2049
2049
2049
2049
2049
2049
2049 | 1793
1793
1793
1793
1793
1793
1793
1793 | Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce
Lièce | E S C S C S C S C S C S C S C S C S C S | LAT
KVL
VAY
HLV
HPI
NLT | E 19 3 Steer
1937 Steer
1933 Star
1938 Star
1938 Star
1938 Star
1934 Star
1934 Star
1934 Star
1934 Star
1934 Star
1937 St |



gi|633095 (100%), 50,282.1 Da

plastidic aspartate aminotransferase [Panicum miliaceum]

7 exclusive unique peptides, 15 exclusive unique spectra, 95 total spectra, 186/457 amino acids (41% coverage)

M A S A A F A L T S PMAPPDPILC LPIEGLAAFT SSPTWGNHKN G I D P T P E QWE SKN L G L Y A E F G E W K Q E M E QN KWH V Y M T K D O	G VS N KA N IF E KI R IG M AG	A P A I A A E A F K A D T A E L L L N D A R V P A D V I Q E A I N V V C R I K N V R S L A G L S	KN DLK <mark>L</mark> GA DNPV WS EYRY KK HMPF SA PEVA QK LYDS	LSAKE	A YI V A V GI VQ GI SQ LI DK SO	N G C R V G R T E E L G T L Q S L S L D F E G M F A S G S L K R L A R F G K D W S F S F H N V S	PYV SGTG AIAD DED PMYS FILR	K N F G R V L N L N V V K K A B S L R L A A A B I E A A P E G S A F S V R L F Y N P P I H G A F Q I G M F S Y T	ENLM FIQR SFVL SFVL KRG RIVA	V D V S R F E G V L E K G E N K E Y Y F P E A K V L I L H G C A H N P T M E V F V A Q S Y N I V G D P T M F K A Q S D N M T D
Valid Seguence V 1.0 (R)FE3VFMAFFDFILOVSEAFE(A) V 1.0 (R)FE3VFMAFFDFILOVSEAFE(A)	Prob Ma 100% 7 100% 6	5.0 50.1 58.3 5.0 50.1 29.9	NTT Modifications 2 Oscilation (†16) 2 Oscilation (†16)	705 28	2,115.83	harge Delis Da De 3 -0.22 -	dia Retent I 110 1750 -94 1760	2027	36art Stop 57 76 57 76	# Offie Offier Frotei Spectrum ID 0 2070: Brom 10566 0 2005: Brom 10615
 IO (R)FEOYFMALTDPLOVSEAFE(A) IO (R)FEOYFMALTDPLOVSEAFE(A) IO (R)FEOYFMALTDPLOVSEAFE(A) IO (R)FEOYFMALTDPLOVSEAFE(A) 	100% 6	4.8 502 7.9	2	700.96 700.95 700.95	2,090 85 2,090 84 2,099 86	3 -0.21 -	100 1800 110 1800 -96 1790	3490 7617 2049	57 76 57 76 57 76	0 2153 Soun 10852 0 2164 Sum of 2 st 0 2148 Soun 10834
 10 (R)FEGVENAFEDERL GVZEAFE(A) 10 (R)FEGVENAFEDERL GVZEAFE(A) 10 (R)FEGVENAFEDERL GVZEAFE(A) 	100% 5	2.5 50.9 6.4 5.6 50.2 6.3	22	700.95 700.95 700.95	2,099.82 2,099.82 2,099.83	3 -0.24 - 3 -0.24 -	(10 1780 (10 1790 (10 1790	1362 2100	57 76 57 76 57 76 57 76	0 2117 Scen 10726 0 2133 Scen 10783 0 2140 Scen 10807
 10 REFERVENCEPTEDUCOVERATION 10 REFERVENCEPTEDUCOVERATION 10 REFERVENCEPTEDUCOVERATION 	100% 4	4.3 50.1 29.0	2 2 2 Oscietation (+15)	1,050 93 1,058 93 1,050 93	2,099 85 2,115 84 2,099 84	2 -0.21 -	-99 1790 100 1740	2105 2638 972 2 2553	57 76 57 76	0 2132 Scan 10750 0 2145 Scan 10750 0 2105 Scan 10478 0 2179 Scan 10931
 10 CONFERMENTARPDUTLOWSEAFE(A) 	100% 4	2.1 50.1 18.9 5.1 50.2 9.6	2 Origitation (+15) 2	705 29	2,115 85 2,092 86	J -0 20 - 2 -0 20 -	-97 1720 -97 1770	758.8	57 76 57 76	0 2016 Scen 10371 0 2115 Scen 10718
10 ROFEGVEMAPDELLOVSEAFE(A) 10 ROFEGVEMAPDELLOVSEAFE(A) 10 ROFEGVEMAPDELLOVSEAFE(A) 10 ROFEGVEMAPDELLOVSEAFE(A)	98% 3	5.4 501 196 3.6 501 168 3.0 501 143	2 Oradation (+15) 2 Oradation (+15) 2 Oradation (+15)	705 28	2,115 83 2,115 85	3 -0.21 -	110 1740 -99 1730 -86 1730	1343 1118 836.2	57 76 57 76 57 76	0 2051: Scen 10505 0 2043: Scen 10462 0 2033: Scen 10427
10 (R)FEOVPMAPPDPILOVERAFK(A) 0.3 (C)LNIGVGAVE(D)	1005 4	4.3 50.1 9.1 1.2 52.2 0.0	2 Oxidation (+16)	1,056 94 1,056 93 481 73 481 75	2,115.87 2,115.85 961.45 961.45	2 -0.21 -	-99 1720 -93 2280	204.9 1220	57 76 57 76 84 92 84 92	0 2026 Scan 10403 2 a)0505932,2 2728 Scan 13881
V 0.3 GOLNLGYGAYR(I) V 0.3 GOLNLGYGAYR(I) V 0.3 GOLNLGYGAYR(I) V 0.3 GOLNLGYGAYR(I)	98% 3 98% 3 92% 2	19 527 0.0	2	481 73 481 74 401 73	961 45 961 46 961 45	2 -0.077 -	-84 1.820 -80 2210 -91 1270	2208 (085 1792	84 92 84 92	 gift005932,g. 1396; Nem 7955 [. gift005932,g. 2619; Nem 13461 gift005932,g. 1320; Rem 7654 [.
V 0.3 (R)TEELOPYVLNVVK(C) 0.3 (R)TEELOPYVLNVVK(C) V 0.3 (R)TEELOPYVLNVVK(C)	93% 2 100% 8 100% 7 100% 7	28 527 0.0 84 527 0.0 53 511 0.0 52 511 0.0 47 511 0.0	2	766.36 511.24 511.24	1,530.70 1,530.71 1,530.71	2 -0.13 -	-84 1510 -77 1550 -79 1530	29.36 0094 4115	9.0 105 9.3 105 9.3 105	2 gif605932.g. 1086 Sten 9130 [2 gif605932.g. 1753 Stem 9363 [2 gif605932.g. 1725 Sten 9266 [
0.3 GOTEELOPYVLNVVKGO 0.3 GOTEELOPYVLNVVKGO	100% 7	47 911 0.0 55 511 0.0 32 511 0.0 84 511 0.0	5	765.37 511.24	1,530 72 1,530 70 1,530 70	2 -0.11 - 3 -0.13	-71 1530 -86 1510 -83 2240	7600 1968 882.5	9.3 105 9.3 105 9.3 105 9.3 105	2 gib605932,g 1724; Bom 9262 [2 gib605932,g 1689; Som 9136 [2 gib605932,g 2661; Som 13675
	91% 2	7.3 51.1 0.0 8.1 50.4 49.5	3	766.36 766.34 631.61	1,530.67	2 -0.16 -	110 2310 -91 1640	885.1 5747	93 105 93 105 115 131	2 gi0605932,g 2786; Sran 14104 1 gi673920919 1896; Sran 9676 [
 0.5 GOOENKEYLPIEOLAAFNK(A) 0.5 GOOENKEVLPIEGLAAFNK(A) 0.5 GOEVLP(EGLAAFNKGA) 	100% 7 100% 5 100% 8	79 904 819 25 904 270 51 512 585	2	631 61 631 61 732 82	1,891 81 1,891 81 1,463 63	3 -0.15	-86 1610 -83 1590 -95 1710	4312 2063 6311	115 131 115 131 119 131	1 gif73021919 1648 Scan 9732 [1 gif73921919 1608 Scan 9583 [1 gif73920919 2000 Scan 10315
0.5 GOEVLP(BGLAAFNE(A) 0.5 GOEVLP(BGLAAFNE(A)	100% 8	2.6 51.2 51.5 4.3 51.2 52.2	2	732.82 732.82 732.82 489.88	1,463.63	2 -0.13 -	-92 1680 -98 1660	2293	119 131 119 131	1 gib73920919 1955; Scen 10143 1 gib73920919 1935; Scen 10151
0.5 GOEVLFIEGLAAFRIK(A) 0.5 GOEVLFIEGLAAFRIK(A) 0.5 GOEVLFIEGLAAFRIK(A)	100% 4	2.9 51.2 21.2 1.6 51.2 11.7 8.3 51.2 19.6 4.0 51.2 13.3	2	483 89	1,463.61 1,463.65 1,463.64 1,463.65	3 -0.11 -	110 1720 -77 1710 -84 1710 -81 1690	2029 2244 2062 1299	119 131 119 131 119 131 119 131 119 131	1 gif73920919 2017 Som 10374 1 gif73920919 2007 Som 10342 1 gif73920919 2001 Som 10318 1 gif73920919 2001 Som 10318 1 gif73920919 1965 Som 10118
V 0.5 GOEVLPIEGLAAFHK(A) V 10 GOATAELLIGADHFVIE(O) V 10 GOATAELLIGADHFVIE(O)	100% 9	1.1 51.1 50.5 3.4 51.1 40.0	2	488 89 508 91 508 91	1,463.65 1,523.71 1,523.70	3 -0.12 - 3 -0.15 - 3 -0.15 -	-81 1690 -98 1570 100 1580	1293 4869 3676	119 131 132 146 132 146	1 gr673920919 1066 Sonn 10184 0 1768 Sonn 9492 [0 1796 Sonn 9540 [
V 10 COATABLLIGADNEVIE(O)	100% 8	10 511 453 14 511 892	3	508.92 762.88 844.41	1,523 72	3 -0.13 -	-87 1560 -88 1550 -75 1640	3891 3182	132 146 132 146	0 1776 Scen 9446 [0 1748 Scen 9345]
 V 10 GOJGLYATIALLIA (1990) V 10 GOJGLYATIALAGU V 10 GOJGLYAT	100226	8.3 50.7 79.3 14 50.7 77.6 10 50.7 69.1 1.7 50.7 67.5	3	844.40	1,695.90 1,695.79 1,695.79	2 -0.13 -	-84 1610 -79 1610	4511 2145 1767	147 163 147 163 147 163	0 1696 Sten 9907 [U 1650 Sten 9742] O 1840 Sten 9697 [
V 10 GCyOLVATLOELSGTOELR(L) V 10 GCQGLVATLOELSGTOELR(L) V 10 GCQGLVATLOELSGTOELR(L)	100% 0	5.4 20.7 40.4 3.1 20.7 22.6	2 2 2	844.40 563.27 563.25	1,655 79 1,655 78 1,655 77	3 -0.15 -	-78 1590 -87 1620 -93 1650	825.7 2377 5751	147 163 147 163 147 163	0 1819: Scan 961.9 [. 0 1856: Scan 9768 [. 0 1903: Scan 9767 [.
V 10 GOOGLVATLOSLSGTGSLR(L) V 10 GOOGLVATLOSLSGTGSLR(L)	100% 4 100% 3 99% 4	7.9 507 289 3.9 507 217	2	563 26 563 26 445 23	1,695.77 1,695.75 898.44	3 -0.17 -	-91 1630 100 1610 -90 2240	3407 1522 2001	147 163 147 163 164 171	0 1676 3con 9636 [0 1644 Bonn 9711] 1 gi673930919 2665 3con 13654
V 0.5 (R)LAAAF(OR(V) V 0.5 (R)LAAAF(OR(V) V 0.5 (R)LAAAF(OR(V)	90% 4	0.9 52.8 7.0 5.2 52.8 4.3	3	445 21	900.40 868.44	2 -0.12 - 2 -0.079 -	130 2390	2375	164 171	1 giB73920919 2751; Bona 13991
V 9.5 (R)LAAAMOR(Y) V 0.5 (R)LAAAMOR(Y) V 0.5 (R)LAAAMOR(Y)	00% 4 07% 4 95% 4	4.7 55.0 9.6	2	445 00 445 45 645 05	000 17 868 88 869 08	2 0.96	300 2060 410 2340 490 2240	2095 2380 2060	164 171 164 171 164 171	1 giE73623019 2705 Ecas 12700 1 giE73623019 2633 Ecas 14267 1 giE73623019 2633 Ecas 14267
0.5 (R)LAAAFOR(V)	94% 4 90% 4	2.3 53.2 11.3 2.8 52.8 6.7	2	445.41 445.33 660.80	858.80 888.65 1.337.58	2 0.29	320 2250 150 2320 -97 1220	2990 2141 907 3	164 171 164 171 178 189	1 gi673920919 2600 Scan 13737 1 gi673920919 2605 Scan 14178
0.3 (C)VL)22PT WONHE(N) 0.3 (R)VPW1EVR(V) 0.3 (R)VPW1EVR(V) 0.3 (R)VPW1EVR(V)	80% 3	7.1 52.2 7.6 9.5 52.2 11.1	â	469 69 469 69	935 37 935 37	2 -0.093 - 2 -0.078 -	-89 1190 -83 1170	21740 3273 1475	1977 203 1977 203	2 gib605932.g 1260 Scim 7395 [2 gib605932.g 1217: Scim 7204 [2 gib605932.g 1180: Scim 7047 [
0.3 (R)VFWSEYR(Y) 0.3 (R)VFWSEYR(Y) 0.5 (C)ADVIORE(C)	82% 2	5.0 52.2 11 J	2	463 71 463 71 453 23	935.41 935.40 914.44	2 -0.057 -	-42 1240 -57 2270 -74 2300	1668	197 203 197 203 252 259	2 gibb05932.g 180 zem 7047 [2 gibb05932.g 1897 Son 7509] 2 gibb05932.g 2715 Som 1880 1 gib73923919 2760 Som 14011
0.5 GOIADVIOEKGO 0.5 GOIADVIOEKGO 0.5 GOIADVIOEKGO 0.5 GOIADVIOEKGO	99% 3 99% 3	80 323 00 64 323 00 52 523 00 14 523 00	9	458 22 458 22 458 23	914 44 914 43 914 44	2 -0.072 -	-79 2180 -85 2400 -78 1120	1521 2705 1792	252 259 252 259 252 259 252 259	1 gE73930919 2576 Son 13220 1 gE73930919 2506 Son 14610 1 gE73930919 1115 Son 6760 [
C 0.5 COLADVIOEKCO	93% 2 92% 2	3.2 52.3 0.0 3.9 52.3 -0.1		459 23 459 23	914 45 914 44	2 -0.055 -	-60 2250 -75 2210	2385 3311	252 259 252 259	1 gib73923919 2583; Soen 13720 1 gib73923919 2521; Som of 2 m
V 0.5 GOLADVIGEEGO V 0.5 GOLADVIGEEGO V 1.0 GORGMEVEPAQSYSK(%)	91% S	98 523 0.0 90 523 0.0 1.4 513 296 1.5 913 215	2	458 23 458 16 501 21	914 45 914 30 1,500 62 1,516 57	2 -0.21 - 3 -0.12	230 1030	3332 4183 2779 1356	252 259 252 259 250 302 250 302	1 gib73923919 2742 Sum of 2 m . 1 gib73923919 954 Som 748 D . 0 1356 Som 749 [. 0 1123 Bonn 6601 [.
10 0CR0MRVFVACSVSK(0) 10 0COMRVFVACSVSK(0) 10 0COMRVFVACSVSK(0) 10 0COMRVFVACSVSK(0)	222	5.5 51.3 21.5 0.4 51.4 60.5 0.5 51.5 62.9	2 Ocatalion (+15) 2 2 Ocatalion (+15)	505 53 673 27 691 25	1,516 57 1,344 52 1,350 49	2 -0.12 -	110 1130 67 1370 110 1170	1350 1165 1330	200 302 291 302 201 302	
10 ROMEYPAQOVER(N)	94% 3	0.4 51.4 27.7 6.0 51.4 17.9	2	673 27 673 32 673 32	1,344 53 1,344 63 1,344 51	2 -0.11 -	81 2380 -7.1 2240 -98 2210	558.3 403.4 460.4	201 302 201 302 201 302	0 2887; Srea, 14519 0 2875; Srea, 12698 0 2617; Srea, 12698
V 10 ROOMEVEYAQEVER(N) V 10 RODA(NVVCSAPEYADR(V) V 10 RODA(NVVCSAPEYADR(V)	100% 7	5.5 51.4 14.7 5.5 50.8 34.2 3.3 50.8 23.9	2 2 Cerbanilonethyl 2 Cerbanilonethyl	835.92 835.86	1,669.83	2 -0.020 - 2 -0.15 -	-12 1390 -89 1340	1281	.311 326 311 326	0 1304: Scen 8407 [. 0 1433: Scen 8118 [.
V 10 REDAINVVCSAFEVADR(V) V 10 REDAINVVCSAFEVADR(V) V 10 REDAINVVCSAFEVADR(V)	100% 2	5.5 50.8 28.7 5.9 50.8 7.4	2 Carbanilomethyl . 2 Carbanilomethyl . 2 Carbanilomethyl .	935 85 557 56 835 85	1,669.69 1,669.65 1,669.69	2 -015 - 3 -020 - 2 -015 -	-91 2290 120 1370 -91 2230	689 1 3568 661 4	311 326 311 326 311 326	0 2753: Scen 13967 0 1476: Scen 8390 f
 V 10 (R)IOA(IN VVC SAFEYADR(V) V 10 (R)IOA(IN VVC SAFEYADR(V) V 10 (R)IOA(IN VVC SAFEYADR(V) V 0.5 (R)IOM/EFYTOLNK(A) 	100% 5 91% 3 100% 4	50 508 138 71 520 326 10 508 25 97 516 301	2 Carbonatomethyl 2 Carbonatomethyl 2 Ocatation (+15)	836 10 557 54 667 76	1,670 19 1,659 60 1,373 54	2 0.34 2 3 -0.24 -	200 2320 150 1350 -90 1330	661.4 713.0 2102 2799	311 326 311 326 311 326 311 326 401 412	0 2557; Scim [162] 0 2792; Scim [41:26] 0 1436; Scim [81:29] [1 gib7/35/21919 1416; Scim [81:44] [
V 0.5 (ROCIGMESYTGLERA) V 10 (COAQEDIMETDE(W)	93% 2	3.9 51.5 1.4.2 3.2 51.6 7.9	2 2	679.78 505.17	1,357.55	2 -0.12 -	-89 1450 -95 639	1847	401 412 413 421	1 gil773920919 1592. Sum of 2 m 615. Sean 4002 ID
V 0.3 (RHELAGLELAKIC) V 0.3 (RHELAGLELAKIC) V 0.3 (RHELAGLELAKIC)	100% 4	7.0 51.9 (4.1 7.8 51.9 1.1	2	486 77 495 77 486 77	971 52 971 52 971 53	2 -0.083 - 2 -0.067 -	-81 1540 -85 1500 -69 1550	2024 7907 1383	432 441 432 441 432 441	2 gib605932.g. 1738; Son 9309 [. 2 gib505932.g. 1669; Son 9063 [2 gib605932.g. 1751; Son 9357 [
0.3 (RHELAGLELAK(C)	100% 4	3.4 51.9 0.0	22	495 77 495 76 495 76	971 53 971 50 971 50	2 -0.058 - 2 -0.100 - 2 -0.10	-69 2250 100 2360 110 2300	1193 1153 1050	432 441 432 441	2 gsb505932.g. 2691 Som 13743 2 gsb505932.g. 2855 Som 14385
V 0.3 (RHELAGLELAK(C) V 0.3 (RHELAGLELAK(C)	80% 2	70 319 59 55 519 33	â	485.75	971 50 971 50	2 -0.10 -	110 2300 110 2280	2304	432 441 432 441	2 gif605932.g. 2774; Son 14055 2 gif605932.g. 2727; Sum of 2 m

Spot # 208

gi|194702912 (100%), 20,753.4 Da

unknown [Zea mays]

2 exclusive unique peptides, 2 exclusive unique spectra, 9 total spectra, 42/193 amino acids (22% coverage)

Μ	GRERAQRSI	V	CQA	AAS	SI	SA	DRVI	DME	KRK	LM	NLL	LL	GA	S I	PTV	GMV	/ V P	Υ (3 A F F	VPAGS
G	NAGGGTYAK	D	KL G	N D	1 T	VΕ	AWLN	ITHG	PND	RΤ	LAQ	GL	KGI) P	TYLV	VEC	DK	Τl	A T Y	GINAV
C	THLGCVVPW	N	G Α Ε	ENK	FI (СΡ	CHGS	SQYN	NQG	ΚV	VRG	PA	PL	S L	ALVH	AD \	DD/	GI	(VLF	VPWVE
T	DFR TGEDPW	14/1	1 1																	
	UFN IGEDFW		A N																	
7alid				Maxo	Maxo	NIT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Stert	Stop	≢0the	Other Protei	Spectrum ID
7alid			Masco	Masco 51.6	Maxo	NI7 2	Modifications	Observed 682.26	Actual Mass 1,362.51	Charge 2	Delta Da -0.16	Delta -120	Retent. 1260	Intensity	TIC 21.56	Start 99	Stop 110	≇Othe O	Other Puotei	Spectrum ID 1127: Scan 7605 [

V	II (K)GDFTYLVVEQDK(T)	100%	48.2	51.5	0.0	2	682.26	1,902.51	2	-0.16	-120	1240	1429	99	110	U	1113: Scan 7521 [
V 0	7 (R)GPAPLSLALYHADVDDGK(Y)	100%	64.8	50.9	16.2	2	592.26	1,773.75	3	-0.18	-100	1490	2609	155	172	2	giB2651B43 1392; Scan 9013 [
V 0	7 (R)GPAPLSLALVHADVDDGK(V)	100%	63.3	50.9	14.0	2	592.26	1,773.77	3	-0.15	-87	1520	3472	155	172	2	giB2651843 1429 Scan 9181 [
▼ 1	0 (K) YLFYP WYETDFR (T)	100%	83.1	51.3	0.0	2	754.34	1,506.66	2	-0.12	-81	1910	5477	173	184	0	1875: Scan 10938
V 1	0 (K) YLFYP WYEIDFR(T)	100%	79.9	51.3	0.0	2	754.34	1,506.67	2	-0.12	-77	1800	13000	173	184	0	1856: Sum of 3 sc
1	0 (K) VLFVP WYEIDFR(T)	100%	64.0	51.3	0.0	2	754.34	1,506.67	2	-0.11	•76	1820	3945	173	184	0	1891 Scan 10996
V 1	0 (K) YLFYP WYEIDFR (T)	100%	57.6	51.3	0.0	2	754.35	1,506.68	2	-0.10	-68	1790	3443	173	184	0	1839 Scan 10822
V 1	0 KIVLEVPWVEIDFR(D)	100%	57.2	51.3	0.0	2	754.34	1,505.66	2	-0.13	-B4	1790	2224	173	184	Û	1834 Scan 10803



gi|118614499 (100%), 54,014.4 Da

ATP synthase CF1 beta subunit (chloroplast) [Sorghum bicolor]

1 exclusive unique peptides, 1 exclusive unique spectra, 23 total spectra, 145/498 amino acids (29% coverage)

GVSIIEEKSV	GRIDQIIGPV	LDIIFPPGKL	PYIYNALIVK	SRDIADKQIN
N N R V R A V A M S	ATDGLMRGME	VIDTGTPLSV	PVGGATLGRI	FNVLGEPIDN
PIHR SAPAFI	ELDTK LSIFE	T G I K <mark>V V D L L A</mark>	PYRRGGKIGL	FGGAGVGKTV
KAHGGVSVFG	GVGER TREGN	DLYMEMKESG	VINEKNIEES	KVALVYGQMN
TSTMLQPRIV	GNEHYETAQR	VKETLQRYKE	LQDIIAILGL	DELSEEDRLT
LSQPFFVAEV	FTGSPGKYVG	LAETIRGFQL	ILSGELDGLP	EQAFYLVGNI
EEESKLKK				
	N N R V R A V A M S P I H R S A P A F I K A H G G V S V F G L T A L T M A E Y F E R I T S T K K G S T S T M L Q P R I V	NNRVRAVAMS ATDGLMRGME PIHRSAPAFI ELDTKLSIFE KAHGGVSVFG GVGERTREGN LTALTMAEYF RDVNKQDVLL ERITSTKKGS ITSIQAVYVP TSTMLQPRIV GNEHYETAQR LSQPFFVAEV FTGSPGKYVG	NNRVRAVAMS ATDGLMRGME VIDTGTPLSV PIHRSAPAFI ELDTKLSIFE TGIKVVDLLA KAHGGVSVFG GVGERTREGN DLYMEMKESG LTALTMAEYF RDVNKQDVLL FIDNIFRFVQ ERITSTKKGS ITSIQAVYVP ADDLTDPAPA TSTMLQPRIV GNEHYETAQR VKETLQRYKE LSQPFFVAEV FTGSPGKYVG LAETIRGFQL	GVSITEEKSV GRIDQITGPV LDTIFPPGKL PYTYNALTVK NNRVRAVAMS ATDGLMRGME VIDTGTPLSV PVGGATLGRI PIHRSAPAFI ELDTKLSIFE TGIKVVDLLA PYRRGKIGL KAHGGVSVFG GVGERTREGN DLYMEMKESG VINEKNIEES LTALTMAEYF RDVNKQDVLL FIDNIFRFVQ AGSEVSALLG ERITSTKKGS ITSIQAVYVP ADDLTDPAPA TTFAHLDATT TSTMLQPRIV GNEHYETAQR VKETLQRYKE LQDIIAILGL LSQPFFVAEV FTGSPGKYVG LAETIRGFQL ILSGELDGLP EEESK LKK KK KK

Yabid		Sequence	Prob	Maxo	Masco	Masco	NTI	Modifications	Observed	Actual Mass	Charge	Delta De	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	03	(R)AVAMSATDGLMR(G)	100%	47.0	51.7	0.0	2		611.74	1,221.47	2	-0.11	-91	1280		97 8.8	76	87	2	gill 3236786, .	1291: Scan 7729 [
	05	(R)SAFAFIELDTK(L)	100%	64.8	51.8	0.0	2		596.26	1,190 50	2	-0.12	-100	1430		2427	135	145	1	gill10915642	1515: Scan 8671 [
1	05	(K)VVDLLAPYR(R)	99%	37.4	52.2	0.0	2		523 25	1,044.48	2	-0.11	-110	1500		2066	155	163	1	gill10915642	1629: Scan 9092 [
	05	(K)VVDLLAFYR(R)	96%	31.9	52.2	0.0	2		523.26	1,044 50	2	-0.100	-95	1490		1644	155	163	1	gill10915642	1610: Scan 9024 [
1	05	(K)VVDLLAPYR (R)	88%	28.4	52.2	0.0	2		523 26	1,044.50	2	-0.095	-91	1520		1596	155	163	1	gill 10915642	1643: Scan 9155 [
V	05	(K)VVDLLAPYR(R)	80%	27.0	52.2	0.0	2		523.26	1,044 50	2	-0.099	-95	1480		1320	155	163	1	gill10915642	1592: Scan 8958 [
V	0.1	(K)IGLFGGAGYGK(T)	100%	59.0	52.6	0.0	2		488.26	974.51	2	-0.049	-50	1420		2325	168	178	17	gil65909168	1495: Scan 8593 [
V	0.1	(K)IGLFGGAGYGK(T)	100%	52.5	52.6	0.0	2		468 25	974.49	2	-0.070	-72	1410		1771	168	178	17	gi65909168	1475: Scan 8515 [
V	03	(K)AHGGVSVFGGYGER(T)	100%	40.9	51.5	0.0	2		664 80	1,327 59	2	-0.078	-59	1230		5 7 7.6	192	205	2	gill 3236786, .	. 1225: Scan 7444 [
7	03	(R)VGLTALTMAEYFR(D)	100%	97.8	51.8	0.0	2		736.31	1,470.60	2	-0.15	-100	1770		1339	249	251	3	gill 3236786, .	2014: Scan 10688
1	03	(R)VGLTALTMAEYFR(D)	100%	66.3	51.8	0.0	2		736.31	1,470.61	2	-0.15	-100	1750		801.0	249	261	3	gill.3236786, .	. 1993: Scan 10592
V	03	(R)VGLTALTMAEVFR(D)	100%	59.5	51.7	0.0	2	Oxidation (+16)	744.32	1,486.63	2	-0.12	-82	1590		941.7	249	261	3	gill 3236786, .	. 1763. Scan 9625 [
1	03	(R)VGLTALTMAEYFR(D)	100%	45.5	51.8	0.0	2		736.32	1,470.63	2	-0.13	-87	1760		913.8	249	261	3	gill 3236786, .	. 2002: Scan 10635
7	03	(R)VGLTALTMAEYFR(D)	97%	31.9	51.7	0.0	2	Oxidation (+16)	744.32	1,486.62	2	-0.13	-87	1580		810.2	249	261	3	gill 3236786,	. 1737: Scan 9519 [
V	03	(R)FYQAGSEVSALLGR(M)	100%	93.8	52.8	0.0	2		717.68	1,433.35	2	0.58	-300	1540		1513	278	291	3	gill 3236786, .	. 1685; Scan 9319 [
V	0.3	(R)FYQAGSEVSALLGR(M)	100%	67.3	515	0.0	2		717.32	1,432.63	2	-0.14	-96	1520		1036	278	291	3	· · ·	. 1647: Sum of 2 sc
7	03	(R)FYQAGSEVSALLGR(M)	100%	79.7	543	0.0	2		717.13	1,432.25	2	-0.52	340	1530		1039	278	291	3	gill 3236786,	. 1668: Scan 9254 [
V	03	(R)FYQAGSEVSALLGR(M)	100%	45.2	515	0.0	2		717.33	1,432.64	2	-0.12	-85	1550		938.5	278	291	3	gill 3236786,	. 1697: Scan 9371 [
	0.3	(R)MPSAYGYQPTLSTEMGSLQER	100%	50.4	50.1	0.0	2		761.31	2,290.90	3	-0.17	-74	1480		1172	292	312	3		. 1591: Scan 8955 [
V	03	(K)GIYPAYDPLDSISTMLQPR(I)	94%	28.7	50.3	0.0	2		1,030.93	2,059.84	2	-0.18	-88	1620		699.7	360	378	3		. 1800: Scan 9766 [
	05	(R)IVGNEHVETAQR(V)	100%	56.7	51.3	0.0	2		708.77	1,415.52	2	-0.16	-110	849		1151	379	390	1	gill10915642	779: Sum of 2 see
		(K)AINLEEESK(L)	100%	53.4	52.2	0.0	2		516.71	1,031.40	2	-0.11	-110	1040		2731	487	495	D		985: Scan 6298 [D
7	1.0	(K)AINLEEESK(L)	100%	45.7	52.2	0.0	2		516.71	1,031.40	2	-0.12	-110	1030		2111	487	495	0		976: Scan 6243 [D

Spot # 470

gi|131176 (100%), 15,456.6 Da

RecName: Full=Photosystem I reaction center subunit IV, chloroplastic; Short=PSI-E; AltName: Full=Photosystem I 10.8 kDa polypeptide; Flags: Precursor 1 exclusive unique peptides, 1 exclusive unique spectra, 2 total spectra, 17/147 amino acids (12% coverage)

MASTNMASAT	SRFMLAAGIP	SGANGGVSSR	VSFLPSNRLG	LKLVARAEEP	ΤΑΑΑΡΑΕΡΑΡ
AADEKPEAAV	ATKEPAKAKP	PPRGPKRGTK	VKILRRESYW	YNGTGSVVTV	DQDPNTRYPV
V V R F A K <mark>V N Y A</mark>	GVSTNNYALD	EIKEVAA			

Vəlid	Sequence	Prob	Masco	Masco	Masco	NII	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	IIC	Start	Stop	# Othe	Other Protei	Spectrum ID
7	1.0 (K)VNYAGVSTNINVALDEIK(E)	100%	47.7	50.5	27.8	2		935.88	1,869.74	2	-0.17	-91	1370		749.3	127	143	0		1047: Scan 8689 [
7	1.0 (KIVNYAGVSTNNYALDEIK(E)	100%	43.7	50.5	221	2		935.89	1,869.77	2	-0.14	-76	1410		475.1	127	143	0		1099: Scan 8900 [

Spot # 666

gi|108773054 (100%), 8,960.2 Da

photosystem I subunit VII (chloroplast) [Acutodesmus obliquus]

1 exclusive unique peptides, 1 exclusive unique spectra, 3 total spectra, 9/81 amino acids (11% coverage)

MSHIVKIYDT CIGCTQCVRA CPLDVLEMVP WNGCKANQMA SAPRTEDCVG CKRCETACPT DFLSIR<mark>VYLS SETTR</mark>SMGLS Y

Valid		Sequence	Frob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent [ntensity	TIC	Start	Stop	≢Othe	Other Protei	Spectrum ID
V	10	(R)VVLSSEITR(S)	100%	53.3	51.3	19.4	2		528.20	1,054.39	2	-0.14	-130	947		1682	67	75	Ũ		799: Scan 5651 [D
1	1.0	(R)VYLSSEITR(S)	100%	40.5	51.3	1.2	2		528 21	1,054.40	2	-0.13	-130	957		27.38	67	75	0		810: Scan 5712 [D
V	1.0	(R)VYLSSEITR(S)	97%	3日4	53.5	4.5	2		528.57	1,055.12	2	0.59	-390	938		1073	67	75	0		793: Scan 5602 [D



gi|108773244 (100%), 10,853.8 Da photosystem I subunit VII [Chara vulgaris] 1 exclusive unique peptides, 1 exclusive unique spectra, 2 total spectra, 13/97 amino acids (13% coverage)

MEKLKLSYFK TNLESLMSHK IKIYDTCIGC TQCVRACPTD VLEMIPWQGC KAKQIASAPR TEDCVGCKR<mark>C</mark> ESACPTDFLS VR</mark>VYLGSETT RSMGLAY

Valid	Sequence	Prob	Maaco	Meco	M800	NII	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent Inte	naty	TIC	Start	Stop	#Othe	Other Protei	Spectrum ID
10	(R)CESACPTDFLSYR(V)	100%	48.9	51.2	175	2	Carbamidomethyl	771.25	1,540.49	2	-0.17	-110	1440		972.3	70	82	0		1236: Scan 8639 [
1.0	(R)CESACPTDELSYR(V)	100%	35.8	51.2	199	2	Carbamadomethyl	771.25	1,540.49	2	-0.18	-120	1430		633.8	70	82	0		1224: Scan 8553 [

SODM4_MAIZE (100%), 25,239.0 Da

Superoxide dismutase [Mn] 3.4, mitochondrial OS=Zea mays GN=SODA.3 PE=2 SV=1 4 exclusive unique peptides, 6 exclusive unique spectra, 16 total spectra, 94/233 amino acids (40% coverage)

MALRTLASKN	ALSFALGGAA	RPSAASARGV	TTVALPDLSY	DFGALEPAIS
GEIMRLHHQK	HHATYVGNYN	KALEQLDAAV	AKGDASAVVQ	LQGAIKFNGG
GHVNHSIFWK	NLKPISEGGG	EPPHGKLGWA	IDEDFGSFEA	LVKRMNAEGA
ALQGSGWVWL	ALDKEPK kls	VETTANQDPL	VTKGASLVPL	LGIDVWEHAY
Y L Q Y K <mark>N V R P D</mark>	YLNNIWK VMN	WKYAGEVYEN	VLA	

SODM1_MAIZE (100%), 25,545.4 Da

Superoxide dismutase [Mn] 3.1, mitochondrial OS=Zea mays GN=SODA.4 PE=2 SV=1 1 exclusive unique peptides, 2 exclusive unique spectra, 9 total spectra, 64/235 amino acids (27% coverage)

MALRTLASKK	VLSFPFGGAG	RPLAAAASAR	GVTTVTLPDL	SYDFGALEPA
ISGEIMRLHH	QKHHATYVAN	YNKALEQLET	AVSKGDASAV	VQLQAAIK FN
GGGHVNHSIF	WKNLKPISEG	GGEPPHGK LG	WAIDEDFGSF	EALVKKMNAE
GAALQGSGWV	WLALDKEAKK	VSVETTANQD	PLVTKGASLV	PLLGIDVWEH
AYYLQYK <mark>NVR</mark>	PDYLNNIWK V	MNWK YAGEVY	ENVLA	

SODM4_MAIZE (100%), 25,239.0 Da

Superoxide dismutase [Mn] 3.4, mitochondrial OS=Zea mays GN=SODA.3 PE=2 SV=1 4 exclusive unique peptides, 6 exclusive unique spectra, 16 total spectra, 94/233 amino acids (40% coverage)

MALRTLASKN	ALSFALGGAA	RPSAASARGV	TTVALPDLSY	DFGALEPAIS
GEIMRLHHQK	HHATYVGNYN	KALEQLDAAV	AKGDASAVVQ	LQGAIKFNGG
GHVNHSIFWK	NLKPISEGGG	EPPHGKLGWA	IDEDFGSFEA	LVKRMNAEGA
ALQGSGWVWL	ALDKEPKKLS	VETTANQDPL	VTK GASLVPL	LGIDVWEHAY
Y L Q Y K <mark>N V R P D</mark>	YLNNIWK VMN	WK YAGEVYEN	VLA	

SODM1_MAIZE (100%), 25,545.4 Da

Superoxide dismutase [Mn] 3.1, mitochondrial OS=Zea mays GN=SODA.4 PE=2 SV=1 1 exclusive unique peptides, 2 exclusive unique spectra, 9 total spectra, 64/235 amino acids (27% coverage)

MALRTLASKK	VLSFPFGGAG	RPLAAAASAR	GVTTVTLPDL	SYDFGALEPA
ISGEIMRLHH	QKHHATYVAN	YNKALEQLET	AVSKGDASAV	VQLQAAIK <mark>FN</mark>
GGGHVNHSIF	WKNLKPISEG	GGEPPHGK LG	WAIDEDFGSF	EALVKKMNAE
GAALQGSGWV	WLALDKEAKK	VSVETTANQD	PLVTKGASLV	PLLGIDVWEH
A Y Y L Q Y K <mark>N V R</mark>	PDYLNNIWKV	M N W K Y A G E V Y	ENVLA	



SODM2_MAIZE (100%), 25,357.0 Da

Superoxide dismutase [Mn] 3.2, mitochondrial OS=Zea mays GN=SODA.1 PE=2 SV=1 1 exclusive unique peptides, 1 exclusive unique spectra, 1 total spectra, 14/232 amino acids (6% coverage)

T T V A L P D L S Y V K <mark>G D A S A V V Q</mark> D E D F G S F E A L A L S F A L G G A A H H A T Y V V N Y N N L K P I S E G G E DFGALEPVIS RPSAASARGV MALRTLASKN K A L E Q L D A V V P P H G K L G W A I GEIMRLHHQK GHFNHSIFWE LQGAIKFNGG V K R M N A E G A A G I D V W E H A Y Y L Q G S G W V W L A L Q Y K N V R P D Y TKGASLVPLL LDKEPKKLSV ETTANQDPLV LNNIWKVMNW KYAGEVYENV LA

Spot # 110

gi|1174391 (100%), 25,239.0 Da

RecName: Full=Superoxide dismutase [Mn] 3.4, mitochondrial; Flags: Precursor

5 exclusive unique peptides, 6 exclusive unique spectra, 6 total spectra, 53/233 amino acids (23% coverage)

MALRTLASKN	ALSFALGGAA	RPSAASARGV	TTVALPDLSY	DFGALEPAIS	GEIMRLHHQK
HHATYVGNYN	KALEQLDAAV	AKGDASAVVQ	LQGAIKFNGG	GHVNHSIFWK	NLKPISEGGG
EPPHGKLGWA	IDEDFGSFEA	LVKRMNAEGA	ALQGSGWVWL	ALDKEPK <mark>kls</mark>	VETTANQDPL
VTKGASLVPL	LGIDVWEHAY	Y L Q Y K <mark>N V R P D</mark>	YLNNIWK VMN	WKYAGEVYEN	VLA

Yalid	Sequence	Prob	Masco	Mexco	Maxo	NII	Modifications	Observed	Actual Mass	Charge	Della Da	Delta	Retent Intensity	ΠC	Start	Stop	#Othe	Other Protei	Spectrum ID
V	10 (K)ALEQLDAAVAK(G)	100%	74.0	51.5	20.0	2		564.82	1,127.62	2	-0.0012	-1.1	1030	1328	72	82	D		207: Sum of 2 sca
V	10 (K)GDASAYYQLQGAIK(F)	100%	95.9	51.3	51.3	2		678.88	1,355.74	2	-0.00060	-0.44	1180	174.7	B3	96	D		266 : Storn of 2 sca
V	1.0 (K)KLEVETTANODPLYTK(G)	100%	113.1	50.9	16.2	2		872.48	l,742.94	2	0.0014	0.80	995	197.8	168	183	D		191 : Sum of 2 sca
V	1.0 (K)KLSYETTANODPLYTK(G)	100%	60.8	50.9	0.0	2		591,99	1,742.94	3	-0.0011	-0.61	990	677.0	169	1B3	D	1	188 : Soun of 2 sca .
7	1.0 (K)LSYETTANODPLYTK(G)	100%	78.8	50.9	0.0	2		808.43	1,614.85	2	-0.00034	-0.21	1070	1190	169	1B3	0		221 : Sum of 2 sca
V	10 (K)NVRPDYLNNEWK(Y)	89%	41.3	51.1	0.2	2		511.27	1,530.79	3	-0.00056	-0.36	1280	119.9	206	217	D		300 : Sturn of 2 sca

Spot # 201

gi|242079005 (100%), 46,381.9 Da

hypothetical protein SORBIDRAFT_07g019320 [Sorghum bicolor]

4 exclusive unique peptides, 4 exclusive unique spectra, 16 total spectra, 148/426 amino acids (35% coverage)

MAALLASSRC	CCSRPSLPPL	PTRGRRSVAR	CALSGGEKRN	SFSWKECAVS
VALSVGLING	APTLGSPAYA	SPLEPVLPDV	SVLISGPPIK	DPGALLR <mark>YAL</mark>
PIDNKAIREV	QKPLEDITDS	LKVAGVRALD	SVERNIKQAS	RALNNGR <mark>SLI</mark>
LAGLAEPKRA	NGEELLNKLA	VGLEELQRIV	EDRNRDAVAP	KQKELLQYVG
TVEEDMVDGF	PYEIPEEYST	MPLLKGRATV	DMKVKIKDNP	NVEDCVFRIV
LDGYNAPVTA	GNFIDLVERK	FYDGMEIQRA	DGFVVQTGDP	EGPAEGFIDP
STGKIRTVPL	EIMVDGDKAP	VYGETLEELG	RYKAQTKLPF	NAFGTMAMAR
EEFDDNSASS	QIFWLLKESE	LTPSNANILD	GRYAVFGYVT	ENEDYLADVK
VGDVIESIQV	VSGLDNLVNP	SYKIVG		

Spot # 61

gi|3914607 (100%), 19,036.4 Da

RecName: Full=Ribulose bisphosphate carboxylase small chain, chloroplastic; Short=RuBisCO small subunit; Flags: Precu 3 exclusive unique peptides, 5 exclusive unique spectra, 15 total spectra, 30/168 amino acids (18% coverage)

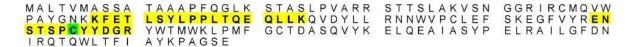


Fig. S2. Validation of identified proteins in leaves of salt-treated CW ecotype by Scaffold.



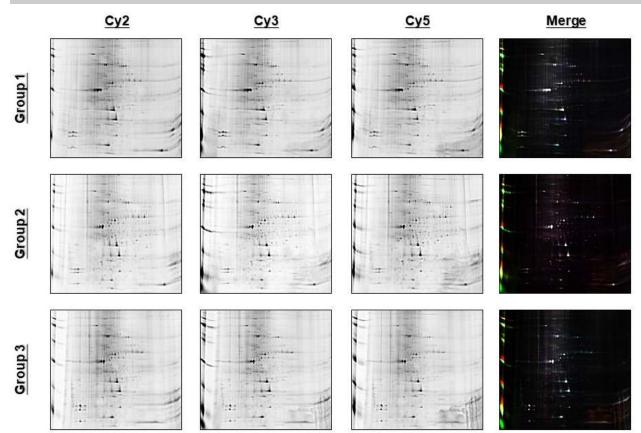


Fig. S3. 2D-DIGE images of leave proteins isolated from salt-treated SL population. The gel images correspond to three representative biological replicates.

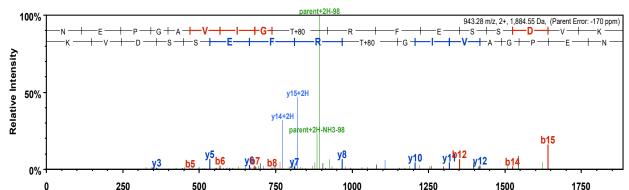


Α.

Unigene22380_SL (100%), 28,149.0 Da

211 981 hypothetical protein SORBIDRAFT_02g036260 [Sorghum bicolor] >gi|241926393|gb|EER99537.1| hypothetical protein SORBI_002G338000 [Sorghum bicolor] 1 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 17/257 amino acids (7% coverage)

GSERQKKPAG PKKATKISSD RPLWFPGAVA PDYLDGSLVG DYGFDPFGLG KPVEYLQFEL DSLDQNLAKN EPGAVIGTRF ESSDVKSTPL QPYSEVFGLQ RFRECELIHG RWAMLATLGA LSVEWLTGVT WQDAGKVELV DGSSYLGQPL PFSISTLIWI EVLVIGYIEF QRNAELDPEK RLYPGGSYFD PLGLAADPEK KERLQLAEIK HARLAMVAFL GFAVQAAATG KGPLNNWATH LSDPLHTTIF DTFGGSS



	200	;	500	750		1000	1200		1900		1/5
					m	z					
в	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y	
1	115.1		98.0		N	1,885.9	943.4	1,868.8	1,867.9	17	
2	244.1		227.1	226.1	E	1,771.8	886.4	1,754.8	1,753.8	16	
3	341.1		324.1	323.1	Р	1,642.8	821.9	1,625.8	1,624.8	15	
4	398.2		381.1	380.2	G	1,545.7	773.4	1,528.7	1,527.7	14	
5	469.2	3	452.2	451.2	A	1,488.7	744.9	1,471.7	1,470.7	13	
6	568.3	284.6	551.2	550.3	Y	1,417.7	709.3	1,400.6	1,399.7	12	
7	681.4	341.2	664.3	663.3	I	1,318.6	659.8	1,301.6	1,300.6	11	
8	738.4	369.7	721.4	720.4	G	1,205.5	603.3	1,188.5	1,187.5	10	
9	919.4	460.2	902.4	901.4	T+80	1,148.5	574.8	1,131.5	1,130.5	9	
10	1,075.5	538.3	1,058.5	1,057.5	R	967.5	484.2	950.5	949.5	8	
11	1,222.6	611.8	1,205.5	1,204.6	F	811.4	406.2	794.4	793.4	7	
12	1,351.6	676.3	1,334.6	1,333.6	E	664.3	332.7	647.3	646.3	6	
13	1,438.6	719.8	1,421.6	1,420.6	s	535.3		518.2	517.3	5	
14	1,525.7	763.3	1,508.6	1,507.7	s	448.2		431.2	430.2	4	
15	1,640.7	820.9	1,623.7	1,622.7	D	361.2	0.0	344.2	343.2	3	
16	1,739.8	870.4	1,722.7	1,721.8	Y	246.2		229.2		2	
17	1,885.9	943.4	1,868.8	1,867.9	K	147.1		130.1		1	
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	1 115.1 2 244.1 3 341.1 4 398.2 5 469.2 6 568.3 7 681.4 8 738.4 9 919.4 10 1,075.5 11 1,222.6 13 1,438.6 14 1,525.7 15 1,640.7 16 1,739.8	B B Ions B+2H 1 115.1 2 244.1 3 341.1 4 398.2 5 469.2 6 568.3 284.6 7 681.4 341.2 8 738.4 369.7 9 919.4 460.2 10 1,075.5 538.3 11 1,222.6 611.8 12 1,351.6 676.3 13 1,438.6 719.8 14 1,525.7 763.3 15 1,640.7 820.9 16 1,739.8 870.4	B B Ions B+2H B-NH3 1 115.1 98.0 2 244.1 227.1 3 341.1 324.1 4 398.2 381.1 5 469.2 452.2 6 568.3 284.6 551.2 7 681.4 341.2 664.3 8 738.4 369.7 721.4 9 919.4 460.2 902.4 10 1,075.5 538.3 1,058.5 11 1,222.6 611.8 1,205.5 12 1,351.6 676.3 1,334.6 13 1,438.6 719.8 1,421.6 14 1,525.7 763.3 1,508.6 15 1,640.7 820.9 1,623.7 16 1,739.8 870.4 1,722.7	B B Ions B+2H B-NH3 B-H2O 1 115.1 98.0 - 2 244.1 227.1 226.1 3 341.1 324.1 323.1 4 398.2 381.1 380.2 5 469.2 452.2 451.2 6 568.3 284.6 551.2 550.3 7 681.4 341.2 664.3 663.3 8 738.4 369.7 721.4 720.4 9 919.4 460.2 902.4 901.4 10 1,075.5 538.3 1,058.5 1,057.5 11 1,222.6 611.8 1,205.5 1,204.6 12 1,351.6 676.3 1,334.6 1,333.6 13 1,438.6 719.8 1,421.6 1,420.6 14 1,525.7 763.3 1,508.6 1,507.7 15 1,640.7 820.9 1,623.7 1,622.7 16 1	B B Ions B+2H B-NH3 B-H2O AA 1 115.1 98.0 N 2 244.1 227.1 226.1 E 3 341.1 324.1 323.1 P 4 398.2 381.1 380.2 G 5 469.2 452.2 451.2 A 6 568.3 284.6 551.2 550.3 Y 7 681.4 341.2 664.3 663.3 I 8 738.4 369.7 721.4 720.4 G 9 919.4 460.2 902.4 901.4 T+80 10 1,075.5 538.3 1,058.5 1,057.5 R 11 1,222.6 611.8 1,205.5 1,204.6 F 12 1,351.6 676.3 1,334.6 1,333.6 E 13 1,438.6 719.8 1,420.6 S 14 1,525.7 763.3 1,508.6	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	m/z B B Ions B+2H B-NH3 B-H2O AA Y Ions Y+2H 1 115.1 98.0 N 1,885.9 943.4 2 244.1 227.1 226.1 E 1,771.8 886.4 3 341.1 324.1 323.1 P 1,642.8 821.9 4 398.2 381.1 380.2 G 1,545.7 773.4 5 469.2 452.2 451.2 A 1,488.7 744.9 6 568.3 284.6 551.2 550.3 Y 1,417.7 709.3 7 681.4 341.2 664.3 663.3 I 1,318.6 659.8 8 738.4 369.7 721.4 720.4 G 1,205.5 603.3 9 919.4 460.2 902.4 901.4 T+80 1,148.5 574.8 10 1,075.5 538.3 1,058.5 1,057.5 R 967.5	m/zBBIonsB+2HB-NH3B-H2OAAYYY+2HY-NH31115.198.0N1,885.9943.41,868.82244.1227.1226.1E1,771.8886.41,754.83341.1324.1323.1P1,642.8821.91,625.84398.2381.1380.2G1,545.7773.41,528.75469.2452.2451.2A1,488.7744.91,471.76568.3284.6551.2550.3Y1,417.7709.31,400.67681.4341.2664.3663.3I1,318.6659.81,301.68738.4369.7721.4720.4G1,205.5603.31,188.59919.4460.2902.4901.4T+801,148.5574.81,131.5101,075.5538.31,058.51,057.5R967.5484.2950.5111,222.6611.81,205.51,204.6F811.4406.2794.4121,351.6676.31,334.61,333.6E664.3332.7647.3131,438.6719.81,421.61,420.6S535.3518.2141,525.7763.31,508.61,507.7S448.2431.2151,640.7820.91,623.71,622.7D361.2344.216<	m/z B B Ions B+2H B-NH3 B-H2O AA Y Ions Y+2H Y-NH3 Y-H2O 1 115.1 98.0 N 1,885.9 943.4 1,868.8 1,867.9 2 244.1 227.1 226.1 E 1,771.8 886.4 1,754.8 1,753.8 3 341.1 324.1 323.1 P 1,642.8 821.9 1,622.8 1,624.8 4 398.2 381.1 380.2 G 1,545.7 773.4 1,528.7 1,527.7 5 469.2 452.2 451.2 A 1,488.7 744.9 1,471.7 1,470.7 6 568.3 284.6 551.2 550.3 Y 1,417.7 709.3 1,400.6 1,399.7 7 681.4 341.2 664.3 663.3 I 1,318.6 659.8 1,301.6 1,300.6 8 738.4 369.7 721.4 720.4 G 1,205.5	m/z m/z B B lons B+2H B-NH3 B-H2O AA Y lons Y+2H Y-NH3 Y-H2O Y 1 115.1 98.0 N 1,885.9 943.4 1,868.8 1,867.9 17 2 244.1 227.1 226.1 E 1,771.8 886.4 1,754.8 1,753.8 16 3 341.1 324.1 323.1 P 1,642.8 821.9 1,625.8 1,624.8 15 4 398.2 381.1 380.2 G 1,545.7 773.4 1,528.7 1,527.7 14 5 668.3 284.6 551.2 550.3 Y 1,417.7 709.3 1,400.6 1,399.7 12 7 681.4 341.2 664.3 663.3 I 1,318.6 659.8 1,301.6 1,300.6 11 8 738.4 369.7 721.4 720.4 G 1,205.5 603.3 1,188.5 1,187.5

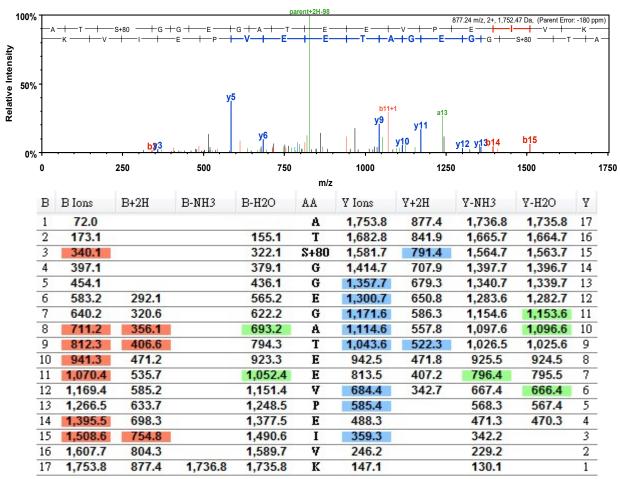
Unigene30507_SL (100%), 16,044.8 Da

150 614 TPA: thylakoid membrane phosphoprotein 14 kDa [Zea mays]

1 exclusive unique peptides, 1 exclusive unique spectra, 1 total spectra, 17/155 amino acids (11% coverage)

ACSSCSFPMA	TACRLAAPLG	LAPLPRVRAS	AGVVAVAAQC	GSKIPRGVAV	R <mark>a t <mark>s</mark> g g e g a t</mark>
<mark>ΕΕΥΡΕΙΥΚ</mark> ΑΑ	QDAWDKVEDK	YAVATIGVAA	IVALWTVVGA	IKAIDKLPLL	PGVLEIVGIG
Y T G W F T Y R N L	IFQPDREALI	GKIKSTYKEI	TGSSS		





B. Partial sequence alignment of thylakoid membrane phosphoprotein 14 kDa protein orthologs in other plant species. Protein sequences from different plant species include XP_015613093.1 (*Oryza sativa Japonica Group*); XP_021314085.1 (*Sorghum bicolor*); XP_021314075.1 (*Sorghum bicolor*); NP_001130557.1 (*Zea mays*); NP_566086.1 (*Arabidopsis thaliana*); XP_015645395.1 (*Oryza sativa Japonica Group*); XP_015645396.1 (*Oryza sativa Japonica Group*); NP_001150124.1 (*Zea mays*); Unigene30507_SL (*Imperata cylindrica*); XP_021308012.1 (*Sorghum bicolor*). Sequence alignment was performed using ClustalW2. The phosphopeptides (ATpSGGEGATEEVPEIVK) identified in leaves of SL population is underline. Conserved phosphorylation sites among different plant species are in gray box.

XP_015613093.1	SFCKRLARNVVAMAAGEA PAAPLAANAE I TEF I NALKQEWDR I EDKYAVTTLAVAA
XP_021314085.1	C KRLARNVVAMATGEP TAAPVADNEELTEFVNALKKEWDR I EDKYAVTTLAVAA
XP_021314075.1	CECKRLARNVVAMATGEP TAAPVADNEELTEFVNALKKEWDRIEDKYAVTTLAVAA
NP_001130557.1	SLYKRLARDVVAMAAGEP A - APQAANEELTEFVDALKKEWDR I EDKYAVTTLAVAA
NP_566086.1	AYCRKIVRNVVTRATTEVGEAPATTTEAETTELPEIVKTAQEAWEKVDDKYAIGSLAFAG
XP_015645395.1	ATGIKYVGLRASRGVAIRAAD-GTGSETEVPEVVKAAQDAWAKVEDKYAVTAIGVAA
XP_015645396.1	ATGIKYGLRASRGVAIRAAD-GTGSETEVPEVVKAAQDAWAKVEDKYAVTAIGVAA
NP_001150124.1	VRCARSSGSKIPRGVAVRATSGGEGATEEVPEIVKAAQDAWDKVEDKYAVATIGVAA
Unigene30507_SL	AAQCGSKIPRGVAVR <u>ATSGGEGATEEVPEIVK</u> AAQDAWDKVEDKYAVATIGVAA
XP_021308012.1	AQCGGSKIPRGVAVRATSGGEGATEDVPEIVKAAQDAWDKVEDKYAVATIGVAA
	. $$ $*$ $$ $$



Partial sequence alignment of chloroplast a/b binding protein CP29 orthologs in other plant species. Protein sequences from different plant species include XP_015646910.1 (*Oryza sativa Japonica Group*); EAZ40279.1 (*Oryza sativa Japonica Group*); NP_001105502.1 (*Zea mays*); NP_001136606.1 (*Zea mays*); Unigene22380_SL (*Imperata cylindrica*); XP_002463016.1 (*Sorghum bicolor*); OAP04488.1 (*Arabidopsis thaliana*); NP_187506.1 (*Arabidopsis thaliana*); AAK43851.1 (*Arabidopsis thaliana*); AAM12979.1 (*Arabidopsis thaliana*); pdb|5MDX|R (*Arabidopsis thaliana*); NP_195773.1 (*Arabidopsis thaliana*). Sequence alignment was performed using ClustalW2. The phosphopeptides (NEPGAVIGpTRFESSDVK) identified in leaves of SL population is underline. Conserved phosphorylation sites among different plant species are in gray box.

XP_015646910.1	WFPGAVAPDYLDGSLVGDYGFDPFGLGKPAEYLQFELDSLDQNLAKNNAGEIIGTRFETG
EAZ40279.1	WFPGAPAEYLQFELDSLDQNLAKNNAGEI IGTRFETG
NP_001105502.1	WFPGAVAPDYLDGSLVGDYGFDPFGLGKPVEYLQFELDSLDQNLAKNEAGGIIGTRFESS
NP_001136606.1	WFPGAVAPDYLDGSLVGDYGFDPFGLGKPVEYLQFELDSLDQNLAKNEAGGIIGTRFESS
Unigene22380_SL	WFPGAVAPDYLDGSLVGDYGFDPFGLGKPVEYLQFELDSLDQNLAK <u>NEPGAVIGTRFESS</u>
XP_002463016.1	WFPGAVAPDYLDGTLVGDYGFDPFGLGKPVEYLQFDLDSLDQNLAKNEPGVVIGTRFESS
OAP04488.1	WFPGAKSPEYLDGSLVGDYGFDPFGLGKPAEYLQFDLDSLDQNLAKNLYGEVIGTRTEAV
NP_187506.1	WFPGAKSPEYLDGSLVGDYGFDPFGLGKPAEYLQFDLDSLDQNLAKNLYGEVIGTRTEAV
AAK82524.1	WYPGAISPDWLDGSLVGDYGFDPFGLGKPAEYLQFDIDSLDQNLAKNLAGDVIGTRTEAA
AAK43851.1	WYPGAISPDWLDGSLVGDYGFDPFGLGKPAEYLQFDIDSLDQNLAKNLAGDVIGTRTEAA
AAM12979.1	WYPGAISPDWLDGSLVGDYGFDPFGLGKPAEYLQFDIDSLDQNLAKNLAGDVIGTRTEAA
pdb 5MDX R	WYPGAISPDWLDGSLVGDYGFDPFGLGKPAEYLQFDIDSLDQNLAKNLAGDVIGTRTEAA
NP_195773.1	WYPGAISPDWLDGSLVGDYGFDPFGLGKPAEYLQFDIDSLDQNLAKNLAGDVIGTRTEAA
	* * * * * * * * * * * * * * * * * * * *

XP 015646910.1 EVKSTPFOPYTEVFGLORFRECELIHGRWAMLATLGALSVEWLTGVTWODAGKVELVDGS EAZ40279.1 EVKSTPFQPYTEVFGLQRFRECELIHGRWAMLATLGALSVEWLTGVTWQDAGKVELVDGS NP 001105502.1 EVKSTPLOPYSEVFGLORFRECELIHGRWAMLATLGALSVEWLTGVTWODAGKVELVDGS NP 001136606.1 DVKSTPLQPYSEVFGLQRFRECELIHGRWAMLATLGALTVEWLTGVTWQDAGKVELVDGS Unigene22380 SL DVKSTPLQPYSEVFGLQRFRECELIHGRWAMLATLGALSVEWLTGVTWQDAGKVELVDGS XP 002463016.1 DVKSTPLOPYSEVFGLORFRECELIHGRWAMLATLGALSVEWLTGVTWODAGKVELVDGS OAP04488.1 DPKSTPFQPYSEVFGLQRFRECELIHGRWAMLATLGAITVEWLTGVTWQDAGKVELVDGS NP 187506.1 DPKSTPF0PYSEVFGL0RFRECELIHGRWAMLATLGAITVEWLTGVTWQDAGKVELVDGS AAK82524.1 DAKSTPFQPYSEVFGIQRFRECELIHGRWAMLATLGALSVEWLTGVTWQDAGKVELVDGS AAK43851.1 DAKSTPFQPYSEVFGIQRFRECELIHGRWAMLATLGALSVEWLTGVTWQDAGKVELVDGS AAM12979.1 DAKSTPFOPYSEVFGIORFRECELIHGRWAMLATLGALSVEWLTGVTWODAGKVELVDGS pdb15MDX1R DAKSTPFQPYSEVFGIQRFRECELIHGRWAMLATLGALSVEWLTGVTWQDAGKVELVDGS

Fig. S4. Identification of two phosphopeptides from data set of our previous study. The study identified phosphopeptides in leaves of CW ecotype and SL population (Wu *et al.*, 2015). **A**, MS/MS fragmentation pattern of the identified phosphopeptides of thylakoid membrane phosphoprotein 14 kDa protein (ATpSGGEGATEEVPEIVK) and a chloroplast a/b binding protein CP29 (NEPGAVIGpTRFESSDVK); **B**, sequence alignment show evolutionarily conserved phosphorylation sites among different plant species.



Spot # 111(755)

Valid		Sequence	Prob	Masco	Maxo	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	1.0	(K)SLAAALMSEAK(F)	100%	68.9	52.2	35.5	2		546.29	1,090.57	2	0.0012	1.1	890		2929	119	129	0		index=2073
V	1.0	(K)SLAAALMSEAK(F)	100%	61.2	52.0	24.5	2	Oxidation (+16)	554.29	1,106.56	2	0.00026	0.24	664		5083	119	129	0		index=2008
V	1.0	(K)SLAAALMSEAK(F)	100%	59.8	52.0	29.7	2	Oxidation (+16)	554.29	1,106.57	2	0.0015	1.3	663		4369	119	129	0		index=2007
V	1.0	(K)FDGADMSEVYMSK(A)	100%	77.3	51.6	51.4	2	Oxidation (+16),	724.30	1,446.59	2	-0.0059	-4.0	450		2607	130	142	0		index=1906
V	1.0	(K)FDGADMSEVYMSK(A)	100%	68.3	51.6	49.6	2	Oxidation (+16),	724.31	1,446.60	2	0.0010	0.72	454		3839	130	142	0		index=1910
V	1.0	(K)GTDFTNAVIDR(V)	100%	95.2	51.6	0.0	2		604.80	1,207.58	2	-0.00082	-0.68	696		6457	152	162	0		index=2026
V	1.0	(K)GTDFTNAVIDR(V)	100%	59.5	51.6	0.0	2		604.80	1,207.58	2	-0.0039	-3.2	692		5137	152	162	0		index=2025

gi|212721648 (100%), 23,654.3 Da

uncharacterized protein LOC100194054 [Zea mays]

3 exclusive unique peptides, 4 exclusive unique spectra, 7 total spectra, 35/225 amino acids (16% coverage)

MASSSCLASP	SGATLCRPRR	PRCRVACSAA	DAGGSTGPAW	AKGAGRLACG	VLAAWSVASA
				LDLRFCDYTN	
A A A L M S E A K F	D G A D <mark>M</mark> S E V V <mark>M</mark>	<mark> </mark>	K <mark>G T D F T N A V I</mark>	<mark>dr</mark> vnfekadl	TGAIFKNTVL
SGSTFDDAKM	DDVVFEDTII	GYIDLQKLCT	NTSISPDARL	ELGCR	

Spot # 835(753)

Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	0.2	(K)LAEQAER(Y)	90%	50.1	53.0	0.0	2		408.71	815.41	2	-0.0016	-1.9	158		2454	17	23	17	giB4888090	index=17636
V	0.2	(K)LAEQAER(Y)	90%	38.1	53.0	-4.3	2		408.71	815.41	2	-0.00076	-0.93	159		2222	17	23	17	giB4888090	index=17638
V	0.7	(R)YEEMVEFMEK(V)	99%	47.9	51.4	1.7	2	Oxidation (+16)	675.78	1,349.55	2	-0.0012	-0.92	711		9793	24	33	4	giB4888090	index=18712
V	0.7	(R)YEEMVEFMEK(V)	90%	33.7	51.6	12.5	2		667.79	1,333.56	2	-0.00042	-0.32	897		2434	24	33	4	giB4888090	index=19054
V	1.0	(K) TVDSEEL TVEER (N)	100%	90.5	51.4	17.1	2		703.84	1,405.66	2	-0.000042	-0.030	549		20020	37	48	0		index=18385
V	1.0	(K) TVDSEEL TVEER (N)	100%	86.8	51.4	16.3	2		703.84	1,405.66	2	-0.00032	-0.23	547		9894	37	48	0		index=18380
V	0.2	(R)NLLSVAYK(N)	88%	33.7	52.4	0.0	2		454.27	906.52	2	0.00026	0.28	725		10820	49	56	17	giB4888090	index=18738
1	0.2	(R)NLLSVAYKNVIGAR(R)	83%	30.4	51.3	7.9	2		506.63	1,516.87	3	-0.00035	-0.23	1030		4468	49	62	17	•	index=19260
V	0.5	(R)HISSIEQKEEGR(G)	100%	95.9	51.4	0.0	2		694.87	1,387.73	2	-0.00092	-0.66	376		31190	68	79	2	~	
V		(R)HISSIEQKEEGR(G)	100%	93.4	51.4	0.0	2		694.87	1,387.73	2	-0.0010	-0.74	374		15540	68	79	2	gil19470124	
V		(R)HSSIEQKEEGR(G)	96%	37.3	51.4	0.0	2		463.58	1,387.73	3	-0.00028	-0.20	.380		260200	68	79	2	gil19470124	
V		(R)HISSIEQKEEGR(G)	91%	33.6	51.4	0.0	2		463.58	1,387.73	3	-0.00055	-0.39	378		172400	68	79	2	gil19470124	index=18029
V	1.0	(K)ICDGILK(L)	90%	40.0	53.0	3.4	2	Carbamidomethyl	409.73	817.44	2	-0.00039	-0.47	492		7298	102	108	0		index=18267
V	1.0	(K)LLESHLVPSSTAPESK(V)	100%	68.2	50.7	26.4	2		847.95	1,693.89	2	0.0021	1.2	586		38490	109	124	0		index=18463
V		(K)LLESHLVPSSTAPESK(V)	100%	54.0	50.7	27.4	2		847.95	1,693.89	2	0.0029	1.7	588		54820	109	124	0		index=18465
V		(K)LLESHLVPSSTAPESK(V)	90%	32.5	50.7	16.4	2		565.64	1,693.89	3	-0.00020	-0.12	583		48180	109	124	0		index=18456
V		(R)KDAAENTMVAYK(A)	100%	106.9	51.3	79.9	2	Oxidation (+16)	678.83	1,355.64	2	0.000063	0.046	239		19160	148	159	0		index=17745
V		(R)KDAAENTMVAYK(A)	100%	101.2	51.3	71.5	2		670.83	1,339.64	2	-0.00062	-0.46	385		32470	148	159	0		index=18045
V		(R)KDAAENTMVAYK(A)	100%	83.2	51.3	58.5	2		670.83	1,339.64	2	-0.00050	-0.37	387		28080	148	159	0		index=18050
V		(R)KDAAENTMVAYK(A)	100%	71.9	51.3	48.8	2	Oxidation (+16)	678.83	1,355.64	2	-0.00042	-0.31	240		20870	148	159	0		index=17748
V		(R)KDAAENTMVAYK(A)	99%	43.0	51.3	23.6	2	Oxidation (+16)	452.89	1,355.64	3	0.00029	0.21	237		14490	148	159	0		index=17742
V		(R)KDAAENTMVAYK(A)	95%	36.6	51.3	14.1	2		447.56	1,339.64	3	-0.00095	-0.71	385		66550	148	159	0		index=18044
V		(K)DAAENTMVAYK(A)	100%	76.1	51.5	49.3	2	0.11.6 (10)	606.78	1,211.55	2	0.00038	0.31	513		12570	149	159	0		index=18310
V	1.0	(K)DAAENTMVAYK(A)	100%	69.2	51.5	47.7	2	Oxidation (+16)	614.78	1,227.54	2	-0.00074	-0.60	336		8804	149	159	0		index=17943
V	1.0	(K)DAAENTMVAYK(A)	100%	67.2	51.5	41.1	2	0.116 640	606.78	1,211.55	2	0.00052	0.43	515		9675	149	159	0		index=18315
1		(K)DAAENTMVAYK(A)	100%	59.7	51.5 50.6	35.3	2	Oxidation (+16)	614.78	1,227.54	2	-0.00054	-0.068	334		9458 17480	149 160	159	5	10 (000000	index=17939
7		(K)AAQDIALAELAPTHPIR(L)	100%	99.8 80.8	50.6		2		893.99	1,785.97	2	-0.00012		888 886				176	5	gil24208202	index=19037
1		(K)AAQDIALAELAPTHPIR(L)	100%	80.8	51.9	0.0	4	Oxidation (+16)	893.99 603.33	1,785.97	2	0.000078	0.044	860		9341 5772	160 222	231) 17	gil24208202 gil84888090	index=19034 index=19416
V	0.2	(K)DSTLIMQLLR(D)	100%	72.2	51.9	0.0	2	Oxidation (+10)	595.33	1,204.05	2	0.00000	0.0025	1180		9896	222	231	17	Q	
	0.2	(K)DSTLIMQLLR(D)	100%	55.5	51.8	0.0	2	Oxidation (+16)	603.33	1,188.05	2	-0.0011	-0.94	1290		3257	222	231	17	Q	index=1948/
7		(K)DSTLIMQLLR(D)	100%	48.7	51.9	0.0	2	(+10) tituatsuaxu	595.33	1,204.05	2	-0.0011	-0.94	1290		7500	222	231	17	gib4888090	
V	0.2	(K)DSTLIMQLLR(D)	100%	90./	J1.0	0.0	4		292.33	1,100.00	2	-0.00022	-0.19	1290		1000	444	201	17	g104000090	umex=19400

gi|242073380 (100%), 29,649.7 Da

hypothetical protein SORBIDRAFT_06g019100 [Sorghum bicolor]

5 exclusive unique peptides, 10 exclusive unique spectra, 32 total spectra, 117/261 amino acids (45% coverage)

MASAELSREE	N	AERYEEMVEF	MEKVAK <mark>TVDS</mark>	EELTVEERNL	L S V A Y K N V I G
ARRASWRIIS	<mark>SIEQKEEGR</mark> G	NEDRVTLIKD	<u>Y R G K I E T E L T</u>	K I <mark>C</mark> D G I L K L L	<mark>E S H L V P S S T A</mark>
PESK VFYLKM	KGDYYRYLAE	F K T G A E R <mark>K D A</mark>	AENT <mark>M</mark> VAYKA	A Q D I A L <mark>A</mark> E L A	<mark>pthpir</mark> lgla
LNFSVFYYEI	LNSPDRACSL	AKQAFDEAIS	ELDTLSEESY	K <mark>D S T L I <mark>M</mark> Q L L</mark>	<mark>R</mark> DNLTLWTSD
ISEDPAEEIR	EAPKRDSSEG	Q			

S20



Spot # 284(74)

Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	1.0	(K)GDPTYLVYEQDK(T)	100%	78.9	51.6	0.0	2		682.34	1,362.67	2	0.00088	0.64	671		2563	99	110	0		index=10241
V	1.0	(K)GDPTYLVYEQDK(T)	100%	64.3	51.6	0.0	2		682.34	1,362.67	2	-0.00012	-0.089	672		4286	99	110	0		index=10242
V	1.0	(K)FICPCHGSQYNNQGK(V)	100%	55.9	52.0	0.0	2	Carbamidomethyl	905.39	1,808.77	2	-0.0020	-1.1	376		4527	137	151	Û		index=10012
V	1.0	(R)TGEDPWWK(-)	87%	33.5	52.3	4.1	2		509.73	1,017.45	2	-0.0013	-1.2	753		3969	185	192	0		index=10281
1	1.0	(R)TGEDPWWKA(-)	100%	65.5	51.9	35.7	2		545.25	1,088.49	2	-0.00034	-0.31	809		13690	185	193	0		index=10294

gi|194702912 (100%), 20,753.4 Da

unknown [Zea mays]

4 exclusive unique peptides, 4 exclusive unique spectra, 5 total spectra, 36/193 amino acids (19% coverage)

MGRERAQRSI VCQAASSISA DRVPDMEKRK LMNLLLLGAI SLPTVGMVVP YGAFFVPAGS GNAGGGTYAK DKLGNDITVE AWLNTHGPND RTLAQGLK<mark>GD PTYLVVEQDK</mark> TLATYGINAV CTHLGCVVPW NGAENK<mark>FICP CHGSQYNNQG K</mark>VVRGPAPLS LALVHADVDD GKVLFVPWVE TDFR**TGEDPW WKA**

Spot # 707(173)

Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei 🖇	Spectrum ID
V	0.5	(K)IYDTCIGCTQCVR(A)	100%	89.6	51.1	62.5	2	Carbamidomethyl	823.36	1,644.71	2	0.00078	0.48	604		7517	23	35	160	giB4501452, ir	udex=17328
V	1.0	(R)VYLSSETTR(S)	100%	46.9	51.3	10.1	2		528.27	1,054.53	2	-0.00032	-0.31	361		8928	67	75	0	ir	ndex=17257
1	1.0	(R)VYLSSETTR(S)	98%	38.8	51.3	9.0	2		528.27	1,054.53	2	0.00066	0.62	359		5058	67	75	0	ÿ	ndex=17256

gi|108773054 (100%), 8,960.2 Da

photosystem I subunit VII (chloroplast) [Acutodesmus obliquus]

1 exclusive unique peptides, 1 exclusive unique spectra, 3 total spectra, 22/81 amino acids (27% coverage)

MSHIVK<mark>IYDT</mark> CIGCTQCVR</mark>A CPLDVLEMVP WNGCKANQMA SAPRTEDCVG CKRCETACPT DFLSIR<mark>VYLS</mark> SETTR<mark>SMGLS</mark> Y

Spot # 214

Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	0.8	(K)LNLGYGAYR(T)	90%	43.1	52.1	0.0	2		481.79	961.56	2	0.026	27	1450		842.2	82	90	1	gil357137439	index=288
V	1.0	(R)TEELQPYVLNVVK(K)	100%	99.2	50.1	0.0	2		766.43	1,530.84	2	0.014	9.1	1840		3055	94	106	0		index=348
V	1.0	(K)ATAELLLGADNPVIK(Q)	100%	68.2	49.9	36.0	2		762.95	1,523.88	2	0.023	15	1860		1447	133	147	0		index=352
V	0.8	(K)IADVIQEK(K)	99%	57.8	51.9	0.0	2		458.27	914.53	2	0.027	30	1040		1524	253	260	1	gil357137439	index=206
V	1.0	(R)ISLAGLSLAK(C)	100%	62.7	51,4	22.8	2		486.82	971.63	2	0.029	29	1780		688.1	433	442	0		index=337

gi|514719430 (100%), 50,192.7 Da

PREDICTED: aspartate aminotransferase, chloroplastic [Setaria italica]

3 exclusive unique peptides, 3 exclusive unique spectra, 5 total spectra, 55/458 amino acids (12% coverage)

MASTAAFAVS	SPAASAVAAR	S	GRIGCRVGIT	<u>R K N F G R</u> V M M A	LAVDVSRFEG
VPMAPPDPIL	G V <u>S E A F K A D K</u>	S D L K <mark>L N L G V G</mark>	AYRTEELQPY	VLNVVK KAEN	LMLEKGEYKE
YLPIEGLAAF	N K <mark>A T A E L L L G</mark>	A D N P V I K Q G L	VATLQSLSGT	GSLRLAAAFI	QRYFPEAKVL
ISSPTWGNHK	NIFNDARVPW	SEYRYYDPKT	VGLDFEGMIA	DIEAAPEGSF	VLLHGCAHNP
TGIDPTPEQW	EK <mark>IADVIQEK</mark>	КНМРЕЕDVAY	QGFASGSLDE	DAFSVRLFVK	RGMEVFVAQS
YSKNLGLYSE	RIGAINVVCS	A	QLKRLARPMY	SNPPIHGARI	VANVVGDPTM
FGEWKQEMEQ	MAGRIKNVRQ	<u>K L</u> Y D S L S V K D	KSGKDWSFIL	RQIGMFSYTG	LNKAQSDNMT
D K W H V Y M T K D	G R <mark>I S L A G L S L</mark>	<mark>ak</mark> cdyladai	IDSFHNVN		



Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent Intensit	y TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	0.5	(K)IYDTCIGCTQCYR(A)	100%	89.4	50.0	66.5	2	Carbamidomethyl	823.37	1,644.73	2	0.023	14	1320	9739	23	35	176	giB4501452,:	index=1102
V	0.5	(K)IYDTCIGCTQCVR(A)	100%	48.3	50.0	24.7	2	Carbamidomethyl	549.25	1,644.73	3	0.027	17	1330	1139	23	35	176	gil34501452,:	index=1104
V	1.0	(R)VYLSSETTR(S)	100%	76.2	50.5	38.3	2		528.29	1,054.56	2	0.028	27	969	2092	67	75	0		index=1074

gi|108773054 (100%), 8,960.2 Da

photosystem I subunit VII (chloroplast) [Acutodesmus obliquus]

1 exclusive unique peptides, 1 exclusive unique spectra, 3 total spectra, 22/81 amino acids (27% coverage)

MSHIVK<mark>IYDT</mark> CIGCTQCVR</mark>A CPLDVLEMVP WNGCKANQMA SAPRTEDCVG CKRCETACPT DFLSIR<mark>VYLS</mark> SETTR<mark>SMGLS</mark> Y

Spot # 452

Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	#0the	Other Protei Spectrum ID
V	1.0	(R)ADEDAAAEPAEGEGVVATKPK	100%	46.5	28.7	37.4	2		685.67	2,054.00	3	0.020	9.8	1090		13730	78	98	0	index=2226
V	1.0	(K)ADKPPPIGPK(R)	90%	28.4	30.4	12.5	2		510.31	1,018.61	2	0.024	23	837		1140	<u>99</u>	108	0	index=2202

CL6460.Contig1_All (100%), 17,924.2 Da

26 529 PREDICTED: photosystem I reaction center subunit IV, chloroplastic-like [Setaria italica]

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 31/168 amino acids (18% coverage)

ARTPHPLTLS	S P S A R A R <u>P T Q</u>	HPRQGEFTPM	ASTNMASATS	<u>R F M L A A G V </u> P T	AGSGSGISGR
VSFAPAPNRL	G R R L V V R <mark>A D E</mark>	DAAAEPAEGE	G V V A T K P K A D	<mark>К Р Р Р І G Р К </mark> R G	AKVKILRRES
YWYNGIGNVV	TVDQDPNTRY	PVVVRFSKVN	YAGVSTNNYA	LDEIKEVK	

Spot # 415

Valid		Sequence	Prob	Masco	Masco	Masco	NTT	Modifications	Observed	Actual Mass	Charge	Delta Da	Delta	Retent	Intensity	TIC	Start	Stop	# Othe	Other Protei	Spectrum ID
V	1.0	(R)TSTGMYVANR(A)	100%	60.2	51.7	36.3	2	Oxidation (+16)	558.27	1,114.53	2	0.023	20	828		1511	44	53	0		index=2930
1	1.0	(R)TSTGMYVANR(A)	100%	48.8	51.6	31.9	2		550.27	1,098.53	2	0.022	20	955		1611	44	53	0		index=2940
1	1.0	(R)SGSAADTQVISDYVR(Y)	100%	111.4	51.0	34.6	2		784.89	1,567.76	2	0.013	8.3	1570		5409	70	84	0		index=3009
1	1.0	(K)VAANLIR(L)	90%	35.6	50.9	1.3	2		378.75	755.49	2	0.023	31	1000		616.7	102	108	0		index=2950
1	1.0	(K)VVSLAMAR(D)	99%	43.4	52.9	14.8	2		423.76	845.51	2	0.026	31	1260		1085	183	190	0		index=2986
1	1.0	(R)TVTINADGVK(R)	99%	37.8	52.1	5.8	2		509.29	1,016.56	2	0.010	10	1120		1943	200	209	0		index=2967

gi|242079721 (100%), 26,207.5 Da

hypothetical protein SORBIDRAFT_07g025030 [Sorghum bicolor]

5 exclusive unique peptides, 6 exclusive unique spectra, 6 total spectra, 50/245 amino acids (20% coverage)

MDASHTGSSS AAGEASTTGE HRMGTTIVGV CYDGGVILGA DSR<mark>TSTGMYV</mark> ANR</mark>ASDKITQ LTDNVYVCR<mark>S GSAADTQVIS DYVR</mark>YFLHQH TIQLGQPATV K<mark>VAANLIR</mark>LL AYQNKNMLQA GMIVGGWDKY EGGQIFSVPL GGTILKQPFA IGGSGSSYLY ALLDHEWKEG MSQEEAEKFV VK<mark>VVSLAMAR</mark> DGASGGVVR<mark>T VTINADGVK</mark>R NFYPGDKLPL WHDELEPHHS LLDILAAGNP DPMVQ

Spot # 56

gi|164698713 (100%), 19,198.3 Da

chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Miscanthus x giganteus] 2 exclusive unique peptides, 2 exclusive unique spectra, 7 total spectra, 20/169 amino acids (12% coverage)

ΜΑΡΤΥΜΑSSΑ	TAVAPFQWLK	STASLPVARR	STTSLAKVSN	GGRIRCMQ <u>VW</u>
PAYGNKKFET	LSYLPPLTEE	QLLKQVDYLL	RNNWVPCLEF	SKEGF <u>VYREN</u>
S T S P C Y Y D G R	YWTMWKLPMF	GCTDASQVYK	EPQEAIASYP	D A Y V R <mark>I L G F D</mark>
NIRQTQCVSF	IAYKPPGSD			



gi|701216950 (100%), 20,781.5 Da

superoxide dismutase [Saccharum spontaneum]

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 25/207 amino acids (12% coverage)

MAAQSFLLAA TATATTAALF AAPYSSARPF HSAHFVAGPG GAAAAARVLV VADASKKAVA VLKGTSEVEG VVTLTQD**EDG PTTVNVR**ITG LTPGLHGFHL HEFGDTTNGC ISTGPHLNPN NLTHGAPEDE VRHAGDLGNI VANAEGVAEA TIVDTQIPLS GPNSVVGRAF VVHELEDDLG K<mark>GGHELSLST GNAGGR</mark>LACG VVGLTPL

Spot # 612

gi|162462282 (100%), 38,605.0 Da

fructose-bisphosphate aldolase, cytoplasmic isozyme [Zea mays] 2 exclusive unique peptides, 2 exclusive unique spectra, 23 total spectra, 123/355 amino acids (35% coverage)

Μ S A Y C G K <mark>Y K D</mark>	ELIKNAAYIG	TPGKGILAAD	ESTGTIGKRL	SSINVENVEE
N R R A L R E L L F	CCPGALQYIS	GVILFEETLY	Q Κ Τ Κ <mark>D G K P F V</mark>	DVLKEGGVLP
<mark>GΙΚVDΚ</mark> GΤΙΕ	VVGTDKETTT	QGHDDLGKRC	AKYYEAGARF	AKWRAVLKIG
PNEPSQLAID	LNAQGLARYA	IICQENGLVP	IVEPEILVDG	<u>phdidrcay</u> v
ТЕТVLААСҮК	ALNEHHVLLE	GTLLKPNMVT	P G S D S K <mark>K V T P</mark>	EVIAEYTVR ^T
LQRTVPAAVP	<u>AVLFLSG</u> GQS	EEEATRN <u>LNA</u>	MNKLSTKKPW	<u>SLSFSFGR<mark>AL</mark></u>
Q A S T L K A W A G	KVENLEKARA	A F L A R C K <mark>A N S</mark>	EATLGTYKGD	A A A D T E S L H V
<mark>κ</mark> ργκγ				

Fig. S5. Validation of identified proteins in leaves of salt-treated SL population by Scaffold.

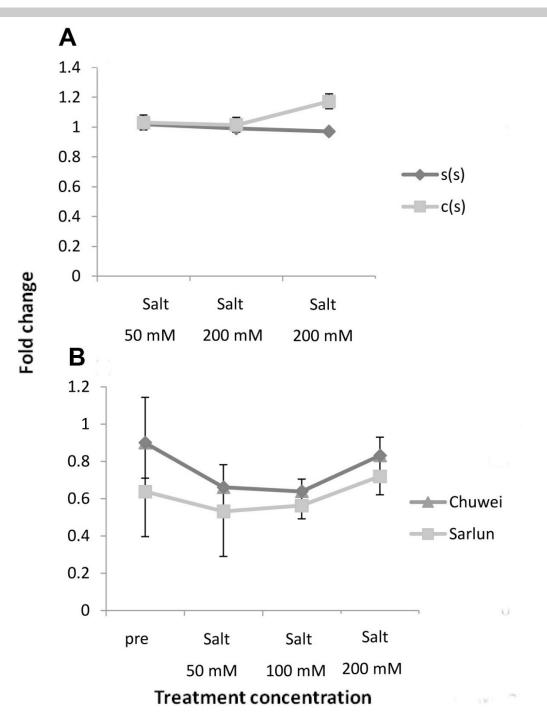


Fig. S6. Chlorophyll fluorescence yield of leaves from salt-treated Chuwei ecotype and Sarlun population. (**A**) and (**B**) shows results of the first and second water culture repeat, respectively; X axis indicates salt treatment by 50 mM, 100 mM, and 200 mM NaCl. Y axis indicates fold ratio against control Kimura's solution only. Pre, the day before treatment. C or Chuwei, samples from Chuwei ecotype; S or Sarlun, samples from Sarlun population. The treatment concentrations were changed every three days, and the last concentration was prolonged for one week. Data are mean \pm S.D, n =10.